



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 101491

**TO: Sheela Huff
Location: CM1/8B07&8E12
Art Unit : 1642
Friday, August 29, 2003**

Case Serial Number: 09/970969

**From : Susan Hanley
Location: Biotech-Chem Library
CM1 6B05
Phone: 305-4053**

susan.hanley@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

101491

From: Huff, Sheela
Sent: Friday, August 22, 2003 5:52 AM
To: STIC-Biotech/ChemLib
Subject: RE: search request for 09/970969

RECEIVED

AUG 22 2003

Not sure what you mean by only 3 sequences. The RSL (which has been marked "entered") in the file says that there are 6 sequences. The paper copy supplied by applicant also says that there are 6 sequences.

(STIC) DIVISION

Sheela

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Wednesday, August 20, 2003 6:30 AM
To: Huff, Sheela
Subject: RE: search request for 09/970969

-----Original Message-----

From: Huff, Sheela
Sent: Tuesday, August 19, 2003 6:12 AM
To: STIC-Biotech/ChemLib
Subject: search request for 09/970969

THERE ARE ONLY 3 SEQ FOR THIS NUMBER. MAUDE
Please search and interference search SEQ ID No. 1-6 of the above application.

Thanks--

*Sheela Huff
Art Unit 1642
CMI-8307
mailbox 8E12
305-7866*

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:43:40 ; Search time 216.333 Seconds
(without alignments)
12241.057 Million cell updates/sec

Title: US-09-970-969-3

Perfect score: 981

Sequence: 1 atggcaggtgctgtggcca.....tgctctccggagaagatgac 981

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
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21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	981	100.0	981	22	AAC91369 Modified human ann
2	977.8	99.7	981	22	AAC91368 Modified human ann
3	976.2	99.5	981	22	AAC91370 Modified human ann
4	958.6	97.7	1803	21	AAAL1241 Annexin V/urokinas
5	958	97.7	1466	10	AAAN91353 vascular anti-coag
6	956.8	97.5	1567	9	AAAN81113 Plasmid contg. pla
7	956.8	97.5	1578	25	ABX63162 Human cDNA #162 di
8	956.8	97.5	1605	10	AAAN91821 Endonexin II compl

9	956.4	97.5	1575	10	AAAN90112 Anticoagulant PP4
10	955.2	97.4	1454	9	AAAN82107 PAP-I cDNA from hu
11	955.2	97.4	1460	12	AAQ12679 PAP-I. Homo sapie
12	954.6	97.3	1466	9	AAAN80801 Sequence encoding
13	953.6	97.2	963	9	AAAN80873 Sequence encoding
14	952	97.0	1574	10	AAAN90599 Human lipocortin-V
15	943.8	96.2	1637	21	AAAF18269 Lung cancer associ
16	882	89.9	1024	25	AB283344 Toxicologically re
17	749.4	76.4	1480	24	ABF199289 Mouse ischaemic co
18	727	74.1	1417	24	ABK63599 Rat sequence diffe
19	518.4	52.8	960	25	AB221925 Human annexin V pr
20	517.8	52.8	2016	25	AB221926 Modified annexin p
21	495.8	50.5	847	25	ABX05088 Human novel polynu
22	412.2	42.0	438	12	AAQ12681 PAP-I-protein C fu
23	412.2	42.0	1529	12	AAQ12680 PAP-I-protein C fu
24	365	37.2	422	25	ABX47939 Bovine EST associa
25	356.2	36.3	409	25	ABX36749 Bovine EST associa
26	351	35.8	1326	10	AAAN90772 Coding strand of c
27	350.4	35.7	410	25	ABX42696 Bovine EST associa
28	349.4	35.6	1982	24	ABX76372 cDNA encoding huma
29	349.4	35.6	2155	21	AAH72826 Human cancer assoc
30	349.4	35.6	2181	22	AAH72826 Human cervical can
31	349.4	35.6	2213	20	AA277514 Human ovarian tumo
32	349.4	35.6	2300	25	ABX63220 Human cDNA #220 di
33	348.2	35.5	2360	11	AAQ02888 Human placenta-der
34	348.2	35.5	2468	23	ABX93800 DNA encoding novel
35	348.2	35.5	2468	24	ABX84730 Human cDNA diffe
36	348.2	35.5	2468	24	ABN97346 Gene #3844 used to
37	346.6	35.3	2016	11	AAQ02887 cDNA of human plac
38	346.6	35.3	2056	25	ABX72249 Human NOVX polynuc
39	319.8	32.6	529	24	ABO59306 Human colon cancer
40	315.2	32.1	686	24	ABT09335 Phase-1 Rat CT gen
41	311	31.7	401	21	AAQ65957 Human lung cancer-
42	311	31.7	401	24	ABQ92362 Human lung cancer
43	311	31.7	401	24	ABL49176 Human lung tumour
44	310.8	31.7	2305	14	AAQ39149 Annexin XI gene in
45	307.6	31.4	2311	14	AAQ39150 Annexin XI gene in

ALIGNMENTS

RESULT 1
AAC91369
ID AAC91369 standard; DNA; 981 BP.
XX AAC91369;
AC AAC91369;
XX
XX 16-MAR-2001 (first entry)
DT Modified human annexin nucleotide sequence, SEQ ID NO: 2.
DE Human; annexin; chelation site; nuclear imaging; apoptosis;
XX Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplant rejection; ds.
XX Homo sapiens.
OS
PN WO200073332-A1.
XX
XX 07-DEC-2000.
XX
XX 25-MAY-2000; 2000WO-US14324.
XX
XX 01-JUN-1999; 99US-0324096.
XX
XX (UNIW) UNIV WASHINGTON.
XX Tait JF, Brown DS;
XX
XX WPI; 2001-080465/09.
DR P-PSDB; AAB50864.
XX
XX Novel modified annexin useful for imaging vascular thrombi and

PT apoptosis, has N-terminal chelation site comprising amino acid
 PT extension which comprises a glycine and a cysteine residue -
 PS Claim 26; Page 31-33; 39pp; English.
 XX The present sequence encodes a modified annexin having an N-terminal
 CC chelation site, which comprises an amino acid extension including a
 CC glycine and a cysteine residue. The modified annexin is useful for
 CC imaging vascular thrombi or apoptosis which is associated with response
 CC to a chemotherapeutic agent or with rejection as a result of
 CC transplantation. The modified annexin can effectively chelate a
 CC radionuclide and retain annexin bioactivity. It can be readily prepared
 CC in high radiochemical yield and with high radiochemical purity. In
 CC contrast to conventional conjugation chemistries that provide a
 CC distribution of conjugation products, the modified annexin has a single
 CC chelation site remote from the site of biological activity.
 XX Sequence 981 BP; 286 A; 187 C; 251 G; 257 T; 0 other;
 SQ

Query Match 100.0%; Score 981; DB 22; Length 981;
 Best Local Similarity 100.0%; Pred. No. 4.5e-275;
 Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAGGTGGCTGTGGCCATATGACACAGGTCTTCAGAGGCACCTGTGACTTCCT 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 1 ATGGCAGGTGGCTGTGGCCATATGACACAGGTCTTCAGAGGCACCTGTGACTTCCT 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 GGATTGTGATGCGGGCTGATCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 GGATTGTGATGCGGGCTGATCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 121 GATGAGGAGAGATCCTGACTCTGTGTGACATCCGGAAGTAACTGTCAGCGCCAGGAAATC 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 121 GATGAGGAGAGATCCTGACTCTGTGTGACATCCGGAAGTAACTGTCAGCGCCAGGAAATC 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 181 TCTGAGCTTTTAAAGACTCTGTTTGGCAGGGATCTCTGGATGACCTGAAATCAGAACTA 240
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 181 TCTGAGCTTTTAAAGACTCTGTTTGGCAGGGATCTCTGGATGACCTGAAATCAGAACTA 240
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 241 ACTGGAATAATTTGAAAAATTAATTTGCTGTGATGAACCCCTCTCGGCTTTATGATGCT 300
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 241 ACTGGAATAATTTGAAAAATTAATTTGCTGTGATGAACCCCTCTCGGCTTTATGATGCT 300
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 301 TATGAACCTGAACATGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 301 TATGAACCTGAACATGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 361 ATTGCTTCAAGGACACCTGGAACACTGAGAGCCATCAACCAAGTTTATGAACAAATAT 420
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 361 ATTGCTTCAAGGACACCTGGAACACTGAGAGCCATCAACCAAGTTTATGAACAAATAT 420
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 421 GGCTCAAGCCTGGAAGATGACCTGTGGGGGACACTTCAGGGTACTACAGCGGATGTTG 480
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 421 GGCTCAAGCCTGGAAGATGACCTGTGGGGGACACTTCAGGGTACTACAGCGGATGTTG 480
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 481 GTGGTTCTCTTCAGGCTTAACAGAGACCCCTGATGCTGAATTTATGAAGCTCAAGTTCAA 540
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 481 GTGGTTCTCTTCAGGCTTAACAGAGACCCCTGATGCTGAATTTATGAAGCTCAAGTTCAA 540
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGAGAGCTTAATTTGGGGACAGATGAAGAAAG 600
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGAGAGCTTAATTTGGGGACAGATGAAGAAAG 600
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 601 TTTATCACCCTTTTGGAAACAGAGTGTGTCTCATTTTGAAGAAAGTGTGTTGACAAAGTAC 660
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 601 TTTATCACCCTTTTGGAAACAGAGTGTGTCTCATTTTGAAGAAAGTGTGTTGACAAAGTAC 660
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 661 ATGACTATATCAGGATTTCAAATTTGAGGAAACCAATTGACCGGAGACTTCTGGCAATTTA 720
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 661 ATGACTATATCAGGATTTCAAATTTGAGGAAACCAATTGACCGGAGACTTCTGGCAATTTA 720
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 721 GAGCAACTACTCTGCTGTGTGAAATCTATTTCGAAGTATACCTGCTACCTTCACAG 780
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 721 GAGCAACTACTCTGCTGTGTGAAATCTATTTCGAAGTATACCTGCTACCTTCAGAG 780
 QY 781 ACCCTCTATTATGCTATGAAGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 781 ACCCTCTATTATGCTATGAAGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
 QY 841 GTTTCAGAGTGAGATGATCTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGGC 900
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 841 GTTTCAGAGTGAGATGATCTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGGC 900
 QY 901 ACCTCTCTTTATCCATGATTAAAGGAGATACCTCTGGGACATATAAGAAAGCTCTCTG 960
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 901 ACCTCTCTTTATCCATGATTAAAGGAGATACCTCTGGGACATATAAGAAAGCTCTCTG 960
 QY 961 CTGCTCTCCGGAAGATGAC 981
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 961 CTGCTCTCCGGAAGATGAC 981

RESULT 2
 AAC91368
 ID AAC91368 standard; DNA; 981 BP.
 XX AAC91368;
 AC AAC91368;
 XX
 DT 16-MAR-2001 (first entry)
 XX
 DE Modified human annexin nucleotide sequence, SEQ ID NO: 1.
 DE Human; annexin; chelation site; nuclear imaging; apoptosis;
 KW transplanted rejection; ds.
 KW
 XX Homo sapiens.
 OS
 XX WO200073332-A1.
 PN
 XX 07-DEC-2000.
 PD
 XX 25-MAY-2000; 2000MO-US14324.
 PF
 XX 01-JUN-1999; 99US-0324096.
 PR
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX Tait JF, Brown DS;
 PI
 XX WPI: 2001-080465/09.
 DR P-PSDB; AAB50863.
 XX
 PT Novel modified annexin useful for imaging vascular thrombi and
 PT apoptosis, has N-terminal chelation site comprising amino acid
 PT extension which comprises a glycine and a cysteine residue -
 XX
 PS Claim 25; Page 28-30; 39pp; English.
 XX
 CC The present sequence encodes a modified annexin having an N-terminal
 CC chelation site, which comprises an amino acid extension including a
 CC glycine and a cysteine residue. The modified annexin is useful for
 CC imaging vascular thrombi or apoptosis which is associated with response
 CC to a chemotherapeutic agent or with rejection as a result of
 CC transplantation. The modified annexin can effectively chelate a
 CC radionuclide and retain annexin bioactivity. It can be readily prepared
 CC in high radiochemical yield and with high radiochemical purity. In
 CC contrast to conventional conjugation chemistries that provide a
 CC distribution of conjugation products, the modified annexin has a single
 CC chelation site remote from the site of biological activity.
 XX
 SQ Sequence 981 BP; 286 A; 187 C; 251 G; 257 T; 0 other;

Query Match 99.7%; Score 977.8; DB 22; Length 981;
 Best Local Similarity 99.8%; Pred. No. 3.8e-274;
 Matches 979; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 361 ATTGTTCAAGGACACCTGAAGAACTGAGAGCCATCAAAACAAGTTTATGAAGAAGATAT 420
 DB 361 ATTGTTCAAGGACACCTGAAGAACTGAGAGCCATCAAAACAAGTTTATGAAGAAGATAT 420
 QY 421 GGCTCAGGCTGGAAGATGACGTGTGGGGGACACTTCAGGTACTACAGCGGATGTTG 480
 DB 421 GGCTCAGGCTGGAAGATGACGTGTGGGGGACACTTCAGGTACTACAGCGGATGTTG 480
 QY 481 GTGGTTCTCCTTCAGGCTAACAGAGACCTGATGCTGGAATTGATGAAGCTCAAGTGA 540
 DB 481 GTGGTTCTCCTTCAGGCTAACAGAGACCTGATGCTGGAATTGATGAAGCTCAAGTGA 540
 QY 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
 DB 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
 QY 601 TTATCACCACCTTTGGACACAGAGTGTCTCATTTTGAGAAAGTGTTCACAAATAC 660
 DB 601 TTATCACCACCTTTGGACACAGAGTGTCTCATTTTGAGAAAGTGTTCACAAATAC 660
 QY 661 ATGACTATATCAGGATTTCAAAATTCAGGAAACCTTACCGGAGACTTCTGSCAATTA 720
 DB 661 ATGACTATATCAGGATTTCAAAATTCAGGAAACCTTACCGGAGACTTCTGSCAATTA 720
 QY 721 GAGCAACTACTCCTTGTCTGTTGAAATCTATTTCGAAGTATACCTGCCTACCTTCGACAG 780
 DB 721 GAGCAACTACTCCTTGTCTGTTGAAATCTATTTCGAAGTATACCTGCCTACCTTCGACAG 780
 QY 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
 DB 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
 QY 841 GTTTCAGGAGTGAGATGATCTGTTTACATCAGGAGGAGCTTTAGGAAGATTTTGC 900
 DB 841 GTTTCAGGAGTGAGATGATCTGTTTACATCAGGAGGAGCTTTAGGAAGATTTTGC 900
 QY 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGAGCTATGAAGAACTCTTCTG 960
 DB 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGAGCTATGAAGAACTCTTCTG 960
 QY 961 CTGCTCTCGGAGAGATGAC 981
 DB 961 CTGCTCTCGGAGAGATGAC 981

RESULT 4

AA11241
 ID AA11241 standard; DNA; 1803 BP.

XX AA11241;

XX AC

XX 25-OCT-2000 (first entry)

XX Annexin V/urokinase fusion construct.

XX Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;
 KW urokinase; insect cell; fibrinolysis; ss.
 XX Unidentified.

XX Key

XX Location/Qualifiers
 FT 1..1803
 CDS /tag= a

FT /product= "annexin V/urokinase fusion protein"
 FT /note= "no start or stop codons are given at the 5'
 FT or 3' ends of the sequence"

XX CN1247195-A.

XX 15-MAR-2000.

XX 12-MAR-1999; 99CN-0113524.

XX 12-MAR-1999; 99CN-0113524.
 PR (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
 PA Wu X, Sun J, Yang G;
 XX WPI: 2000-413098/36.
 DR P-PSDB; AAY92930.
 XX New thrombolytic fusion protein for targetting thrombus - comprises
 PT fusion of Annexin V and urokinase
 PS Claim 2; Page 2-4; 20pp; Chinese.
 XX Annexin V, which has high affinity for active thrombocytes, is used
 CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion
 CC protein. The protein is the result of expression of a fusion gene
 CC (this sequence) comprising the Annexin V gene and a low-molecular
 CC urokinase gene, in insect cells. The Annexin V-scu-PA-32 fusion protein,
 CC expressed in insect cell strain Tn-581-4, has high affinity for active
 CC thrombocytes and has the fibrinolytic activity of urokinase.
 XX Sequence 1803 BP; 495 A; 415 C; 462 G; 431 T; 0 other;

Query Match 97.7%; Score 958.6; DB 21; Length 1803;
 Best Local Similarity 98.6%; Pred. No. 2e-268;
 Matches 967; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGGCAGGTGGCTGTGGCCATATGCGACAGGTTCTCAGAGGACACTGTGACTGACTTCCT 60
 DB 820 ATTCAGAGAAGATATCTCGAGATGCGACAGGTTCTCAGAGGACACTGTGACTGACTTCCT 879
 QY 61 GATTGTGATGCGGGCTGATGCGAAACTCTTCGGAAGGCTATCAAGGCTTGGGCACA 120
 DB 880 GATTGTGATGCGGGCTGATGCGAAACTCTTCGGAAGGCTATCAAGGCTTGGGCACA 939
 QY 121 GATGAGGAGAGCATCCTGACTCTGTTGACATCCCGAAGTAACTCTCAGCGCCAGGAATC 180
 DB 940 GATGAGGAGAGCATCCTGACTCTGTTGACATCCCGAAGTAACTCTCAGCGCCAGGAATC 999
 QY 181 TCTGAGCTTTTAAAGTCTGTTTGGCAGGGATCTTCGGATGACCTGAATCAGAACTA 240
 DB 1000 TCTGAGCTTTTAAAGTCTGTTTGGCAGGGATCTTCGGATGACCTGAATCAGAACTA 1059
 QY 241 ACTGGAATAATTGAAAAATTAATTCTGCTCTGATGAACCCCTCTCGGCTTTATGATGCT 300
 DB 1060 ACTGGAATAATTGAAAAATTAATTCTGCTCTGATGAACCCCTCTCGGCTTTATGATGCT 1119
 QY 301 TATGAACCTGAACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAAT 360
 DB 1120 TATGAACCTGAACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAAT 1179
 QY 361 ATTGTTCAAGGACACCTGGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
 DB 1180 ATTGTTCAAGGACACCTGGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 1239
 QY 421 GGCTCAAGCTGGAAGATGACGTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTG 480
 DB 1240 GGCTCAAGCTGGAAGATGACGTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTG 1299
 QY 481 GTGGTTCTCCTTCAGGCTAACAGAGACCTGATGCTGGAATTGATGAAGCTCAAGTGA 540
 DB 1300 GTGGTTCTCCTTCAGGCTAACAGAGACCTGATGCTGGAATTGATGAAGCTCAAGTGA 1359
 QY 541 CAAGATGCTCAGGCTTTTATTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
 DB 1360 CAAGATGCTCAGGCTTTTATTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 1419
 QY 601 TTTATCACCACCTTTTGGAAACAGGAAGTGTGCTCATTTTGAAGAGTGTGTTGACAGTAC 660
 DB 1420 TTTATCACCACCTTTTGGAAACAGGAAGTGTGCTCATTTTGAAGAGTGTGTTGACAGTAC 1479

Qy 661 ATGACTATATCAGGATTTCAAAATTGAGAAACCATTGACCGGAGACTTCTGGCAATTTA 720
 Db 1480 ATGACTATATCAGGATTTCAAAATTGAGAAACCATTGACCGGAGACTTCTGGCAATTTA 1539
 Qy 721 GAGCAACTACTCCTTGTGTTGTTGCAATCTATTGCAAGTATACCTGCTACCTTGCAGAG 780
 Db 1540 GAGCAACTACTCCTTGTGTTGTTGCAATCTATTGCAAGTATACCTGCTACCTTGCAGAG 1599
 Qy 781 ACCCTCTATTATGCTATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCATG 840
 Db 1600 ACCCTCTATTATGCTATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCATG 1659
 Qy 841 GTTTCAGGAGTGAATGATCTGTTTAAATCATCAGGAGGAGTTTAGGAAGATTTTGGC 900
 Db 1660 GTTTCAGGAGTGAATGATCTGTTTAAATCATCAGGAGGAGTTTAGGAAGATTTTGGC 1719
 Qy 901 ACCCTCTCTTATTCATGATTAGGGAGATACATCTCGGACATATAGGAAGCTCTTCTG 960
 Db 1720 ACCCTCTCTTATTCATGATTAGGGAGATACATCTCGGACATATAGGAAGCTCTTCTG 1779
 Qy 961 CTGCTCTCCGAGAGATGAC 981
 Db 1780 CTGCTCTGGAGAGATGAC 1800

RESULT 5

AA91353 ID AA91353 standard; DNA; 1466 BP.
 AC AA91353;
 AC AA91353;
 DT 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 30-JUL-1989 (first entry)
 XX Vascular anti-coagulating protein-alpha cDNA.
 XX Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas; ss.
 RW Chimeric - Homo sapiens.
 OS Chimeric - Mus musculus.
 XX Key Location/Qualifiers
 FT CDS 35..996
 FT /*tag= a
 FT /label=VAC-alpha cDNA
 PN DE3810331-A.
 XX
 PD 05-OCT-1989.
 XX
 PF 26-MAR-1988; 88DE-3810331.
 XX
 PR 26-MAR-1988; 88DE-3810331.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM.
 XX
 PI Gunther A;
 XX
 DR WPI; 1989-293724/41.
 DR P-FSDB; AAP91953.
 XX
 PT Monoclonal antibodies to vascular anti-coagulating proteins - and
 PT hybridomas producing such antibodies.
 XX
 PS Disclosure; fig 1; 11pp; German.
 XX
 CC The vascular anti-coagulating protein (VAC)-alpha encoded by this cDNA
 CC is used in the preparation of monoclonal antibodies (MABs). The
 CC VAC-alpha is injected into a host animal, in conjugation with eg keyhole
 CC limpet haemocyanin, and the B-cells from the immunised hosts are then
 CC fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9)
 CC produce Abs specific to VAC-alpha. The Abs can be used as immunoassay

CC reagents to detect VAC proteins, as affinity ligands for purificn. of
 CC VACs and as medicaments for binding and/or neutralising VAC proteins in
 CC vivo. See also AA91354 and Ep-181465.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1466 BP; 423 A; 291 C; 327 G; 425 T; 0 other;

SQ Query Match 97.7%; Score 958; DB 10; Length 1466;

Best Local Similarity 99.5%; Pred. No. 2.7e-268;

Matches 961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 16 GGCCATATGACACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGG 75
 Db 29 CTGCTATGACACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGG 88
 Qy 76 GCTGATGACACAACTCTTCGGAAGGCTATGAAGGCTTGGGACAGATGAGGAGGATC 135
 Db 89 GCTGATGACACAACTCTTCGGAAGGCTATGAAGGCTTGGGACAGATGAGGAGGATC 148
 Qy 136 CTGACTCTGTTGACATCCCGAAGTAACTGCTCAGCGCCAGGAAATCTCTGCGCTTTTAAAG 195
 Db 149 CTGACTCTGTTGACATCCCGAAGTAACTGCTCAGCGCCAGGAAATCTCTGCGCTTTTAAAG 208
 Qy 196 ACTCTGTTGGCAGGATCTCTGGATGACCTGGAATCAGAACTCACTGGAATTTGAA 255
 Db 209 ACTCTGTTGGCAGGATCTCTGGATGACCTGGAATCAGAACTCACTGGAATTTGAA 268
 Qy 256 AAATTAATTTGCTCTGATCAAACTCTCGGCTTATGATGCTTATGATGCTTAACTCAACAT 315
 Db 269 AAATTAATTTGCTCTGATCAAACTCTCGGCTTATGATGCTTATGATGCTTAACTCAACAT 328
 Qy 316 GCCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATATTGCTTCAAGGACA 375
 Db 329 GCCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATATTGCTTCAAGGACA 388
 Qy 376 CTTGAAGACTGAGAGCCATCAACAAAGTTTATGAAGAAATATGCTCAAGCTCGAA 435
 Db 389 CTTGAAGACTGAGAGCCATCAACAAAGTTTATGAAGAAATATGCTCAAGCTCGAA 448
 Qy 436 GATGACGTGTGGGGGACACTTTCAGGCTACTTACAGCGGATGTTGGTGTCTCTCAG 495
 Db 449 GATGACGTGTGGGGGACACTTTCAGGCTACTTACAGCGGATGTTGGTGTCTCTCAG 508
 Qy 496 GCTAACAGAGACCTGATGCTGGAATTTGATGAAGTCAAGTTGAACAAAGTCTCAGGCT 555
 Db 509 GCTAACAGAGACCTGATGCTGGAATTTGATGAAGTCAAGTTGAACAAAGTCTCAGGCT 568
 Qy 556 TTATTTGAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTT 615
 Db 569 TTATTTGAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTT 628
 Qy 616 GGAACAGAGTGTGCTCATTTGAGAAAGTGTGACAGAGTACATGATATATCAGGA 675
 Db 629 GGAACAGAGTGTGCTCATTTGAGAAAGTGTGACAGAGTACATGATATATCAGGA 688
 Qy 676 TTTCAAAATTCAGGAAACCATTTGACCGGAGACTTCTGCAATTTTAGACCAACTACTCCTT 735
 Db 689 TTTCAAAATTCAGGAAACCATTTGACCGGAGACTTCTGCAATTTTAGACCAACTACTCCTT 748
 Qy 736 GCTGTTGAAATCTATTCGAAAGTATACCTGCTTACCTTGGCAGAGCCCTTATATGCT 795
 Db 749 GCTGTTGAAATCTATTCGAAAGTATACCTGCTTACCTTGGCAGAGCCCTTATATGCT 808
 Qy 796 ATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGCTTCCAGGATGAG 855
 Db 809 ATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGCTTCCAGGATGAG 868
 Qy 856 ATTGATCTGTTTAAACATCAGGAGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATGCC 915
 Db 869 ATTGATCTGTTTAAACATCAGGAGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATGCC 928
 Qy 916 ATGATTAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTGCTCTCCGGAGAA 975

Db 929 ATGATTAAAGGAGATACATCTGGGACTATAAGAAAGCTTCTGCTGCTGTGGAGAA 988
 QY 976 GATGAC 981
 Db 989 GATGAC 994

RESULT 6
 AAN81113
 ID AAN81113 standard; DNA; 1567 BP.
 XX AAN81113;
 XX 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 12-NOV-1990 (first entry)
 XX Plasmid contg. placental coagulation inhibitor gene.
 XX Placental coagulation inhibitor; disseminated vascular coagulation;
 KW thrombosis; ss.
 XX Homo sapiens.
 XX Location/Qualifiers
 FH 136..1098
 CDS
 FT /*tag= a
 FT /label=placental coagulation inhibitor
 FT 1568
 FT /*tag= b
 XX
 XX EP279459-A.
 PN JP03219875-A.
 PN
 XX 24-AUG-1988.
 PD
 XX 19-FEB-1988; 88EP-0102468.
 PF
 XX 20-FEB-1987; 87JP-0037227.
 PR
 XX 23-JUL-1987; 87JP-0184428.
 PR
 XX (KOWA) KOWA CO LTD.
 PA
 XX Saino Y, Iwasaki A, Suda M;
 PI WPI: 1988-236733/34.
 DR WPI: 1991-329110/45.
 DR P-PSDB; AAP80511.
 XX
 XX Recombinant placental coagulation inhibitor - useful for the prevention
 PT and treatment of thromboses or disseminated intra-vascular coagulation.
 PT
 XX Disclosure; Page ?; p: English.
 PS
 XX This recombinant DNA sequence comprises a promoter region, ribosome
 CC binding site, initiation sequence, termination codon and a trans-
 CC cription terminator in addition to the placental coagulation inhibitor
 CC gene. The polypeptide produced on culturing of transformed host cells
 CC exhibits strong anticoagulant activities and is useful for the treat-
 CC ment and prevention of eg thrombosis or disseminated intravascular
 CC coagulation in the brain, heart and peripheral blood vessels.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC

SO Sequence 1567 BP; 430 A; 332 C; 358 G; 447 T; 0 other;
 Query Match 97.5%; Score 956.8; DB 9; Length 1567;
 Best Local Similarity 99.8%; Pred. No. 6.3e-268;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
 Db 136 ATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 195
 QY 82 GCAGAACTCTTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGAGAGCATCCTGACT 141
 Db 196 GCAGAACTCTTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGAGAGCATCCTGACT 255
 QY 142 CTGTTGACATCCCGAAGTAATCTCAGCGCAGGAAATCTCTGACGCTTTTAAAGACTCTG 201
 Db 256 CTGTTGACATCCCGAAGTAATCTCAGCGCAGGAAATCTCTGACGCTTTTAAAGACTCTG 315
 QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
 Db 316 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 375
 QY 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAATCTGAACATGCCCTG 321
 Db 376 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAATCTGAACATGCCCTG 435
 QY 322 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 Db 436 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 495
 QY 382 GAACTGAGAGCCATCAACAACTTTATGAAGAAGATATGGCTCAAGGCTGGAAGATGAC 441
 Db 496 GAACTGAGAGCCATCAACAACTTTATGAAGAAGATATGGCTCAAGGCTGGAAGATGAC 555
 QY 442 GTGGTGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 501
 Db 556 GTGGTGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 615
 QY 502 AGAGACCTGATGCTGGAAATTCGATGAAGTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 561
 Db 616 AGAGACCTGATGCTGGAAATTCGATGAAGTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 675
 QY 562 CAGGCTGGAGAACTTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA 621
 Db 676 CAGGCTGGAGAACTTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA 735
 QY 622 CGAAGTGTCTCATTTTGAAGAAAGTGTGTCAGCAAGTACATGACTATATCAGGATTTCAA 681
 Db 736 CGAAGTGTCTCATTTTGAAGAAAGTGTGTCAGCAAGTACATGACTATATCAGGATTTCAA 795
 QY 682 ATTGAGAAACATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTT 741
 Db 796 ATTGAGAAACATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTT 855
 QY 742 GTGAAATCTATTGCAAGTATACCTGCTACCTTGCGAGAGCCCTCTATTATGCTATGAAG 801
 Db 856 GTGAAATCTATTGCAAGTATACCTGCTACCTTGCGAGAGCCCTCTATTATGCTATGAAG 915
 QY 802 CGAGCTGGGACAGATGATCATCCCTCATCAGATCATGTTTCCAGGAGTGAGATTGAT 861
 Db 916 CGAGCTGGGACAGATGATCATCCCTCATCAGATCATGTTTCCAGGAGTGAGATTGAT 975
 QY 862 CTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGGCACTCTCTTTTATTTCCATGAT 921
 Db 976 CTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGGCACTCTCTTTTATTTCCATGAT 1035
 QY 922 AAGGAGATACATCTGGGGACTATGAAGAAAGTCTCTCTGCTGCTCCGGAGAGATGAC 981
 Db 1036 AAGGAGATACATCTGGGGACTATGAAGAAAGTCTCTCTGCTGCTGCTGGAGAGATGAC 1095

RESULT 7
 ABX63162
 ID ABX63162 standard; cDNA; 1578 BP.
 XX
 AC ABX63162;
 XX
 DT 25-FEB-2003 (first entry)
 XX

DE Human cDNA #162 differentially expressed in activated vascular tissue.
 XX Human; gene; ss: vascular tissue; cytostatic; atherosclerosis;
 KW cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke;
 XX
 OS Homo sapiens.
 XX
 XX US2002137081-A1.
 PN
 XX
 PD 26-SEP-2002.
 XX
 XX 08-JAN-2002; 2002US-0044090.
 XX
 XX 28-JUL-2000; 2000US-222469P.
 PR
 PR 08-JAN-2001; 2001US-260483P.
 XX
 PA (BAND/) BANDMAN O.
 XX
 XX Bandman O;
 XX
 XX WPI: 2003-110597/10.
 DR
 XX
 PT Combination for diagnosing, staging, treating, or monitoring the
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several cDNAs that are differentially expressed in activated
 PT vascular tissue.
 XX
 XX Claim 1; Page -: 18pp; English.
 PS
 XX This invention relates to a combination comprising several cDNAs that
 CC are differentially expressed in activated vascular tissue. The invention
 CC also discloses a high throughput method for detecting differentially
 CC expressed cDNAs in a sample. The cDNAs of the invention may have
 CC antiatherosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
 CC gynaecological; vasotropic and cerebroprotective activities and may be
 CC used in gene therapy. The cDNAs of the invention may be used in a
 CC high-throughput methods for detecting differential expression of one or
 CC more cDNAs in a sample, or screening several molecules or compounds to
 CC identify a molecule or compound that specifically binds a cDNA of the
 CC invention. A protein encoded by the cDNA may be used to screen several
 CC molecules or compounds to identify a ligand that specifically binds to
 CC the protein, or to produce or purify an antibody to the protein that can
 CC be used to detect a protein in a sample or purify a natural or
 CC recombinant protein from a sample. The nucleotides may be useful for
 CC diagnosing, staging, treating, or monitoring the progression of
 CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
 CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-
 CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used
 CC for large-scale genetic or gene expression analysis of several new
 CC nucleic acid molecules. Antibodies to the proteins encoded by the
 CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic
 CC or acute diseases associated with abnormalities in the expression,
 CC amount or distribution of the protein. The present sequence
 CC represents a cDNA of the invention that is differentially expressed in
 CC activated vascular tissue.
 CC Note: The sequence data for this patent did not form part of the
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>.
 XX
 XX Sequence 1578 BP; 432 A; 335 C; 360 G; 451 T; 0 other;
 S0
 Query Match 97.58; Score 956.8; DB 25; Length 1578;
 Best Local Similarity 99.8; Pred. No. 6.3e-268;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 22 ATGGCAGAGTTCTCAGAGCAGCTGTGACTTCCTCGATTGTGATGAGCGGCTGAT 81
 DB 142 ATGGCAGAGTTCTCAGAGCAGCTGTGACTTCCTCGATTGTGATGAGCGGCTGAT 201
 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGATCCTGACT 141

202	GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGACT	261
142	CTCTTGACATCCCGAGTAACTGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG	201
262	CTGTTGACATCCCGAGTAACTGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG	321
202	TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	261
322	TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	381
262	ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG	321
382	ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG	441
322	AAGGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA	381
442	AAGGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA	501
382	GAACTGAGAGCCATCAAACTGATGCTGCTGGAATTTATGAAAGAGATATGCTCAAGCCTGGAAGATGAC	441
502	GAACTGAGAGCCATCAAACTGATGCTGCTGGAATTTATGAAAGAGATATGCTCAAGCCTGGAAGATGAC	561
442	GTGCTGGGGGACACTTCAGGGTACTACACGGGATGTTGGTGTCTCTCTTCAGGCTAAC	501
562	GTGCTGGGGGACACTTCAGGGTACTACACGGGATGTTGGTGTCTCTCTTCAGGCTAAC	621
502	AGAGACCTCTGATGCTGGAATTTGATGAAGCTCAAGTTGCAACAAGATGCTCAGGCTTTATTT	561
622	AGAGACCTCTGATGCTGGAATTTGATGAAGCTCAAGTTGCAACAAGATGCTCAGGCTTTATTT	681
562	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA	621
682	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA	741
622	CGAAGTGTCTCTATTTGGAAGAGTGTGTTGACAAAGTACATGACTATATCAGGATTTCAA	681
742	CGAAGTGTCTCTATTTGGAAGAGTGTGTTGACAAAGTACATGACTATATCAGGATTTCAA	801
682	ATTGAGAAACCACTTACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTCTGCTGTT	741
802	ATTGAGAAACCACTTACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTCTGCTGTT	861
742	GTGAAATCTATTCGAAGTATACCTGCTACCTTGCAGAGACCTCTTATGCTTATGAAG	801
862	GTGAAATCTATTCGAAGTATACCTGCTACCTTGCAGAGACCTCTTATGCTTATGAAG	921
802	GGAGCTGGGACAGATGATACCTCATCAGAGTATGTTTCCAGGAGTGAGATTGAT	861
922	GGAGCTGGGACAGATGATACCTCATCAGAGTATGTTTCCAGGAGTGAGATTGAT	981
862	CTGTTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTCCACCTCTCTTTATTCATGATT	921
982	CTGTTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTCCACCTCTCTTTATTCATGATT	1041
922	AAGGGAGATACATCTGGGGAGCTATATAAGAAAGCTCTTCTGCTGCTCTCGGAGAAAGATGAC	981
1042	AAGGGAGATACATCTGGGGAGCTATATAAGAAAGCTCTTCTGCTGCTCTCGGAGAAAGATGAC	1101

RESULT 8
 AAN91821
 ID AAN91821 standard; DNA; 1605 BP.
 XX
 AC AAN91821;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1990 (first entry)
 XX
 DE Endonexin II complete cDNA.
 XX
 KW Placenta; blood coagulation
 XX

OS Homo sapiens (human).
 XX Key Location/Qualifiers
 FH 160..1119
 FT /*tag= a
 FT CDS
 XX
 PN EP339285-A.
 XX
 XX 02-NOV-1989.
 XX
 XX 30-MAR-1989; 89EP-0105626.
 PF
 XX 31-MAR-1988; 88US-0176802.
 PR
 XX (RORE) RORER INT OVERSEAS INC.
 PA
 XX Kaplan R, Jaye M;
 XX WPI; 1989-317181/44.
 DR P-PSDB; AAP91021.
 XX
 XX Recombinant human endonexin II - which inhibits blood coagulation
 PT and phospholipase A2 and is used as an antiinflammatory agent
 PT
 XX Claim 1; fig. 1; 13pp; English.
 PS
 XX hENII is a calcium and phospholipid binding protein.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX Sequence 1605 BP; 447 A; 337 C; 366 G; 455 T; 0 other;
 SQ

Query Match 97.5%; Score 956.8; DB 10; Length 1605;
 Best Local Similarity 99.8%; Pred. No. 6.3e-268;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
 DB 160 ATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 219
 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141
 DB 220 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 279
 QY 142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCG 201
 DB 280 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCG 339
 QY 202 TTTGGCAGGGATCTTCTGGATGACCTGGAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
 DB 340 TTTGGCAGGGATCTTCTGGATGACCTGGAATCAGAACTAACTGGAATAATTTGAAAAATTA 399
 QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTCTTG 321
 DB 400 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTCTTG 459
 QY 322 AAGGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTGCTTCAAGGACACCTGAA 381
 DB 460 AAGGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTGCTTCAAGGACACCTGAA 519
 QY 382 GAACCTGAGAGCCATCAACAACTTTATGAAGATATGCTCAAGCCTGGAAGATGAC 441
 DB 520 GAACCTGAGAGCCATCAACAACTTTATGAAGATATGCTCAAGCCTGGAAGATGAC 579
 QY 442 GTGGTGGGGACACTTCAGGGTACTACACGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 501
 DB 580 GTGGTGGGGACACTTCAGGGTACTACACGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 639
 QY 502 AGAGACCCCTGATGCTGGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 DB 640 AGAGACCCCTGATGCTGGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 699
 QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 621
 DB 1119

Db 700 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGCTTTATCACCATCTTTGGAACA 759
 QY 622 CGAAGTGTCTCTCATTGTGACAAAGGTGTTTGAACAAGTACATGACTATATCAGGATTTCAA 681
 Db 760 CGAAGTGTCTCTCATTGTGACAAAGGTGTTTGAACAAGTACATGACTATATCAGGATTTCAA 819
 QY 682 ATTGAGGAAACCACTTGACCGCGAGACTTCTGCGCAATTTAGAGCAACTACTCTCTGCTGTT 741
 Db 820 ATTGAGGAAACCACTTGACCGCGAGACTTCTGCGCAATTTAGAGCAACTACTCTCTGCTGTT 879
 QY 742 GTGAATCTATTTCGAAGTATACCTGCCTACCTTGACAGACCCCTCTATTATGCTATGAAG 801
 Db 880 GTGAATCTATTTCGAAGTATACCTGCCTACCTTGACAGACCCCTCTATTATGCTATGAAG 939
 QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT 861
 Db 940 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT 999
 QY 862 CTGTTTAACTCAGGAAGGAGTTTAGGAAGAATTTTGCACCTCTCTTTTATTTCCATGATT 921
 Db 1000 CTGTTTAACTCAGGAAGGAGTTTAGGAAGAATTTTGCACCTCTCTTTTATTTCCATGATT 1059
 QY 922 AAGGAGATACATCTGGGACTATGAAGAAGCTCTTCTGCTGCTCTCCGGAGAAAGATGAC 981
 Db 1060 AAGGAGATACATCTGGGACTATGAAGAAGCTCTTCTGCTGCTCTGCTGCTGAGAAAGATGAC 1119

RESULT 9
 AAN90112
 ID AAN90112 standard; DNA; 1575 BP.
 XX
 AC AAN90112;
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE Anticoagulant PP4 DNA.
 KW Anticoagulant; PP4 protein; thromboplastin.
 XX
 OS Homo sapiens (human).
 XX
 FH Key Location/Qualifiers
 FT polYA_signal 1539..1575
 FT /*tag= a
 FT CDS 107..1066
 FT /*tag= b
 XX
 PN EP318703-A.
 XX
 PD 07-JUN-1989.
 PF 29-OCT-1988; 88EP-0118039.
 XX
 PR 03-NOV-1987; 87DE-3737239.
 XX
 PA (BEHW) BEHRINGERWERKE AG.
 XX
 PI Grundmann U, Abel KJ, Kupper H;
 XX WPI; 1989-166767/23.
 DR
 XX
 PT New DNA sequence encoding anticoagulant PP4 protein
 PT - and new recombinant protein, vectors, antibodies, etc.,
 PT useful therapeutically and diagnostically.
 XX
 PS Claim 1; table 1; 14pp; German.
 XX
 CC DNA sequence encoding anticoagulant PP4 protein. This
 CC inhibits blood coagulation at the thromboplastin stage.
 CC The derived protein is 320 amino acids.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 1575 BP; 461 A; 322 C; 351 G; 441 T; 0 other;

Query Match 97.5%; Score 956.4; DB 10; Length 1575;

Best Local Similarity 99.4%; Pred. No. 8.2e-268;

Matches 960; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 16 GCCCATATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGTGAGCGG 75
Dy 101 GTCGCTATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGTGAGCGG 160
Qy 76 GCTGATGAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 135
Dy 161 GCTGATGAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 220
Qy 136 CTGACTCTGTGACATCCCGAAGTAATGCTCAGCGGCAAGAAATCTCTGAGCTTTAAG 195
Dy 221 CTGACTCTGTGACATCCCGAAGTAATGCTCAGCGGCAAGAAATCTCTGAGCTTTAAG 280
Qy 196 ACTCTGTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAACTGGAATAATTTGAA 255
Dy 281 ACTCTGTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAACTGGAATAATTTGAA 340
Qy 256 AAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACAT 315
Dy 341 AAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACAT 400
Qy 316 GCCTTGAAGGAGCTGGAACAAATGAAGTAAGTCTGACAGAAATTTATGCTTCAAGGACA 375
Dy 401 GCCTTGAAGGAGCTGGAACAAATGAAGTAAGTCTGACAGAAATTTATGCTTCAAGGACA 460
Qy 376 CCTGAAGAACTGAGAGCCTCAACAAATTTATGAAGAAATATGCTCAAGCCTGGAA 435
Dy 461 CCTGAAGAACTGAGAGCCTCAACAAATTTATGAAGAAATATGCTCAAGCCTGGAA 520
Qy 436 GATGAGCTGTGGGGGACACTTCAAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAG 495
Dy 521 GATGAGCTGTGGGGGACACTTCAAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAG 580
Qy 496 GCTAACAGAGACCTGATGCTGGAAATGATGAAGCTCAAGTTGAACAGATGCTCAGGCT 555
Dy 581 GCTAACAGAGACCTGATGCTGGAAATGATGAAGCTCAAGTTGAACAGATGCTCAGGCT 640
Qy 556 TTATTTCAAGCTGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCACCTTT 615
Dy 641 TTATTTCAAGCTGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCACCTTT 700
Qy 616 GGAACAGAGAGTGTCTCAATTTGAGAAAGTGTGACAAAGTACATGACTATATCAGGA 675
Dy 701 GGAACAGAGAGTGTCTCAATTTGAGAAAGTGTGACAAAGTACATGACTATATCAGGA 760
Qy 676 TTCAATTTAGGAAACCATTTGACGGGAGACTTCTGCGAATTTAGAGCAACTACTCCTT 735
Dy 761 TTCAATTTAGGAAACCATTTGACGGGAGACTTCTGCGAATTTAGAGCAACTACTCCTT 820
Qy 736 GCTGTGTGAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCT 795
Dy 821 GCTGTGTGAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCT 880
Qy 796 ATGAAGGAGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGGTTTCAGGAGTGAG 855
Dy 881 ATGAAGGAGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGGTTTCAGGAGTGAG 940
Qy 856 ATTGATCTGTTTACATCAGAGAGGTTTATGGAAGAAATTTTGGCACCTCTCTTTATTC 915
Dy 941 ATTGATCTGTTTACATCAGAGAGGTTTATGGAAGAAATTTTGGCACCTCTCTTTATTC 1000
Qy 916 ATGATTAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTCTCTCGGAGAA 975
Dy 1001 ATGATTAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTCTCTCGGAGAA 1060
Qy 976 GATGAC 981

Db 1061 GATGAC 1066

RESULT 10

AAN82107

ID AAN82107 standard; cDNA; 1454 BP.

XX AC AAN82107;

XX DT 25-MAR-2003 (updated)

XX DT 13-NOV-1990 (first entry)

XX PAP-1 cDNA from human placenta, used for anticoagulant production.

XX PAP-1; anticoagulant; anti-inflammatory agent; phospholipid;

XX phospholipase A2; disseminated intravascular coagulation; human placenta;

XX deep vein thrombosis; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 13..972

XX FT /*tag= a

XX FT /product=PAP-I

XX PN W08805659-A.

XX PD 11-AUG-1988.

XX PF 05-FEB-1988; 88WO-US00340.

XX PR 06-FEB-1987; 87US-0011782.

XX PR 05-JUN-1987; 87US-0059355.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Fujikawa K, Irani MH, Carter BLA;

XX WPI; 1988-235049/33.

XX P-PSDB; AAP82317.

XX Human proteins having anticoagulant and antiinflammatory activity -

XX isolated from biological fluid by anion-exchange chromatograph media.

XX Disclosure: Page ?; p; English.

XX A human placenta cDNA library (Clontech) was screened to obtain
CC this sequence. The cDNA does not contain a leader peptide sequence,
CC indicating that PAP-1 is probably not constitutively secreted.
CC The product binds to phospholipid and inhibits phospholipase A2.
CC The protein can substitute heparin or other anticoagulants in
CC the treatment of disseminated intravascular coagulation, deep vein
CC thrombosis, or other disorders. It also has antiinflammatory
CC properties.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1454 BP; 434 A; 280 C; 324 G; 416 T; 0 other;

Query Match 97.4%; Score 955.2; DB 9; Length 1454;

Best Local Similarity 99.7%; Pred. No. 1.8e-267;

Matches 957; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 22 ATGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGTGATGAGCGGCTGAT 81

Dy 13 ATGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGTGATGAGCGGCTGAT 72

Qy 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141

Dy 73 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 132

Qy 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAGACTCTG 201

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Db 133 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGAAATCTCTGACGCTTTTAGACTCTG 192
QY 202 TTGGCAGGATCTCTCGATGACCTGAATCAGAACTAGAACTGGAATAATTTGAAAAATTA 261
Db 193 TTGGCAGGATCTCTCGATGACCTGAATCAGAACTAGAACTGGAATAATTTGAAAAATTA 252
QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTTG 321
Db 253 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTTG 312
QY 322 AAGGGAGCTGGAAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 313 AAGGGAGCTGGAAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372
QY 382 GAACTCAGAGCCATCAACAAGTTTATGAAGAAGATATGGCTCAAGCTGGAAGATGAC 441
Db 373 GAACTCAGAGCCATCAACAAGTTTATGAAGAAGATATGGCTCAAGCTGGAAGATGAC 432
QY 442 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
Db 433 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 492
QY 502 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 561
Db 493 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 552
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCAACCATCTTTTGAACA 621
Db 553 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCAACCATCTTTTGAACA 612
QY 622 CGAAGTGTCTCATTTGAGAAAGGTTTGAACAAGTATGATGATGATGATGATGATGATGAT 681
Db 613 CGAAGTGTCTCATTTGAGAAAGGTTTGAACAAGTATGATGATGATGATGATGATGATGAT 672
QY 682 ATTGAGAAACCACTTACCGGAGACTTCTGSCAATTTAGACCAACTACTCTCTGCTTT 741
Db 673 ATTGAGAAACCACTTACCGGAGACTTCTGSCAATTTAGACCAACTACTCTCTGCTTT 732
QY 742 GTGAAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 801
Db 733 GTGAAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 792
QY 802 GGAGCTGGACAGATGATCAATACCCCTCATCAGATCATGTTTCCAGGAGTGAATGAT 861
Db 793 GGAGCTGGACAGATGATCAATACCCCTCATCAGATCATGTTTCCAGGAGTGAATGAT 852
QY 862 CTGTTTAACTCAGGAAGGAGTTTAGGAAGAATTTTGCACCTCTCTTTATCCATGATT 921
Db 853 CTGTTTAACTCAGGAAGGAGTTTAGGAAGAATTTTGCACCTCTCTTTATCCATGATT 912
QY 922 AAGGGAGATACATCTGGGACTATAGAAGCTCTTCTGCTCTCTCCGAGAGATGAC 981
Db 913 AAGGGAGATACATCTGGGACTATAGAAGCTCTTCTGCTCTCTGCTGCTGGAGAGATGAC 972
```

RESULT 11

AAQ12679

ID AAQ12679 standard; cDNA; 1460 BP.

XX AC AAQ12679;

XX AC AAQ12679;

DT 25-MAR-2003 (updated)

DT 30-SEP-1991 (first entry)

XX AC AAQ12679;

XX AC AAQ12679;

XX PAP-I.

KW Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;

KW gla-domain; VKDP; ss.

XX OS Homo sapiens.

XX OS Homo sapiens.

XX OS Homo sapiens.

FH Key

Location/Qualifiers

FT CDS

FT 13..972

FT /*tag= a

FT /product= PAP-I

XX WO9109953-A.

PN 11-JUL-1991.

XX 13-DEC-1990;

XX 90WO-US07335.

XX 29-DEC-1989;

XX 89US-0459082.

XX (ZYMO) ZYMOGENETICS INC.

XX Foster DC;

XX WPI; 1991-222905/30.

XX P-PSDB; AAK13082.

XX Recombinant prodn. of hybrid phospholipid-binding proteins -

XX comprising lipocortin phospholipid-binding domain and

XX vitamin K-dependent protein

XX Dislosure; Fig 7; 57pp; English.

XX This sequence, or a fragment of it, is used in the construction of

XX DNA sequences encoding hybrid phospholipid-binding proteins (PBP)

XX comprising at least one lipocortin phospholipid binding domain (PBD),

XX e.g. of PAP-I, joined to a gla-domainless vitamin K-dependent

XX protein, e.g. protein C or activated protein C.

XX See AAQ12680-81 for such examples.

XX A human placenta cDNA library was screened using affinity-

XX purified antibody against PAP-I in order to obtain this cDNA.

XX See also AAQ12678-81.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1460 BP; 436 A; 280 C; 323 G; 421 T; 0 other;

XX Query Match 97.4%; Score 955.2; DB 12; Length 1460;

XX Best Local Similarity 99.7%; Pred. No. 1.8e-267;

XX Matches 957; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 22 ATGGCAGAGTCTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81

Db 13 ATGGCAGAGTCTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 72

QY 82 GCAGAAACTCTTCGGAAGGCTATGAAAGCTTGGGCACAGATGAGGAGAGCATCTGACT 141

Db 73 GCAGAAACTCTTCGGAAGGCTATGAAAGCTTGGGCACAGATGAGGAGAGCATCTGACT 132

QY 142 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGAAATCTCTGACGCTTTTAAAGACTCTG 201

Db 133 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGAAATCTCTGACGCTTTTAAAGACTCTG 192

QY 202 TTTGGCAGGATCTCTCGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261

Db 193 TTTGGCAGGATCTCTCGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 252

QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTTG 321

Db 253 ATTGTGGCTCTTATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTTG 312

QY 322 AAGGGAGCTGGAAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381

Db 313 AAGGGAGCTGGAAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372

QY 382 GAACTCAGAGCCATCAACAAGTTTATGAAGAAGATATGGCTCAAGCTGGAAGATGAC 441

Db 373 GAACTCAGAGCCATCAACAAGTTTATGAAGAAGATATGGCTCAAGCTGGAAGATGAC 432

QY 442 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501

Db 433 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 492

502 AGAGCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 493 AGAGCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 552
 562 CAGGCTGGAGAACTTAATAGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAA 621
 553 CAGGCTGGAGAACTTAATAGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAA 612
 622 CGAAGTGTCTCATTTGAGAAAGTGTGACAAAGTACATGACTATATCAGGATTTCAA 681
 613 CGAAGTGTCTCATTTGAGAAAGTGTGACAAAGTACATGACTATATCAGGATTTCAA 672
 682 ATTGAGAAACCATTTGACCGGACACTTCTGGCAATTTAGAGCAACTACTCTTCGCTGTT 741
 673 ATTGAGAAACCATTTGACCGGACACTTCTGGCAATTTAGAGCAACTACTCTTCGCTGTT 732
 742 GTGAATCTATTCGAAGTATACCTGCTACCTTCGAGAGACCCCTTATATGCTATGAAG 801
 733 GTGAATCTATTCGAAGTATACCTGCTACCTTCGAGAGACCCCTTATATGCTATGAAG 792
 802 GGAGCTGGAGAGATGATACCTCATCAGAGTCAATGCTTCCAGAGTGAGATTGAT 861
 793 GGAGCTGGAGAGATGATACCTCATCAGAGTCAATGCTTCCAGAGTGAGATTGAT 852
 862 CTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGCACCTCTCTTTATTCATGATT 921
 853 CTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGCACCTCTCTTTATTCATGATT 912
 922 AAGGAGATACATCTGGGAGCTATGAAGAGCTCTCTGCTGCTCTCCGGAAGAGATGAC 981
 913 AAGGAGATACATCTGGGAGCTATGAAGAGCTCTCTGCTGCTCTGGAAGAGATGAC 972

RESULT 12

AAN80801
 ID AAN80801 standard; DNA; 1466 BP.

XX AC AAN80801;

XX DT 25-MAR-2003 (updated)
 DT 12-SEP-1990 (first entry)

Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha (Glu22).

Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant; antiinflammatory; phospholipase inhibitory.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT mat_peptide 35..997

FT /*tag= a
 /note=-claimed in claim 2, page 160-161*

XX PN W08807576-A.

XX PD 06-OCT-1988.

XX PF 26-MAR-1988; 88WO-EP00266.

XX PR 28-MAR-1987; 87DE-3710309.

XX PR 28-MAR-1987; 87DE-3710364.

XX PR 28-MAR-1987; 87DE-3710430.

XX PR 04-NOV-1987; 87DE-3737367.

XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX PI Hauptmann R, Maurer-Fogy I, Bodo G, Swetly P, Stratowa C, Falkner E;

XX PI Adolf G, Reutlingsperger CMP;

XX DR WPI; 1988-292861/41.

DR P-PSDB: AAP80714.

XX New vascular anti-coagulating proteins -
 PT useful as thrombin inhibitors, antiinflammatory agents, etc

XX PS Disclosure; Fig 4/1-4/3; 183pp; German.

XX CC The DNA is produced by determining the amino acid sequence of isolated
 CC and highly purified VAPs, constructing DNA probes on the basis of this
 CC sequence, using that probes to search through suitable cDNA libraries,
 CC isolating cDNA that hybridises with the probes, by inserting the cDNA
 CC into a suitable vector, and using the vector to transform a host
 CC organism. VAC-alpha has anticoagulant activity under certain
 CC conditions, but loses this activity in the event of severe bleeding.
 CC It acts by inhibiting conversion of factor X to factor Xa and conversion
 CC of prothrombin to thrombin. It is structurally related to lipocortin I
 CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
 CC has similar antiinflammatory and phospholipase inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1466 BP; 422 A; 289 C; 328 G; 424 T; 3 other;

Query Match 97.3%; Score 954.6; DB 9; Length 1466;

Best Local Similarity 99.6%; Pred: No. 2.6e-267;

Matches 957; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 21 TATGGCAGAGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGA 80
 Db 34 TATGGCAGAGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGA 93

Qy 81 TCGAGAAACTCTTCGGAAGGCTATGAAAGGCTTCGGCACAGATGAGGAGACATCCCTGAC 140
 Db 94 TCGAGAAACTCTTCGGAAGGCTATGAAAGGCTTCGGCACAGATGAGGAGACATCCCTGAC 153

Qy 141 TCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAAATCTCTGACGTTTTAAGACTCT 200
 Db 154 TCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAAATCTCTGACGTTTTAAGACTCT 213

Qy 201 GTTTGGCAGGATCTCTGGATGACCTCAATCAGAACTAACTGAAATTTGAAATTT 260
 Db 214 GTTTGGCAGGATCTCTGGATGACCTCAATCAGAACTAACTGAAATTTGAAATTT 273

Qy 261 AATTGTGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTT 320
 Db 274 AATTGTGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTT 333

Qy 321 GAAGGAGCTGGAAACAATGAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGA 380
 Db 334 GAAGGAGCTGGAAACAATGAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGA 393

Qy 381 AGAACTGAGAGCCATCAACAAGTTTATGAAGAAGATATGCTCAAGCCCTGGAAGATGA 440
 Db 394 AGAACTGAGAGCCATCAACAAGTTTATGAAGAAGATATGCTCAAGCCCTGGAAGATGA 453

Qy 441 CGTGGTGGGACACACTTTCAGGCTACTACCCAGCGGATGTTGGTGGTCTCTCCTCAGGCTAA 500
 Db 454 CGTGGTGGGACACACTTTCAGGCTACTACCCAGCGGATGTTGGTGGTCTCTCCTCAGGCTAA 513

Qy 501 CAGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 560
 Db 514 CAGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 573

Qy 561 TCAGGCTGGAACTTAAATGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAAC 620
 Db 574 TCAGGCTGGAACTTAAATGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAAC 633

Qy 621 ACGAAGTGTGCTCATTTGAGAAAGGTTTGAACAAGTACATGACTATATCAGGATTTCA 680
 Db 634 ACGAAGTGTGCTCATTTGAGAAAGGTTTGAACAAGTACATGACTATATCAGGATTTCA 693

Qy 681 AATTGAGGAAACCATTTGACCCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGGCTGT 740
 Db 681 AATTGAGGAAACCATTTGACCCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGGCTGT 740

Db 694 AATTCAGGAACCATTCACCGGACACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT 753
 QY 741 TGTGAATCTATTTCGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAA 800
 Db 754 TGTGAATCTATTTCGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAA 813
 QY 801 GGGAGCTGGGACAGATGATACCTCATCAGATGCTGTTTCCAGAGTGAATGGA 860
 Db 814 GGGAGCTGGGACAGATGATACCTCATCAGATGCTGTTTCCAGAGTGAATGGA 873
 QY 861 TCTGTTTAAACATCAGGAAGGAGTTAGGAAGAAATTTGGCACCTCTCTTTATTCATGAT 920
 Db 874 TCTGTTTAAACATCAGGAAGGAGTTAGGAAGAAATTTGGCACCTCTCTTTATTCATGAT 933
 QY 921 TAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTCTCCGAGAGATGA 980
 Db 934 TAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTCTGCTGAGAGATGA 993
 QY 981 C 981
 Db 994 C 994

RESULT 13

AAN80873 standard; DNA; 963 BP.

XX AAN80873;
 XX AC AAN80873;
 XX DT 25-MAR-2003 (updated)
 XX DT 12-SEP-1990 (first entry)
 XX DE Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
 XX DE (Asp22).
 XX KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
 XX KW antinflammatory; phospholipase inhibitor.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT mat_peptide 35..963
 XX FT /*tag- a
 XX XN W08807576-A.
 XX XP 06-OCT-1988.
 XX XP 26-MAR-1988; 88WO-EP00266.
 XX PR 28-MAR-1987; 87DE-3710309.
 XX PR 28-MAR-1987; 87DE-3710364.
 XX PR 28-MAR-1987; 87DE-3710430.
 XX PR 04-NOV-1987; 87DE-3737367.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX PI Hauptmann R, Maurer-Fogy I, Bodo G, Svetly P, Stratowa C, Falkner E;
 XX PI Adolf G, Reutlingsperger CMP;
 XX DR WPI; 1988-292861/41.
 XX DR P-PSDB; AAP80242.
 XX New vascular anti-coagulating proteins -
 XX useful as thrombin inhibitors, antinflammatory agents, etc
 XX Claim 2: Page 160-161; 183pp; German.
 XX The DNA is produced by determining the amino acid sequence of isolated
 XX and highly purified VAPs, constructing DNA probes on the basis of this
 XX sequence, using the probes to search through suitable cDNA libraries,
 XX isolating cDNA that hybridises with the probes, by inserting the cDNA
 XX into a suitable vector, and using the vector to transform a host

CC organism. VAC-alpha has anticoagulant activity under certain
 CC conditions, but loses this activity in the event of severe bleeding.
 CC It acts by inhibiting conversion of factor X to factor Xa and conversion
 CC of prothrombin to thrombin. It is structurally related to lipocortin I
 CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
 CC has similar antiinflammatory and phospholipase inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 963 BP; 284 A; 183 C; 242 G; 254 T; 0 other;
 QY Query Match 97.2%; Score 953.6; DB 9; Length 963;
 Db Best Local Similarity 99.6%; Pred. No. 4.2e-267;
 Mismatches 956; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 22 ATGGCACAGTCTTCAGAGGCACCTGTGACTGTACTTCCCTGGATTTGATCAGCGGGCTGAT 81
 Db 1 ATGGCACAGTCTTCAGAGGCACCTGTGACTGTACTTCCCTGGATTTGATCAGCGGGCTGAT 60
 QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCTGACT 141
 Db 61 GCAGACACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCTGACT 120
 QY 142 CTGTTGACATCCGGAAGTAACTGCTCAGGCCAGGAATCTCTGCAGCTTTTAAAGACTCTG 201
 Db 121 CTGTTGACATCCGGAAGTAACTGCTCAGGCCAGGAATCTCTGCAGCTTTTAAAGACTCTG 180
 QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAATAATTA 261
 Db 181 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAATAATTA 240
 QY 262 ATTGTGGCTCTGATGAAACCCCTCTGGCTTTATGATGCTTATGAACTGAAACATGCTTTG 321
 Db 241 ATTGTGGCTCTGATGAAACCCCTCTGGCTTTATGATGCTTATGAACTGAAACATGCTTTG 300
 QY 322 AAGGAGCTGGAAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 Db 301 AAGGAGCTGGAAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 360
 QY 382 GAACCTGAGAGCCATCAACAACTTTATGAAGAAGATATGGCTCAAGCTGGAAGATGAC 441
 Db 361 GAACCTGAGAGCCATCAACAACTTTATGAAGAAGATATGGCTCAAGCTGGAAGATGAC 420
 QY 442 GTGGTGGGGACACTTCAAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCCAGGCTAAC 501
 Db 421 GTGGTGGGGACACTTCAAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCCAGGCTAAC 480
 QY 502 AGAGACCTGATGCTGGAAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 Db 481 AGAGACCTGATGCTGGAAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 540
 QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 621
 Db 541 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 600
 QY 622 CGAGTGTCTCTCATTTTGAAGAAAGTGTGTTGACAAAGTACATGACTATATCAGGATTTCAA 681
 Db 601 CGAGTGTCTCTCATTTTGAAGAAAGTGTGTTGACAAAGTACATGACTATATCAGGATTTCAA 660
 QY 682 ATTGAGAAACCATTTGACCGGAGACTTCTGCGCAATTTAGAGCAACTACTCTCTCTGCTGT 741
 Db 661 ATTGAGAAACCATTTGACCGGAGACTTCTGCGCAATTTAGAGCAACTACTCTCTCTGCTGT 720
 QY 742 GTGAATCTATTTCGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 801
 Db 721 GTGAATCTATTTCGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 780
 QY 802 GGAGCTGGACAGATGATCATCCCTCATCAGAGTCATGTTTCCAGGAGTGAGATTCAT 861
 Db 781 GGAGCTGGACAGATGATCATCCCTCATCAGAGTCATGTTTCCAGGAGTGAGATTCAT 840
 QY 862 CTGTTTACATCAGGAAGGAGTTTGGCAAGAAATTTGGCCACCTCTCTTTATTCATGAT 921
 Db 840 CTGTTTACATCAGGAAGGAGTTTGGCAAGAAATTTGGCCACCTCTCTTTATTCATGAT 900

Db 841 CTGTTTAAACATCAGGAAGAGGTTTGTAGGAAGAAATTTGCCACCTCTCTTTTATTCATGATT 900
Qy 922 AAGGAGATACATCTGGGACTATAAGAAAGCTTCTGCTGCTCTCCGGAGAGATGAC 981
Db 901 AAGGAGATACATCTGGGACTATAAGAAAGCTTCTGCTGCTCTGGAGAAGATGAC 960

RESULT 14
AAN90599 standard; cDNA; 1574 BP.
XX AC AAN90599;
XX 22-DEC-1989 (first entry)
DE Human lipocortin-V.
XX Human lipocortin-V; lambdaRliipo V-1; anti-inflammatory agent.
XX Homo sapiens.
FH Key Location/Qualifiers
FT mat_peptide complement (143..1102)
ET /*tag= a
XX EP330396-A.
XX 30-AUG-1989.
XX 20-FEB-1989; 89EP-0301603.
XX 26-FEB-1988; 88US-0160866.
XX (BIOJ) BIOGEN INC.
XX Wallner BP, Pepinsky RB, Browning JL;
XX WPI; 1989-250486/35.
DR P-PSDB; AAP91363.
XX Human lipocortin cpds. III, IV, V, and VI - used in treatment of
PT arthritic, allergic, dermatologic, ophthalmic and collagen disorders
PT involving inflammatory processes.
XX Claim 4; fig 4; 32pp; English.
XX Human lipocortin-V was isolated from a lambda gt10 human peripheral
CC blood lymphocyte cDNA library with rat lipocortin-V cDNA of lambda
CC Rliipo V-1 as probe. Lipocortins are anti-inflammatory agents and can
CC be used to treat arthritic, allergic, dermatologic, ophthalmic, and
CC collagen diseases.
CC See also AAP91362, AAN90598, and AAP91363.
XX Sequence 1574 BP; 428 A; 334 C; 366 G; 446 T; 0 other;

Query Match 97.0%; Score 952; DB 10; Length 1574;
Best Local Similarity 99.5%; Pred. No. 1.6e-266;
Matches 955; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 22 ATGCACAGGTTCTCAGAGGCATCTGACTGCTCCCTGGATTGTAGCGGGCTGAT 81
Db 143 ATGCACAGGTTCTCAGAGGCATCTGACTGCTCCCTGGATTGTAGCGGGCTGAT 202
Oy 82 GCAGAACTCTTCGGAAGGCTATCAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
Db 203 GCAGAACTCTTCGGAAGGCTATCAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 262
Oy 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201
Db 263 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 322
Oy 202 TTGGGAGGATCTCTCGATGACCTGAAATCAGAACTAATCGAAAATTTGAAAAATTA 261
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Db 323 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 382
Qy 262 ATTGTGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACGAAACATGCCTTG 321
Db 383 ATTGTGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACGAAACATGCCTTG 442
Oy 322 AAGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 443 AAGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 502
Oy 382 GAAGTGAAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 441
Db 503 GAAGTGAAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 562
Oy 442 GTGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCTTCAGGCTAAC 501
Db 563 GTGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCTTCAGGCTAAC 622
Oy 502 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
Db 623 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 682
Oy 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAACA 621
Db 683 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAACA 742
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Db 743 CGAAGTGTCTCATTTGAGTTCGTTGGTTCACAAAGTACATGACTATATCAGGATTTCAA 802
Oy 682 ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTCGCTGTT 741
Db 803 ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTCGCTGTT 862
Oy 742 GTGAATCTATTTCGAAGTATACCTGCTTCCAGAGACCTCTTATTCATGCTATGAG 801
Db 863 GTGAATCTATTTCGAAGTATACCTGCTTCCAGAGACCTCTTATTCATGCTATGAG 922
Oy 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTTCATGGTTTCCAGAGGTGAGATGAT 861
Db 923 GGAGCTGGGACAGATGATCATACCTCATCAGAGTTCATGGTTTCCAGAGGTGAGATGAT 982
Oy 862 CTGTTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTTGGCCACCTCTCTTTATTCATGATT 921
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Oy 922 AAGGAGATACATCTGGGACTATAAGAAAGCTTCTCTGCTGCTCTCCGGAGAGATGAC 981
Db 1043 AAGGAGATACATCTGGGACTATAAGAAAGCTTCTCTGCTGCTCTGFGGAGAGATGAC 1102

RESULT 15
AAF18269
ID AAF18269 standard; DNA; 1637 BP.
XX AC AAF18269;
XX 14-MAR-2001 (first entry)
XX Lung cancer associated polynucleotide sequence SEQ ID 288.
DE Human; lung cancer associated protein; neuroprotective; cytostatic;
XX cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antineoplastic; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disease; reproductive;
KW proliferative disorder; wound healing; infectious disease; ds.
XX Homo sapiens.
OS WO2000055180-A2.
PN 21-SEP-2000.
XX PD
XX

PF 08-MAR-2000; 2000WO-US05918.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Ruben SM;
XX
XX WPI: 2000-587514/55.
DR P-PSDB; AAB58393.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX
XX Claim 1; Page 746; 1425pp; English.
XX
XX Polynucleotide sequences AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX
XX
SQ Sequence 1637 BP; 455 A; 349 C; 378 G; 450 T; 5 other;

Query Match 96.2%; Score 943.8; DB 21; Length 1637;
Best Local Similarity 99.6%; Pred. No. 3.9e-264;
Matches 956; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 293 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCGCAGCTTTTAAAGACTCTG 352
QY 202 TTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAATA 261
DB 353 TTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAATA 412
QY 262 ATTGCGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 321
DB 413 ATTGCGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 472
QY 322 AAGGGAGCTGGAAACAAATCAAAAGTACTGACAGAAATTTTGGCTTCAAGGACACCTGAA 381
DB 473 AAGGGAGCTGGAAACAAATCAAAAGTACTGACAGAAATTTTGGCTTCAAGGACACCTGAA 532
QY 382 GAACGTAGAGCCATCAACAAAGTTTATGAAGAGATATGGCTCAGGCTGGAAGATGAC 441
DB 533 GAACGTAGAGCCATCAACAAAGTTTATGAAGAGATATGGCTCAGGCTGGAAGATGAC 592
QY 442 GTGGTGGGGGACACTTCAGGGTACTACGAGCGGATGTGGTGGTCTCCTTCAGGCTAAC 501
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DB 593 GTGGTGGGGGACACACTTCAGGGTACTACACGCGATGTTGGTGTCTCTCCTTCAGGCTAAC 652
QY 502 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAAACAAGATGCTCAGGCTTTATTT 561
DB 653 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAAACAAGATGCTCAGGCTTTATTT 712
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTTGAACA 621
DB 713 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTTGAACA 772
QY 622 CGAAGTGTCTCTCATTTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 681
DB 773 CGAAGTGT-NCATTTGAGAAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 831
QY 682 ATTGAGGAACCATTTGACCGGAGACTTCTGSCAATTTAGAGCAACTACTCCTTCGCTGT 741
DB 832 ATTGAGGAACCATTTGACCGGAGACTTCTGSCAATTTAGAGCAACTACTCCTTCGCTGT 891
QY 742 GTGAATCTATTTCGAAGTATAGCTGCTACCTTTCGAGAGACCTCTCTATTATGCTATGAAG 801
DB 892 GTGAATCTATTTCGAAGTATAGCTGCTACCTTTCGAGAGACCTCTCTATTATGCTATGAAG 951
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QY 862 CTGTTTAAACATCAGGAAGGAGTTAGGAAGAATTTGCCACCTCTCTTTTATCCCATGAT 921
DB 1012 CTGTTTAAACATCAGGAAGGAGTTAGGAAGAATTTGCCACCTCTCTTTTATCCCATGAT 1071
QY 922 AAGGAGATACATCTGGGGACTATAGAAGGCTCTTCTGCTGCTCTCCGGAGAAGATGAC 981
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Search completed: August 28, 2003, 16:03:35
Job time : 218.333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:43:40 ; Search time 216.333 Seconds
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	981	100.0	981	22 AAC91368 Modified human ann
2	977.8	99.5	981	22 AAC91369 Modified human ann
3	976.2	99.5	981	22 AAC91370 Modified human ann
4	958.2	97.7	1466	10 AAN91353 Vascular anti-coag
5	956.8	97.5	1567	9 AAN81113 Plasamid contg. pla
6	956.8	97.5	1578	25 ABX63162 Human cDNA #162 di
7	956.8	97.5	1605	10 AAN91821 Endonexin II compl
8	956.6	97.5	1575	10 AAN90112 Anticoagulant PP4

9	956	97.5	1803	21 AAAL1241 Annexin V/uokinas
10	955.2	97.4	1454	9 AAN82107 PAP-I cDNA from hu
11	955.2	97.4	1460	12 AAQ12679 PAP-I. Homo sapie
12	954.6	97.3	1466	9 AAN80801 Sequence encoding
13	953.6	97.2	963	9 AAN80873 Sequence encoding
14	952	97.0	1574	10 AAN90599 Human lipocortin-V
15	943.8	96.2	1637	21 AAF18269 Lung cancer associ
16	882	89.9	1024	25 ABX83344 Toxicologically re
17	749.4	76.4	1480	24 AB199289 Mouse ischaemic co
18	727	74.1	1417	24 ABK63699 Rat sequence diffe
19	518.4	52.8	960	25 AB221925 Human annexin V pr
20	517.8	52.8	2016	25 AB221926 Modified annexin p
21	495.8	50.5	847	25 ABX05088 Human novel polynu
22	412.2	42.0	438	12 AAQ12681 PAP-I-protein C fu
23	412.2	42.0	1529	12 AAQ12680 PAP-I-protein C fu
24	365	37.2	422	25 ABX47939 Bovine EST associa
25	356.2	36.3	409	25 ABX36749 Bovine EST associa
26	351	35.8	1326	10 AAN90772 Coding strand of c
27	350.4	35.7	410	25 ABX42696 Bovine EST associa
28	349.4	35.6	1982	24 ABX76372 cDNA encoding huma
29	349.4	35.6	2155	21 AAC77826 Human cancer assoc
30	349.4	35.6	2181	22 AAH72826 Human cervical can
31	349.4	35.6	2213	20 AAZ77514 Human ovarian tumo
32	349.4	35.6	2300	25 ABX63220 Human cDNA #220 di
33	348.2	35.5	2360	11 AAQ02888 Human placenta-der
34	348.2	35.5	2468	23 AAS93800 DNA encoding novel
35	348.2	35.5	2468	24 ABK84730 Human cDNA differe
36	348.2	35.5	2468	24 ABN97346 Gene #3844 used to
37	346.6	35.3	2016	11 AAQ02887 cDNA of human plac
38	346.6	35.3	2056	25 ABX72249 Human NOVX polynuc
39	319.8	32.6	529	24 ABQ59306 Human colon cancer
40	315.2	32.1	686	24 ABT09335 Phase-1 Rat CT gen
41	311	31.7	401	21 AAC65957 Human lung cancer-
42	311	31.7	401	24 ABQ92362 Human lung cancer
43	311	31.7	401	24 ABL49176 Human lung tumour
44	310.8	31.7	2305	14 AAQ39149 Annexin XI gene in
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ALIGNMENTS

RESULT 1	
AAC91368	
ID AAC91368 standard; DNA; 981 BP.	
XX	
AC AAC91368;	
XX	
DT 16-MAR-2001 (first entry)	
XX	
DE Modified human annexin nucleotide sequence, SEQ ID NO: 1.	
XX	
KW Human; annexin; chelation site; nuclear imaging; apoptosis;	
KW transplant rejection; ds.	
XX	
OS Homo sapiens.	
XX	
PN WO200073332-A1.	
XX	
PD 07-DEC-2000.	
XX	
PF 25-MAY-2000; 2000WO-US14324.	
XX	
PR 01-JUN-1999; 99US-0324096.	
XX	
PA (UNIW) UNIV WASHINGTON.	
XX	
PI Tait JF, Brown DS;	
XX	
DR WPI: 2001-080465/09.	
DR P-PSDB; AAB50863.	
XX	
PT Novel modified annexin useful for imaging vascular thrombi and	

Query Match 99.7%; Score 977.8; DB 22; Length 981;
Best Local Similarity 99.8%; Pred. No. 6.6e-274;
Matches 979; Conservative 0; Mismatches 2; Indels 0;


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1 ATGCGAGTGGCTGTGCCATATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCT 60
QY 61 GGATTTGATCAGGGGCTGATGAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GGATTTGATCAGGGGCTGATGAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
QY 121 GATGAGGAGAGCACTCTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATC 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 GATGAGGAGAGCACTCTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATC 180
QY 181 TCTGCACTTTTAAGACTCTGTTGGCAGGAGTCTTCTGATGACCTGAAATCAGAACTA 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 241 ACTGGAAATTTGAAATAATTAATGTCCTGATGAAACCTCTCGGCTTTATGATGCT 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 301 TATGAATGAACATGCTTTGAAGGAGCTGGAAACAAATGAAAAGTACTGACAGAAAT 360
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TATGAATGAACATGCTTTGAAGGAGCTGGAAACAAATGAAAAGTACTGACAGAAAT 360
QY 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAATAT 420
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAATAT 420
QY 421 GGCTCAAGCTGGAAGATGCTGTTGGGGGACACTTCAGGGTACTACCGCGGATCTTG 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
421 GGCTCAAGCTGGAAGATGCTGTTGGGGGACACTTCAGGGTACTACCGCGGATCTTG 480
QY 481 GTGCTTCTCCTTCAAGGCTAAGAGACCTGATGCTGGAATTTGATGAAGTCAAGTTGAA 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 GTGCTTCTCCTTCAAGGCTAAGAGACCTGATGCTGGAATTTGATGAAGTCAAGTTGAA 540
QY 541 CAAGATGCTCAGGCTTTATTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
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541 CAAGATGCTCAGGCTTTATTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
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QY 661 ATGACTATATCAGGATTTCAAATTTAGGAAACCAATTCACCGCGAGACTTCTGGCAATTA 720
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661 ATGACTATATCAGGATTTCAAATTTAGGAAACCAATTCACCGCGAGACTTCTGGCAATTA 720
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RESULT 3

AAC91370

ID AAC91370 standard; DNA; 981 BP.

XX

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AC AAC91370;
XX 16-MAR-2001 (first entry)
DE Modified human annexin nucleotide sequence, SEQ ID NO: 5.
XX Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplant rejection; ds.
XX Homo sapiens.
XX WO200073332-A1.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US14324.
XX 01-JUN-1999; 99US-0324096.
XX (UNIW ) UNIV WASHINGTON.
XX Tait JF, Brown DS;
XX WPI; 2001-080465/09.
XX P-PSDB; AAB50865.
XX Novel modified annexin useful for imaging vascular thrombi and
PT apoptosis, has N-terminal chelation site comprising amino acid
PT extension which comprises a glycine and a cysteine residue.
XX
XX Claim 27; Page 35-37; 39pp; English.
XX
CC The present sequence encodes a modified annexin having an N-terminal
CC chelation site, which comprises an amino acid extension including a
CC glycine and a cysteine residue. The modified annexin is useful for
CC imaging vascular thrombi or apoptosis which is associated with response
CC to a chemotherapeutic agent or with rejection as a result of
CC transplantation. The modified annexin can effectively chelate a
CC radionuclide and retain annexin bioactivity. It can be readily prepared
CC in high radiochemical yield and with high radiochemical purity. In
CC contrast to conventional conjugation chemistries that provide a
CC distribution of conjugation products, the modified annexin has a single
CC chelation site remote from the site of biological activity.
XX
SQ Sequence 981 BP; 286 A; 187 C; 250 G; 258 T; 0 other;
Query Match 99.5%; Score 976.2; DB 22; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.9e-273;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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1 ATGCGATGTCGGGTGCCCATATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCT 60
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241 ACTGGAAATTTGAAATAATTAATGTCCTGATGAAACCTCTCGGCTTTATGATGCT 300
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QY 421 GGCTCAAGCCTGGAAGATGACGTGTGGGGGACACTTCAGGTACTACACGGGATGTG 480
DB 421 GGCTCAAGCCTGGAAGATGACGTGTGGGGGACACTTCAGGTACTACACGGGATGTG 480
QY 481 GTGGTCTCCTTCAGGCTAACAGAGACCCTGATGCTGGAATGATGAAGCTCAAGTTGAA 540
DB 481 GTGGTCTCCTTCAGGCTAACAGAGACCCTGATGCTGGAATGATGAAGCTCAAGTTGAA 540
QY 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
DB 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
QY 601 TTATACACCATTTTGGAAACAGAAAGTGTCTCATTTGAGAAAGTGTTCACAAATGAC 660
DB 601 TTATACACCATTTTGGAAACAGAAAGTGTCTCATTTGAGAAAGTGTTCACAAATGAC 660
QY 661 ATGACTATATCAGGATTTCAAAATTCAGGAAACCATTTGACCGGAGACTTCTGCAATTTA 720
DB 661 ATGACTATATCAGGATTTCAAAATTCAGGAAACCATTTGACCGGAGACTTCTGCAATTTA 720
QY 721 GAGCAACTACTCCTTGTCTGTGTGAAATCTATTGAAAGTATACCTGCTTACCTTGCAGAG 780
DB 721 GAGCAACTACTCCTTGTCTGTGTGAAATCTATTGAAAGTATACCTGCTTACCTTGCAGAG 780
QY 781 ACCCTTATATGCTATGAGGAGCTGGGACAGATGATCATACCTCATCAGATCATG 840
DB 781 ACCCTTATATGCTATGAGGAGCTGGGACAGATGATCATACCTCATCAGATCATG 840
QY 841 GTTTCAGGAGTGAGATGATCTGTTTAAACATCAGGAGGAGTTTAGGAAGAAATTTTGC 900
DB 841 GTTTCAGGAGTGAGATGATCTGTTTAAACATCAGGAGGAGTTTAGGAAGAAATTTTGC 900
QY 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGAGCTATAAAGAAAGCTCTTCTG 960
DB 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGAGCTATAAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGGAGAGATGAC 981
DB 961 CTGCTCTCCGGAGAGATGAC 981
```

RESULT 4

AA91353
ID AA91353 standard; DNA; 1466 BP.

AC AA91353;

DT 25-MAR-2003 (updated)

DT 10-MAR-2003 (updated)

DT 30-JUL-1989 (first entry)

DE Vascular anti-coagulating protein-alpha cDNA.

KW Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas; ss.

OS Chimeric - Homo sapiens.

OS Chimeric - Mus musculus.

FH Key Location/Qualifiers

FT CDS 35..996

FT /tag= a

FT /label=VAC-alpha cDNA

PN DE3810331-A.

XX 05-OCT-1989.

PF 26-MAR-1988; 88DE-3810331.

XX 26-MAR-1988; 88DE-3810331.
PR (BOEH) BOEHRINGER INGELHEIM.
PA
XX Gunther A;
XX WPI: 1989-293724/41.
XX P-PSDB; AAP91953.
XX Monoclonal antibodies to vascular anti-coagulating proteins - and
XX hybridomas producing such antibodies.
XX Disclosure; fig 1; 11pp; German.
XX The vascular anti-coagulating protein (VAC)-alpha encoded by this cDNA
XX is used in the preparation of monoclonal antibodies (MABs). The
XX VAC-alpha is injected into a host animal, in conjunction with eg keyhole
XX limpet haemocyanin, and the B-cells from the immunised hosts are then
XX fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9)
XX produce Abs specific to VAC-alpha. The Abs can be used as immunosay
XX reagents to detect VAC proteins, as affinity ligands for purification of
XX VACs and as medicaments for binding and/or neutralising VAC proteins in
XX vivo. See also AAN91354 and EP-181465.
XX (Updated on 10-MAR-2003 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 1466 BP; 423 A; 291 C; 327 G; 425 T; 0 other;

Query Match 97.7%; Score 958.2; DB 10; Length 1466;
Best Local Similarity 99.2%; Pred. No. 4e-268;
Matches 963; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 11 GCGGTGGCCATATGCGACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATG 70
DB 24 GAGTACTGCTATGCGACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATG 83
QY 71 AGCGGGCTGATGCGAAGAACTCTTCGGAAGGCTTATGAAAGGCTTGGGCAAGATGAGGAGA 130
DB 84 AGCGGGCTGATGCGAAGAACTCTTCGGAAGGCTTATGAAAGGCTTGGGCAAGATGAGGAGA 143
QY 131 GCATCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGCAAAATCTCTGCAGCTT 190
DB 144 GCATCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGCAAAATCTCTGCAGCTT 203
QY 191 TTAAGACTCTGTTGGCAGGGATCTTCTGGATGACTTGAATCAGAACTAAGTGAAGAAAT 250
DB 204 TTAAGACTCTGTTGGCAGGGATCTTCTGGATGACTTGAATCAGAACTAAGTGAAGAAAT 263
QY 251 TTGAAAAATTAATTGTGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGACTGA 310
DB 264 TTGAAAAATTAATTGTGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGACTGA 323
QY 311 AACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATATTGCTTCAA 370
DB 324 AACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATATTGCTTCAA 383
QY 371 GGACACCTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGAAATATGCTCAAGCC 430
DB 384 GGACACCTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGAAATATGCTCAAGCC 443
QY 431 TGAAGAGTACGTGTGGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCC 490
DB 444 TGAAGAGTACGTGTGGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCC 503
QY 491 TTCAGGCTAACAGAGACCCCTGATGCTGGAATGATGAAGCACTCAAGTTGACAGATGCTC 550
DB 504 TTCAGGCTAACAGAGACCCCTGATGCTGGAATGATGAAGCACTCAAGTTGACAGATGCTC 563
QY 551 AGGCTTTTATTTTCAGGCTGAGAACTTAAATGGGGGACAGATGAAGAAAAAGTTTATCAGCA 610
DB 564 AGGCTTTTATTTTCAGGCTGAGAACTTAAATGGGGGACAGATGAAGAAAAAGTTTATCAGCA 623

Qy 611 TCTTTGGAACACGAAAGTGTCTCATTTTGAGAAAGGTGTTTGACAAGTACATGACTATAT 670
 Db 624 TCTTTGGAACACGAAAGTGTCTCATTTTGAGAAAGGTGTTTGACAAGTACATGACTATAT 683
 Qy 671 CAGGATTTCAAATTGAGAAACCATTCACCGGAGACTCTGGCAATTAGAGCAACTAC 730
 Db 684 CAGGATTTCAAATTGAGAAACCATTCACCGGAGACTCTGGCAATTAGAGCAACTAC 743
 Qy 731 TCCCTGTGTGTGAAATCTATTGCGAAGTATACCTGCTTACCTTTGCGAGACCCCTCTATT 790
 Db 744 TCCCTGTGTGTGAAATCTATTGCGAAGTATACCTGCTTACCTTTGCGAGACCCCTCTATT 803
 Qy 791 ATGCTATGAGGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGTTTCCAGGA 850
 Db 804 ATGCTATGAGGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGTTTCCAGGA 863
 Qy 851 GTGAGATTGATCTCTTTAAACATCAGGAGGAGTTTAGGAAGATTTTGCCACCTCTCTTT 910
 Db 864 GTGAGATTGATCTCTTTAAACATCAGGAGGAGTTTAGGAAGATTTTGCCACCTCTCTTT 923
 Qy 911 ATTCCATGATTAAAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCCG 970
 Db 924 ATTCCATGATTAAAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTG 983
 Qy 971 GAGAAGATGAC 981
 Db 984 GAGAAGATGAC 994

RESULT 5

AA81113
 ID AA81113 standard; DNA; 1567 BP.
 XX
 AC AA81113;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 12-NOV-1990 (first entry)
 XX
 DE Plasmid contg. placental coagulation inhibitor gene.
 XX
 KW Placental coagulation inhibitor; disseminated vascular coagulation;
 KW thrombosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 136..1098
 FT /*tag= a
 FT /label=placental coagulation inhibitor
 FT polyA_signal 1568
 FT /*tag= b
 XX
 PN EP279459-A.
 PN JP03219875-A.
 XX
 PD 24-AUG-1988.
 XX
 PF 19-FEB-1988; 88EP-0102458.
 XX
 PR 20-FEB-1987; 87JP-0037227.
 PR 23-JUL-1987; 87JP-0184428.
 XX
 PA (KOWA) KOWA CO LTD.
 XX
 PI Saino Y, Iwasaki A, Suda M;
 XX
 DR WPI; 1988-236733/34.
 DR WPI; 1991-329110/45.
 DR P-PSDB; AAP80511.
 XX
 PT Recombinant placental coagulation inhibitor - useful for the prevention
 PT and treatment of thromboses or disseminated intra-vascular coagulation.

XX Disclosure; Page ?; p; English.
 XX

CC This recombinant DNA sequence comprises a promoter region, ribosome
 CC binding site, initiation sequence, termination codon and a trans-
 CC cription terminator in addition to the placental coagulation inhibitor
 CC gene. The polypeptide produced on culturing of transformed host cells
 CC exhibits strong anticoagulant activities and is useful for the treat-
 CC ment and prevention of eg thrombosis or disseminated intravascular
 CC coagulation in the brain, heart and peripheral blood vessels.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 1567 BP; 430 A; 332 C; 358 G; 447 T; 0 other;

Query Match 97.5%; Score 956.8; DB 9; Length 1567;
 Best Local Similarity 99.8%; Pred. No. 1.le-267;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 22 ATGCGACAGGTTCTCAGAGGCACGTGACTGCTTCCCTGGATTGTGATGAGCGGCTGAT 81
 Db 136 ATGCGACAGGTTCTCAGAGGCACGTGACTGCTTCCCTGGATTGTGATGAGCGGCTGAT 195
 Qy 82 GCAGAACTCTTTCGAAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGCATCCTGACT 141
 Db 196 GCAGAACTCTTTCGAAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGCATCCTGACT 255
 Qy 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAAGACTG 201
 Db 256 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAAGACTG 315
 Qy 202 TTTGCGAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATTTGAAAAATTA 261
 Db 316 TTTGCGAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATTTGAAAAATTA 375
 Qy 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACATGAAACATG 321
 Db 376 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACATGAAACATG 435
 Qy 322 AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 Db 436 AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 495
 Qy 382 GAACTGAGAGCCATCAACAAAGTTTATCAAGAAAGATATGCTCAAGCTCGAAGATCAC 441
 Db 496 GAACTGAGAGCCATCAACAAAGTTTATCAAGAAAGATATGCTCAAGCTCGAAGATCAC 555
 Qy 442 GTGTTGGGGACACTTCAGGGTACTTACCAGCGGATGTTGGTGTCTCTCTTCAGGCTAAC 501
 Db 556 GTGTTGGGGACACTTCAGGGTACTTACCAGCGGATGTTGGTGTCTCTCTTCAGGCTAAC 615
 Qy 502 AGAGACCTGATGCTGGAATTTGAAAGTCAAGTGAACAGATGCTCAGGCTTTTATT 561
 Db 616 AGAGACCTGATGCTGGAATTTGAAAGTCAAGTGAACAGATGCTCAGGCTTTTATT 675
 Qy 562 CAGGCTGGAGACTTAATGGGGACAGATCAAGAAAGTTTATCACCATCTTTGGAACA 621
 Db 676 CAGGCTGGAGACTTAATGGGGACAGATCAAGAAAGTTTATCACCATCTTTGGAACA 735
 Qy 622 CGAAGTGTCTCATTTTGAGAAAGTGTCTTGCACAGTACATGACTATATCAGGATTTCAA 681
 Db 736 CGAAGTGTCTCATTTTGAGAAAGTGTCTTGCACAGTACATGACTATATCAGGATTTCAA 795
 Qy 682 ATTGAGGAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGTCTTT 741
 Db 796 ATTGAGGAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGTCTTT 855
 Qy 742 GTGAATCTATTTCGAAGTATACCTTGCCTTACCTTCAGAGAGCCCTCTATTATGCTATGAG 801
 Db 856 GTGAATCTATTTCGAAGTATACCTTGCCTTACCTTCAGAGAGCCCTCTATTATGCTATGAG 915

QY 802 GGAGCTGGGACAGATGATCATCCCTCATCAGAGTCATGGTTCCAGGAGTGAGATTGAT 861
 DB 916 GGAGCTGGGACAGATGATCATCCCTCATCAGAGTCATGGTTCCAGGAGTGAGATTGAT 975
 QY 862 CTGTTTAAATCAGGAGAGGAGTTAGGAGAAATTTGGCCACCTCTCTTTATCCATGATT 921
 DB 976 CTGTTTAAATCAGGAGAGGAGTTAGGAGAAATTTGGCCACCTCTCTTTATCCATGATT 1035
 QY 922 AAGGAGATACATCTGGGAGCTATAGAAAGCTCTTCTGCTCTCCGGAGAGATGAC 981
 DB 1036 AAGGAGATACATCTGGGAGCTATAGAAAGCTCTTCTGCTCTGGAGAGATGAC 1095

RESULT 6
 ABX63162
 ID ABX63162 standard; cDNA; 1578 BP.

XX ABX63162;

DT 25-FEB-2003 (first entry)

DE Human cDNA #162 differentially expressed in activated vascular tissue.

XX Human; gene; 88; vascular tissue; cytostatic; atherosclerosis;
 KW cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke;

XX Homo sapiens.

XX US2002137081-A1.

XX 26-SEP-2002.

XX 08-JAN-2002; 2002US-0044090.

XX 28-JUL-2000; 2000US-222459P.

XX 08-JAN-2001; 2001US-260483P.

XX (BAND/) BANDMAN O.

XX Bandman O;

XX WPI; 2003-110597/10.

DR Combination for diagnosing, staging, treating, or monitoring the
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several cDNAs that are differentially expressed in activated
 PT vascular tissue -

XX Claim 1; Page -; 18pp; English.

XX This invention relates to a combination comprising several cDNAs that
 CC are differentially expressed in activated vascular tissue. The invention
 CC also discloses a high throughput method for detecting differentially
 CC expressed cDNAs in a sample. The cDNAs of the invention may have
 CC antiatherosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
 CC gynaecological; vasotropic and cerebroprotective activities and may be
 CC used in gene therapy. The cDNAs of the invention may be used in a
 CC high-throughput methods for detecting differential expression of one or
 CC more cDNAs in a sample, or screening several molecules or compounds to
 CC identify a molecule or compound that specifically binds a cDNA of the
 CC invention. A protein encoded by the cDNA may be used to screen several
 CC molecules or compounds to identify a ligand that specifically binds to
 CC the protein, or to produce or purify an antibody to the protein that can
 CC be used to detect a protein in a sample or purify a natural or
 CC recombinant protein from a sample. The nucleotides may be useful for
 CC diagnosing, staging, treating, or monitoring the progression of
 CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
 CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-
 CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used
 CC for large-scale genetic or gene expression analysis of several new

CC nucleic acid molecules. Antibodies to the proteins encoded by the
 CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic
 CC or acute diseases associated with abnormalities in the expression,
 CC amount or distribution of the protein. The present sequence
 CC represents a cDNA of the invention that is differentially expressed in
 CC activated vascular tissue.
 CC Note: The sequence data for this patent did not form part of the
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>.

XX Sequence 1578 BP; 432 A; 335 C; 360 G; 451 T; 0 other;

Query Match 97.5%; Score 956.8; DB 25; Length 1578;
 Best Local Similarity 99.8%; Pred. No. 1.1e-267;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTCATCAGCGGCTGAT 81
 DB 142 ATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTCATCAGCGGCTGAT 201
 QY 82 GCAGAAACTCTTCGGAGAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCTGACT 141
 DB 202 GCAGAAACTCTTCGGAGAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCTGACT 261
 QY 142 CTGTTGACATCCCGAAGTAATGCTCAGCCCGAGGAAATCTCTGACGCTTTTAAAGACTCTG 201
 DB 262 CTGTTGACATCCCGAAGTAATGCTCAGCCCGAGGAAATCTCTGACGCTTTTAAAGACTCTG 321
 QY 202 TTTGGCAGGAGTCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAATAATTA 261
 DB 322 TTTGGCAGGAGTCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAATAATTA 381
 QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAACATGCTCTTG 321
 DB 382 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAACATGCTCTTG 441
 QY 322 AAGGAGCTGGGAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 DB 442 AAGGAGCTGGGAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 501
 QY 382 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGGCTCAAGCCTCGAAGATGAC 441
 DB 502 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGGCTCAAGCCTCGAAGATGAC 561
 QY 442 GTGGTGGGGACACTTCAGGGTACTACACGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 501
 DB 562 GTGGTGGGGACACTTCAGGGTACTACACGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 621
 QY 502 AGAGACCCCTGATGCTGGAAATTCATGAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 DB 622 AGAGACCCCTGATGCTGGAAATTCATGAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 681
 QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 621
 DB 682 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 741
 QY 622 CGAAGTGTCTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 681
 DB 742 CGAAGTGTCTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 801
 QY 682 ATTGAGGAACCATTTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTTT 741
 DB 802 ATTGAGGAACCATTTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTTT 861
 QY 742 GTGAATCTATTTCGAGATATAGCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 801
 DB 862 GTGAATCTATTTCGAGATATAGCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 921
 QY 802 GGAGCTGGGACAGATGATCATCCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT 861
 DB 922 GGAGCTGGGACAGATGATCATCCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT 981
 QY 862 CTGTTTAAATCAGGAGAGGAGTTAGGAGAAATTTGGCCACCTCTCTTTATCCATGATT 921

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Db      982 CTGTTTAACATCAGGAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTCATGATT 1041
Qy      922 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAGATGAC 981
Db      1042 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCTGTGGAGAAGATGAC 1101

RESULT 7
AAN91821
ID      AAN91821 standard; DNA; 1605 BP.
XX
AC      AAN91821;
XX
DT      25-MAR-2003 (updated)
DT      16-MAR-1990 (first entry)
XX
DE      Endonexin II complete cDNA.
XX
KW      Placenta; blood coagulation
XX
OS      Homo sapiens (human).
XX
FH      Key      Location/Qualifiers
FT      CDS      160..1119
FT      FT      /*tag= a
XX
PN      EP339285-A.
XX
PD      02-NOV-1989.
XX
PF      30-MAR-1989; 89EP-0105626.
XX
PR      31-MAR-1988; 88US-0176802.
XX
PA      (RORE ) RORER INT OVERSEAS INC.
XX
PI      Kaplan R, Jaye M;
XX
DR      WPI; 1989-317181/44.
XX
DR      P-PSDB; AAN91021.
XX
PT      Recombinant human endonexin II - which inhibits blood coagulation
PT      and phospholipase A2 and is used as an antiinflammatory agent
XX
PS      Claim 1: fig. 1; 13pp; English.
XX
CC      hENII is a calcium and phospholipid binding protein.
CC      (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ      Sequence 1605 BP; 447 A; 337 C; 366 G; 455 T; 0 other;

Query Match      97.5%; Score 956.8; DB 10; Length 1605;
Best Local Similarity 99.8%; Pred. No. 1.1e-267;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      22 ATGSCACAGGTTCTCAGAGGCACCTGTGACTTCCCTGATTTGATGAGCGGCTGAT 81
Db      160 ATGSCACAGGTTCTCAGAGGCACCTGTGACTTCCCTGATTTGATGAGCGGCTGAT 219
Qy      82 GCAGAAACTCTTGGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
Db      220 GCAGAAACTCTTGGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 279
Qy      142 CTGTTGACATCCCGAAGTATGCTCAGCGCCAGGAATCTGTCAGCTTTTAAGACTCTG 201
Db      280 CTGTTGACATCCCGAAGTATGCTCAGCGCCAGGAATCTGTCAGCTTTTAAGACTCTG 339
Qy      202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTTAATGGAATAATTTGAAAAATTA 261
Db      340 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTTAATGGAATAATTTGAAAAATTA 399
Qy      262 ATTGTGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCGCTTG 321

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Db      400 ATTGTGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCCCTTG 459
Qy      322 AAGGAGCTGAACAAATGAAAAGTACTGACAGAAATATTGCTTCAAGCACACCTGAA 381
Db      460 AAGGAGCTGAACAAATGAAAAGTACTGACAGAAATATTGCTTCAAGCACACCTGAA 519
Qy      382 GAACGTGAGAGCATCAAAAGTATTATGAAGAAGAAATATGGCTCAAGCTCGAAGATGAC 441
Db      520 GAACGTGAGAGCATCAAAAGTATTATGAAGAAGAAATATGGCTCAAGCTCGAAGATGAC 579
Qy      442 GTGTGGGGGACACTTCAGGCTACTACACGGGATGTTGGTGGTCTCTCTCAGGCTAAC 501
Db      580 GTGTGGGGGACACTTCAGGCTACTACACGGGATGTTGGTGGTCTCTCTCAGGCTAAC 639
Qy      502 AGACACCTGATGCTGGNAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 561
Db      640 AGACACCTGATGCTGGNAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 699
Qy      562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTATTATCACCACCTCTTTGGAACA 621
Db      700 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTATTATCACCACCTCTTTGGAACA 759
Qy      622 CGAAGTGTCTCATTTGAGAAAGGTGTTGACAAGTACATGACTATATCAGGATTTCAA 681
Db      760 CGAAGTGTCTCATTTGAGAAAGGTGTTGACAAGTACATGACTATATCAGGATTTCAA 819
Qy      682 ATTGAGGNAACCATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGCCTGTT 741
Db      820 ATTGAGGNAACCATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGCCTGTT 879
Qy      742 GTGAAATCTATTGAAAGTATACCTGCCTTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 801
Db      880 GTGAAATCTATTGAAAGTATACCTGCCTTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 939
Qy      802 GGAGCTGGACAGATGATCATACCCCTCATCAGATCATGGTTTCCAGAGTGAAGATGAT 861
Db      940 GGAGCTGGACAGATGATCATACCCCTCATCAGATCATGGTTTCCAGAGTGAAGATGAT 999
Qy      862 CTGTTTAACATCAGGAAGGAGCTTTAGGAAGAAATTTGCCACCTCTCTTTATTTCCATGATT 921
Db      1000 CTGTTTAACATCAGGAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTTCCATGATT 1059
Qy      922 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC 981
Db      1060 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCTGTGTGGAGAAGATGAC 1119

RESULT 8
AAN90112
ID      AAN90112 standard; DNA; 1575 BP.
XX
AC      AAN90112;
XX
DT      25-MAR-2003 (updated)
DT      01-NOV-1989 (first entry)
XX
DE      Anticoagulant PP4 DNA.
XX
KW      Anticoagulant; PP4 protein; thromboplastin.
XX
OS      Homo sapiens (human).
XX
FH      Key      Location/Qualifiers
FT      polyA_signal 1539..1575
FT      FT      /*tag= a
FT      CDS      107..1066
FT      FT      /*tag= b
XX
PN      EP318703-A.
XX
XX      07-JUN-1989.
XX
PD

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PF 29-OCT-1988; 88EP-0118039.
PR 03-NOV-1987; 87DE-3737239.
XX (BEHW) BEHRINGWERKE AG.
XX Grundmann U, Abel KJ, Kupper H;
XX WPI; 1989-166767/23.
XX New DNA sequence encoding anticoagulant p4 protein
XX - and new recombinant protein, vectors, antibodies, etc.,
XX useful therapeutically and diagnostically.
XX Claim 1; table 1; 14pp; German.
XX DNA sequence encoding anticoagulant p4 protein. This
XX inhibits blood coagulation at the thromboplastin stage.
XX The derived protein is 320 amino acids.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PR field.)
XX (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 1575 BP; 461 A; 322 C; 351 G; 441 T; 0 other;
Query Match 97.58; Score 956.6; DB 10; Length 1575;
Best Local Similarity 99.18; Pred. No. 1.2e-267;
Matches 962; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 11 GCGGTGCCATGGACAGGTTCTCAGAGGCACTGACTGACTCCCTGGATTTGATG 70
DB 96 GAGTAGTCGTATGGCCACAGGTTCTCAGAGGCACTGACTGACTCCCTGGATTTGATG 155
QY 71 AGCGGGCTGATGACAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGA 130
DB 156 AGCGGGCTGATGACAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGA 215
QY 131 GCATCTGACTCTGTTGACATCCCGAAGTAATGCTCAGGCCAGGAAATCTCTGCAGCTT 190
DB 216 GCATCTGACTCTGTTGACATCCCGAAGTAATGCTCAGGCCAGGAAATCTCTGCAGCTT 275
QY 191 TTAAAGACTCTGTTGGCAGGATCTCTGATGACCTGAACTGAACTGAACTGAACTGAACT 250
DB 276 TTAAAGACTCTGTTGGCAGGATCTCTGATGACCTGAACTGAACTGAACTGAACTGAACT 335
QY 251 TTGAAAAATTAATTTGGTCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGA 310
DB 336 TTGAAAAATTAATTTGGTCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGA 395
QY 311 AACATGCTTGAAGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAA 370
DB 396 AACATGCTTGAAGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAA 455
QY 371 GGACACTGAAGAACTGAGAGCCATCAACAACTTTATGAAAGAAATATGGCTCAAGCC 430
DB 456 GGACACTGAAGAACTGAGAGCCATCAACAACTTTATGAAAGAAATATGGCTCAAGCC 515
QY 431 TGAAGATGACGTGGTGGGGACACTTACAGGGTACTACAGCGATGTTGGTGGTCTCC 490
DB 516 TGAAGATGACGTGGTGGGGACACTTACAGGGTACTACAGCGATGTTGGTGGTCTCC 575
QY 491 TTCAGGCTACAGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTC 550
DB 576 TTCAGGCTACAGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTC 635
QY 551 AGGCTTTATTTACAGGCTGAGAACTTAAATGGGGACAGATGAGAAAGTTTATCACC 610
DB 636 AGGCTTTATTTACAGGCTGAGAACTTAAATGGGGACAGATGAGAAAGTTTATCACC 695
QY 611 TCTTTGGAACACAGAGTGTCTCATTTTGAAGAAAGTGTGTTGACAAAGTACATGACTATAT 670
DB 696 TCTTTGGAACACAGAGTGTCTCATTTTGAAGAAAGTGTGTTGACAAAGTACATGACTATAT 755

QY 671 CAGGATTTCAAAATTGAGGAAACCATTCACCGCAGAGACTTCTGGCAATTTAGAGCAACTAC 730
DB 756 CAGGATTTCAAAATTGAGGAAACCATTCACCGCAGAGACTTCTGGCAATTTAGAGCAACTAC 815
QY 731 TCCTTGCTGTTGTAATCTATTGGAAGTATACCTGCCTACCTTGCAGAGACCCCTCTATT 790
DB 816 TCCTTGCTGTTGTAATCTATTGGAAGTATACCTGCCTACCTTGCAGAGACCCCTCTATT 875
QY 791 ATGCTATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCTGTTTCCAGGA 850
DB 876 ATGCTATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCTGTTTCCAGGA 935
QY 851 GTGAGATGATCTGTTTAAACATCAGGAAGGAGTTTAGAAGAATTTGGCCACCTCTCTTT 910
DB 936 GTGAGATGATCTGTTTAAACATCAGGAAGGAGTTTAGAAGAATTTGGCCACCTCTCTTT 995
QY 911 ATTCCATGATTAAGGAGATACATCTGGGACATATAAGAAGCTCTCTGCTGCTCTCCG 970
DB 996 ATTCCATGATTAAGGAGATACATCTGGGACATATAAGAAGCTCTCTGCTGCTCTGTG 1055
QY 971 GAGAAGATGAC 981
DB 1056 GAGAAGATGAC 1066
RESULT 9
AAAL1241
ID AAAL1241 standard; DNA: 1803 BP.
XX AAAL1241;
XX 25-OCT-2000 (first entry)
XX Annexin V/urokinase fusion construct.
DE Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;
XX urokinase; insect cell; fibrinolysis; ss.
KW Unidentified.
XX Key Location/Qualifiers
FT 1..1803
FT CDS
FT /*tag= a
FT /product= "annexin V/urokinase fusion protein"
FT /note= "no start or stop codons are given at the 5'
FT or 3' ends of the sequence"
XX
XX CNL247195-A.
XX 15-MAR-2000.
XX 12-MAR-1999; 99CN-0113524.
XX 12-MAR-1999; 99CN-0113524.
XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
XX Wu X, Sun J, Yang G;
XX WPI; 2000-413098/36.
XX P-PSDB; AAY92930.
XX New thrombolytic fusion protein for targeting thrombus - comprises
XX fusion of Annexin V and urokinase
XX Claim 2; Page 2-4; 20pp; Chinese.
XX Annexin V, which has high affinity for active thrombocytes, is used
XX as a carrier molecule to build a thrombus-targeting thrombolytic fusion
XX protein. The protein is the result of expression of a fusion gene
XX (this sequence) comprising the Annexin V gene and a low-molecular
XX urokinase gene, in insect cells. The Annexin V-scu-PA-32 fusion protein,
XX expressed in insect cell strain Tn-5B1-4, has high affinity for active

Sequence 1803 BP; 495 A; 415 C; 462 G; 431 T; 0 other;

Matches 959; Conservative 0; Mismatches 5; Indels 0

837 CGAGATGGCACAGGTTCTCAGAGGCACTCTGACTGACTTCCCTGGATTGATGAGCGGGC 896

[illegible]

150 GAGCGCTGTGAGCATCCCGGAGGAGATATCTCCAGGCTTTTAGAGC 157

198 TCTGTTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAATTGAAA 257

258 ATTAATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATCAACTCAAAACATGC 317

.....

113/ CTGTGAAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACC 1196

1197 TGAAGAACTGAGAGCCATCAACAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGAAGA 1256

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[illegible]

558 ATTCAGGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTATCACCATCTTTGG 617

618 AACACCAAGCTGTCCTCATTTCAGAGAAGCGTCTTTGACACACACATCACCATCCATT 677

.....

1497 TCAATTGAGGAAACCAATTGACCGGAGACTTCTGGCAATTAGAGCAACTACTCTTGC 1556

1557 TGTGTGAAATCTTATTCGAAGTATACCTGGCTACCTTGCAGAGACCCCTCTATTATGCTAT 1616

838 TGATCTGTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTCGCCACCTCTCTTATTATCCAT 917

918 GATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGA 977

Db 1797 TGAC 1800

ID AAN8

DT 25-MAR-20

DE PAP-I CDN

KW
phosphorus
KW
deep vein

XX

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XX

05 - FEB - 19

XX
XX

XX 11

DK WF1, 1988
DR P-PSDB: A

PT isolated

XX 22

The product

CC thrombosis

Sequence	XX	XY
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Best Local S

22
Qy

82 Qy


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Db 133 CTGTTGACATCCGGAAGTAATGCTCAGCCGAGAAATCTCTGACGCTTTTAAGACTCTG 192
QY 202 TTTGGCAGGATCTCTCGATGACCTGAATCAGAACTAAGTGAAGAAATTTGAAAAATTA 261
Db 193 TTTGGCAGGATCTCTCGATGACCTGAATCAGAACTAAGTGAAGAAATTTGAAAAATTA 252
QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAACATGCCCTG 321
Db 253 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAACATGCCCTG 312
QY 322 AAGGGAGCTGGACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 313 AAGGGAGCTGGACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372
QY 382 GAAGTGAAGCCATCAACAAAGTTTATGAAGAGATATGGCTCAAGCCTGGAAGATGAC 441
Db 373 GAAGTGAAGCCATCAACAAAGTTTATGAAGAGATATGGCTCAAGCCTGGAAGATGAC 432
QY 442 GTGGTGGGGGACATTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 501
Db 433 GTGGTGGGGGACATTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 492
QY 502 AGAGACCCCTGATGCTGGAATTTGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 561
Db 493 AGAGACCCCTGATGCTGGAATTTGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 552
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 621
Db 553 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 612
QY 622 CGAAGTGTCTCATTTTGAAGAAGTGTGTTGACAAAGTACATGATATATCAGGATTTCAA 681
Db 613 CGAAGTGTCTCATTTTGAAGAAGTGTGTTGACAAAGTACATGATATATCAGGATTTCAA 672
QY 682 ATTGAGAAACATTTGACGCGAGACTTCTGGCAATTTAGACCAACTACTCTCTGCTGTT 741
Db 673 ATTGAGAAACATTTGACGCGAGACTTCTGGCAATTTAGACCAACTACTCTCTGCTGTT 732
QY 742 GTGAATCTATTTCGAAGTATACCTGCTACCTTTGAGAGACCTCTATTATCTATGAAG 801
Db 733 GTGAATCTATTTCGAAGTATACCTGCTACCTTTGAGAGACCTCTATTATCTATGAAG 792
QY 802 GGAGCTGGGACAGATGATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATGAT 861
Db 793 GGAGCTGGGACAGATGATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATGAT 852
QY 862 CTGTTTAACATCAGGAAGGATTTAGGAAGAAATTTGGCACCTCTCTTTATTCATGAT 921
Db 853 CTGTTTAACATCAGGAAGGATTTAGGAAGAAATTTGGCACCTCTCTTTATTCATGAT 912
QY 922 AAGGGAGATACATCTGGGACTATGAAGAGCTCTTCTGCTGCTCTCGGAGAGATGAC 981
Db 913 AAGGGAGATACATCTGGGACTATGAAGAGCTCTCTGCTGCTCTGTGGAGAGATGAC 972
```

RESULT 11

AAQ12679
ID AAQ12679 standard; cdna; 1460 BP.

XX AAQ12679;

AC AAQ12679;

XX (updated)

DT 25-MAR-2003 (first entry)

DT 30-SEP-1991

XX PAP-I.

DE Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;

KW glia-domain; VKDP; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

Location/Qualifiers

CDS

FT 13..972
FT /*tag= a
FT /product= PAP-I

XX WO9109953-A.

XX 11-JUL-1991.

XX 13-DEC-1990; 90WO-US07335.

XX 29-DEC-1989; 89US-0459082.

XX (ZYMO) ZYMOGENETICS INC.

XX Foster DC;

XX WPI; 1991-222905/30.

XX P-PSDB; AARI3082.

XX Recombinant prodn. of hybrid phospholipid-binding proteins -

XX comprising lipocortin phospholipid-binding domain and

XX vitamin K-dependent protein

XX Disclosure: Fig 7; 57pp; English.

XX This sequence, or a fragment of it, is used in the construction of

XX DNA sequences encoding hybrid phospholipid-binding proteins (PBP)

XX comprising at least one lipocortin phospholipid binding domain (PBD),

XX e.g. of PAP-I, joined to a gla-domainless vitamin K-dependent

XX protein, e.g. protein C or activated protein C.

XX See AAQ12680-81 for such examples.

XX A human placenta cDNA library was screened using affinity-

XX purified antibody against PAP-I in order to obtain this cDNA.

XX See also AAQ12678-81.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX SQ

Sequence 1460 BP; 436 A; 280 C; 323 G; 421 T; 0 other;

Query Match 97.4%; Score 955.2; DB 12; Length 1460;

Best Local Similarity 99.7%; Pred. No. 3e-267;

Matches 957; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 22 ATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGGGGCTGAT 81

Db 13 ATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGGGGCTGAT 72

QY 82 GCAGAACTCTTCGGAAGGCTATGAAGCTTGGGCACAGATGAGGAGCATCTGACT 141

Db 73 GCAGAACTCTTCGGAAGGCTATGAAGCTTGGGCACAGATGAGGAGCATCTGACT 132

QY 142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201

Db 133 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 192

QY 202 TTTGGCAGGATCTCTCGATGACCTGAAATCAGAACTAAGTGAAGAAATTTGAAAAATTA 261

Db 193 TTTGGCAGGATCTCTCGATGACCTGAAATCAGAACTAAGTGAAGAAATTTGAAAAATTA 252

QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAACATGCCCTG 321

Db 253 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAACATGCCCTG 312

QY 322 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381

Db 313 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372

QY 382 GAAGTGAAGCCATCAACAAAGTTTATGAAGAGATATGGCTCAAGCCTGGAAGATGAC 441

Db 373 GAAGTGAAGCCATCAACAAAGTTTATGAAGAGATATGGCTCAAGCCTGGAAGATGAC 432

QY 442 GTGGTGGGGGACATTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 501

Db 433 GTGGTGGGGGACATTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 492

QY 502 AGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
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Db 493 AGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 552
|||||
QY 562 CAGGCTGGAGAACTTAATGGGGGACAGATGAAGAAAGTTATACCACTCTTTGGAACA 621
|||||
Db 553 CAGGCTGGAGAACTTAATGGGGGACAGATGAAGAAAGTTATACCACTCTTTGGAACA 612
|||||
QY 622 CGAAGTGTCTCATTTGAGAAAGGTTTGACAAGTACATGACTATATCAGGATTTCAA 681
|||||
Db 613 CGAAGTGTCTCATTTGAGAAAGGTTTGACAAGTACATGACTATATCAGGATTTCAA 672
|||||
QY 682 ATTGAGAAACCAATGACCGGAGACTCTTGGAATTTAGAGCAACTACTCTTGTGTT 741
|||||
Db 673 ATTGAGAAACCAATGACCGGAGACTCTTGGAATTTAGAGCAACTACTCTTGTGTT 732
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QY 742 GTCAATCTATTGGAAGTACCTGCTTACCTTGCAGAGACCTCTATATGCTATGAAG 801
|||||
Db 733 GTCAATCTATTGGAAGTACCTGCTTACCTTGCAGAGACCTCTATATGCTATGAAG 792
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QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCTGTTTCCAGGAGTGAATGAT 861
|||||
Db 793 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCTGTTTCCAGGAGTGAATGAT 852
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QY 862 CTGTTTAACATCAGGAGGAGTTTAGAAGAAATTTGCCACCTCTCTTTATCCATGATT 921
|||||
Db 853 CTGTTTAACATCAGGAGGAGTTTAGAAGAAATTTGCCACCTCTCTTTATCCATGATT 912
|||||
QY 922 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTCTCCGAGAGATGAC 981
|||||
Db 913 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTCTGTGGAGAAGATGAC 972
|||||

RESULT 12
AAN80801
ID AAN80801 standard; DNA; 1466 BP.
XX AC AAN80801;
XX DT 25-MAR-2003 (updated)
DT 12-SEP-1990 (first entry)
XX DE
DE DE
DE DE
KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant;
KW antiinflammatory; phospholipase inhibitory.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH mat_peptide 35..997
FT /*tag= a
FT /note="claimed in claim 2, page 160-161"
XX FT
XX PN WO8807576-A.
XX PD 06-OCT-1988.
XX PF 26-MAR-1988; 88WO-EP00266.
XX PR 28-MAR-1987; 87DE-3710309.
XX PR 28-MAR-1987; 87DE-3710364.
XX PR 28-MAR-1987; 87DE-3710430.
XX PR 04-NOV-1987; 87DE-3737367.
XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX PI Hauptmann R, Maurer-Fogy I, Bodo G, Swetly P, Stratowa C, Falkner B;
PI Adolf G, Reutlingsperger CMP;
XX WI 1988-292861/41.
DR WPI; 1988-292861/41.

DR P-PSDB; AAP80714.
XX New vascular anti-coagulating proteins -
PT useful as thrombin inhibitors, anti-inflammatory agents, etc
PS Disclosure; Fig 4/1-4/3; 183pp; German.
XX The DNA is produced by determining the amino acid sequence of isolated
CC and highly purified VAPs, constructing DNA probes on the basis of this
CC sequence, using the probes to search through suitable cDNA libraries,
CC isolating cDNA that hybridises with the probes, by inserting the cDNA
CC into a suitable vector, and using the vector to transform a host
CC organism. VAC-alpha has anticoagulant activity under certain
CC conditions, but loses this activity in the event of severe bleeding.
CC It acts by inhibiting conversion of factor X to factor Xa and conversion
CC of prothrombin to thrombin. It is structurally related to lipocortin I
CC (Nature 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
CC has similar antiinflammatory and phospholipase inhibitory activity.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 1466 BP; 422 A; 289 C; 328 G; 424 T; 3 other;
Query Match 97.3%; Score 954.6; DB 9; Length 1466;
Best Local Similarity 99.6%; Pred. No. 4.5e-267;
Matches 957; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 21 TATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTCGATGCGGGCTGA 80
|||||
Db 34 TATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTCGATGCGGGCTGA 93
|||||
QY 81 TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCTCGAC 140
|||||
Db 94 TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCTCGAC 153
|||||
QY 141 TCTGTTGACATCCCGAAGTAAATGCTCAGCGCCGAGGAAATCTCTGCACGCTTTTAAAGACTCT 200
|||||
Db 154 TCTGTTGACATCCCGAAGTAAATGCTCAGCGCCGAGGAAATCTCTGCACGCTTTTAAAGACTCT 213
|||||
QY 201 GTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGSGAAATTTGAAAAATTT 260
|||||
Db 214 GTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGSGAAATTTGAAAAATTT 273
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QY 261 AATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTT 320
|||||
Db 274 AATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTT 333
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QY 321 GAAGGGAGCTGGAACAANTGAAAAAGTACTACAGAAATTTATGCTTCAAGGACACCTGA 380
|||||
Db 334 GAAGGGAGCTGGAACAANTGAAAAAGTACTACAGAAATTTATGCTTCAAGGACACCTGA 393
|||||
QY 381 AGAACTGAGAGCCATCAACAAGTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGA 440
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Db 394 AGAACTGAGAGCCATCAACAAGTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGA 453
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QY 441 CGTGGTGGGGACACTTCAGGGTACTACACCGGATGTTGGTGGTCTCTCCTTCAGGCTAA 500
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Db 454 CGTGGTGGGGACACTTCAGGGTACTACACCGGATGTTGGTGGTCTCTCCTTCAGGCTAA 513
|||||
QY 501 CAGAGACCCCTGATGCTGGAATTTGATGAAGTCAAGTTGAACAAGATGCTCAGGCTTTATT 560
|||||
Db 514 CAGAGACCCCTGATGCTGGAATTTGATGAAGTCAAGTTGAACAAGATGCTCAGGCTTTATT 573
|||||
QY 561 TCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAC 620
|||||
Db 574 TCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAC 633
|||||
QY 621 ACCAAGTGTCTCTCATTGAGAAAGGTTTGGACAAGTACATGACTATATCAGGATTTCA 680
|||||
Db 634 ACCAAGTGTCTCTCATTGAGAAAGGTTTGGACAAGTACATGACTATATCAGGATTTCA 693
|||||
QY 681 AATTGAGGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGT 740
|||||

Db 694 AATTCAGGAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGCTGT 753
 QY 741 TCTGAATCTATTTCGAAGTATACCTGCCTACCTTCGAGAGCCCTCTATTATGCTATGAA 800
 Db 754 TGTGAATCTATTTCGAAGTATACCTGCCTACCTTCGAGAGCCCTCTATTATGCTATGAA 813
 QY 801 GGGAGCTGGGACAGATGATCATACCTCATCAGAGTCTGTTTCCAGGAGTGAGATTGA 860
 Db 814 GGGAGCTGGGACAGATGATCATACCTCATCAGAGTCTGTTTCCAGGAGTGAGATTGA 873
 QY 861 TCTGTTTACATCAGGAGGAGTTTAGGAGAAATTTTGGCACCCTCTCTTTATTCATGAT 920
 Db 874 TCTGTTTACATCAGGAGGAGTTTAGGAGAAATTTTGGCACCCTCTCTTTATTCATGAT 933
 QY 921 TAAGGAGATACATCTGGGAGCTATAGAAGAGCTCTTCTGCTGCTCTCCGGAGAGATGA 980
 Db 934 TAAGGAGATACATCTGGGAGCTATAGAAGAGCTCTTCTGCTGCTCTGGGAGAGATGA 993
 QY 981 C 981
 Db 994 C 994

RESULT 13

AA080873
 ID AA080873 standard; DNA; 963 BP.
 XX
 AC AA080873;
 XX
 DT 25-MAR-2003 (updated)
 DT 12-SEP-1990 (first entry)
 XX
 DE Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
 (Asp22).
 DE
 XX Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
 KW antinflammatory; phospholipase inhibitory.
 KW
 XX Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT mat_peptide 35..963
 ET /*tag= a
 XX
 PN W08807576-A.
 XX
 PD 06-OCT-1988.
 XX
 PE 26-MAR-1988; 88WO-EP00266.
 XX
 PR 28-MAR-1987; 87DE-3710309.
 PR 28-MAR-1987; 87DE-3710364.
 PR 28-MAR-1987; 87DE-3710430.
 PR 04-NOV-1987; 87DE-3737367.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Hauptmann R, Maurer-Fogy I, Bodo G, Swetly P, Stratowa C, Falkner E;
 PI Adolf G. Reutlingsperger CMP;
 XX
 DR WPI: 1988-292861/41.
 DR P-PSDB; AAP80242.
 XX
 PT New vascular anti-coagulating proteins -
 PT useful as thrombin inhibitors, antinflammatory agents, etc
 XX
 PS Claim 2; Page 160-161; 183pp; German.
 XX

CC The DNA is produced by determining the amino acid sequence of isolated
 CC and highly purified VAPs, constructing DNA probes on the basis of this
 CC sequence, using the probes to search through suitable cDNA libraries,
 CC isolating cDNA that hybridises with the probes, by inserting the cDNA
 CC into a suitable vector, and using the vector to transform a host

CC organism. VAC-alpha has anticoagulant activity under certain
 CC conditions, but loses this activity in the event of severe bleeding.
 CC It acts by inhibiting conversion of factor X to factor Xa and conversion
 CC of prothrombin to thrombin. It is structurally related to lipocortin I
 CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
 CC has similar antiinflammatory and phospholipase inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 963 BP; 284 A; 183 C; 242 G; 254 T; 0 other;

Query Match 97.2%; Score 953.6; DB 9; Length 963;
 Best Local Similarity 99.6%; Pred. No. 7.2e-267;
 Matches 956; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 81
 Db 1 ATGGCACAGGTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 60
 QY 82 GCAGAACTCTTCGGAAGGCTATGAAGCTTGGCCAGAGTGGAGAGCATCTGACT 141
 Db 61 GCAGACACTCTTCGGAAGGCTATGAAGCTTGGCCAGAGTGGAGAGCATCTGACT 120
 QY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201
 Db 121 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 180
 QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGGAAATTTGAAAAATTA 261
 Db 181 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGGAAATTTGAAAAATTA 240
 QY 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTTATGAACTGAAACATGCCCTG 321
 Db 241 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTTATGAACTGAAACATGCCCTG 300
 QY 322 AAGGAGCTGGAAACAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 381
 Db 301 AAGGAGCTGGAAACAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 360
 QY 382 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGGCTCAAGCTGGAAGATGAC 441
 Db 361 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGGCTCAAGCTGGAAGATGAC 420
 QY 442 GTGGTGGGGACACTTTCAGGGTACTACCGAGGATGTTGGTGGTCTCTCTCAGGCTAAC 501
 Db 421 GTGGTGGGGACACTTTCAGGGTACTACCGAGGATGTTGGTGGTCTCTCTCAGGCTAAC 480
 QY 502 AGAGACCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTTATT 561
 Db 481 AGAGACCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTTATT 540
 QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA 621
 Db 541 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA 600
 QY 622 CGAAGTGTCTCTATTTCAGAAAGTGTGTCACAAAGTACATGACTATATCAGGATTTCAA 681
 Db 601 CGAAGTGTCTCTATTTCAGAAAGTGTGTCACAAAGTACATGACTATATCAGGATTTCAA 660
 QY 682 ATTGAGGAACACCTTGACCGGAGACTTCTGCGCAATTTAGAGCACTACTCTCTGCTGT 741
 Db 661 ATTGAGGAACACCTTGACCGGAGACTTCTGCGCAATTTAGAGCACTACTCTCTGCTGT 720
 QY 742 GTGAATCTATTTCGAAGTATACCTGCTACCTTTCAGAGAGCCCTCTATTATGCTATGAAG 801
 Db 721 GTGAATCTATTTCGAAGTATACCTGCTACCTTTCAGAGAGCCCTCTATTATGCTATGAAG 780
 QY 802 GGAGCTGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT 861
 Db 781 GGAGCTGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT 840
 QY 862 CTGTTTACATCAGGAAGAGTTTGAAGAAATTTTGGCACCCTCTCTTTATTCATGAT 921
 Db 840 CTGTTTACATCAGGAAGAGTTTGAAGAAATTTTGGCACCCTCTCTTTATTCATGAT 900

Db 841 CTGTTTAAACATCAGGAGGAGTTTAGGAGAAATTTTGGCACCTCTCTTTATTCCTGATTT 900

QY 922 AAGGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCCCGAGAGATGAC 981
 |||||
 Db 901 AAGGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCTGTGGAGAGATGAC 960

RESULT 14

AA90599 standard; cDNA; 1574 BP.

XX AC AA90599;

XX 22-DEC-1989 (first entry)

XX Human lipocortin-V.

XX Human lipocortin-V; lambdaBARTipo V-1; anti-inflammatory agent.

XX Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide complement (143..1102)

FT /*tag= a

XX EP330396-A.

XX 30-AUG-1989.

XX 20-FEB-1989; 89EP-0301603.

XX 26-FEB-1988; 88US-0160866.

XX (BIOJ) BIOGEN INC.

XX Wallner BP, Pepinsky RB, Browning JL;

XX WPI; 1989-250486/35.

DR P-PSDB; AAP91363.

XX Human lipocortin cpds. III, IV, V, and VI - used in treatment of

PT arthritic, allergic, dermatologic, ophthalmic and collagen disorders

PT involving inflammatory processes.

XX Claim 4; fig 4; 32pp; English.

XX Human lipocortin-V was isolated from a lambda gt10 human peripheral

CC blood lymphocyte cDNA library with rat lipocortin-V cDNA of lambda

CC RIipo V-1 as probe. Lipocortins are anti-inflammatory agents and can

CC be used to treat arthritic, allergic, dermatologic, ophthalmic, and

CC collagen diseases.

CC See also AAP91362, AA90598, and AAP91363.

XX

SQ Sequence 1574 BP; 428 A; 334 C; 366 G; 446 T; 0 other;

Query Match 97.0%; Score 952; DB 10; Length 1574;

Best Local Similarity 99.5%; Pred. No. 2.7e-266;

Matches 955; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 22 ATGGCACAGTTCTCAGAGCACTGTGACTGCTTCCTCGATTTGATGAGCGGCTGAT 81
 |||||

Db 143 ATGGCACAGTTCTCAGAGCACTGTGACTGCTTCCTGGATTTGATGAGCGGCTGAT 202
 |||||

QY 82 GCAGAACTCTCGGAAGGCTATTGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
 |||||

Db 203 GCAGAACTCTCGGAAGGCTATTGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 262
 |||||

QY 142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCGACGCTTTTAAGACTCTG 201
 |||||

Db 263 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCGACGCTTTTAAGACTCTG 322
 |||||

QY 202 TTGGGAGGATCTCTTGGATGACCTGGAATCAGAACTACTCGAAATTTGAAAATTA 261
 |||||

Db 323 TTTGGGAGGATCTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 382

QY 262 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCTTG 321
 |||||

Db 383 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCTTG 442
 |||||

QY 322 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 |||||

Db 443 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 502
 |||||

QY 382 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGCTCAAGCCCTGGAAGATGAC 441
 |||||

Db 503 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGCTCAAGCCCTGGAAGATGAC 562
 |||||

QY 442 GTGTGGGGGACACTTTCAGGCTACTACACGGGATGTTGGTGGTTCCTTCCTTCAGGCTAAC 501
 |||||

Db 563 GTGTGGGGGACACTTTCAGGCTACTACACGGGATGTTGGTGGTTCCTTCCTTCAGGCTAAC 622
 |||||

QY 502 AGAGACCTCTGATGCTGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 561
 |||||

Db 623 AGAGACCTCTGATGCTGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 682
 |||||

QY 562 CAGGCTGGACAACCTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGGAACA 621
 |||||

Db 683 CAGGCTGGAGAAGCTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGGAACA 742
 |||||

QY 622 CGAAGTGTCTCTCATTTGAAAAGGTTTGAACAAGTACATGACTATATCAGGATTTCAA 681
 |||||

Db 743 CGAAGTGTCTCTCATTTGAGTTTGGCTGTTTGAACAAGTACATGACTATATCAGGATTTCAA 802
 |||||

QY 682 ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTTCTCTGCTGTT 741
 |||||

Db 803 ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTTCTCTGCTGTT 862
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QY 742 GTGAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 801
 |||||

Db 863 GTGAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 922
 |||||

QY 802 GGAGCTGGGACAGATGATCATCCCTCATCAGAGTATGTTTCCAGAGCTGAGATTGAT 861
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Db 923 GGAGCTGGGACAGATGATCATCCCTCATCAGAGTATGTTTCCAGAGCTGAGATTGAT 982
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QY 862 CTCTTTAAACATCAGGAGGAGTTTAGGAAGAATTTGCCACCTCTCTTTATTCATGATT 921
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Db 983 CTCTTTAAACATCAGGAGGAGTTTAGGAAGAATTTGCCACCTCTCTTTATTCATGATT 1042
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QY 922 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCCGAGAGATGAC 981
 |||||

Db 1043 AAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTGTGGAAGATGAC 1102
 |||||

RESULT 15

AAF18269 standard; DNA; 1637 BP.

XX AC AAF18269;

XX 14-MAR-2001 (first entry)

XX Lung cancer associated polynucleotide sequence SEQ ID 288.

XX Human; lung cancer associated protein; neuroprotective; cytosolic;

XX cardioactive; immunomodulatory; muscular active; vulnerable;

XX gastrointestinal; nephrotropic; anti-infective; gynecological;

XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;

XX proliferative disorder; wound healing; infectious disease; ds.

XX Homo sapiens.

XX WO200055180-A2.

XX 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05918.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX
PI Ruben SM;
XX
XX WPI; 2000-587514/55.
DR P-PSDB; AAB58393.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer.
XX
PS Claim 1; Page 746; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnarary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
XX sequences.
XX
SQ Sequence 1637 BP; 455 A; 349 C; 378 G; 450 T; 5 other;

Query Match 96.2%; Score 943.8; DB 21; Length 1637;
Best Local Similarity 99.6%; Pred. NO. 6.6e-264;
Matches 956; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 22 ATGGCACAGTCTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 81
DB 173 ATGGCACAGTCTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 232
QY 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 233 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCTGACT 292
QY 142 CTGTTGACATCCGGAAGTAACTGCTCAGCCGCGGAAATCTCTGCACTTTTAAAGACTCTG 201
DB 293 CTGTTGACATCCGGAAGTAACTGCTCAGCCGCGGAAATCTCTGCACTTTTAAAGACTCTG 352
QY 202 TTTGGCAGGATCTCTGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
DB 353 TTTGGCAGGATCTCTGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 412
QY 262 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 321
DB 413 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 472
QY 322 AAGGAGCTGGAAACAAATGAAAGTACTTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB 473 AAGGAGCTGGAAACAAATGAAAGTACTTGACAGAAATTTATGCTTCAAGGACACCTGAA 532
QY 382 GAACCTGAGAGCCATCAACAACTTTATGAGAAAGATATGGCTCAAGCCTGGAAGATGAC 441
DB 533 GAACCTGAGAGCCATCAACAACTTTATGAGAAAGATATGGCTCAAGCCTGGAAGATGAC 592
QY 442 GTGGTGGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 501
DB 592

DB 593 GTGGTGGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 652
QY 502 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAAACAAGATGCTCAGGCTTTATTT 561
DB 653 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAAACAAGATGCTCAGGCTTTATTT 712
QY 562 CAGGCTGGAGAACTTTAAATGGGGGACAGATGAAGAAAACCTTTATACCAATCTTTGGAACA 621
DB 713 CAGGCTGGAGAACTTTAAATGGGGGACAGATGAAGAAAACCTTTATACCAATCTTTGGAACA 772
QY 622 CGAAGTGTCTCTCATTTTGAGAAAAGGTGTTTGACAAGTACATGACTATATCAGSATTTCAA 681
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QY 682 ATTGAGGAAACCATTTGACCGGAGACTTCTGGCAATTTTAGAGCAACTACTCTCTTGTGTT 741
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QY 742 GTGAAATCTATTTCGAAGTATACCTGCTACCTTTGCAGAGACCCCTCTATTATGCTATGAAG 801
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DB 952 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCATGGTTTCCAGGAGTGAAGATTGAT 1011
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DB 1012 CTGTTTAAACATCAGGAAGGAGTTTAGGAAGAATTTTGCACCCCTCTCTTTTATTCATGATT 1071
QY 922 AAGGAGATACATCTGGGGACTATAGAAGCTCTTCTGCTCTCTCCGGAGAAAGATGAC 981
DB 1072 AAGGAGATACATCTGGGGACTATAGAAGCTCTTCTGCTGCTCTGTGGGAGAAAGATGAC 1131

Search completed: August 28, 2003, 16:03:33
Job time : 220.333 secs

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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:49:00 ; Search time 55.3333 Seconds
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Title: US-09-970-969-5

Perfect score: 981

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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	976.2	99.5	981	4	US-09-324-096A-1
3	976.2	99.5	981	4	US-09-324-096A-3
4	956.8	97.5	1460	6	5225537-3
5	956.8	97.5	1567	1	US-08-125-746-2
6	953.8	97.2	957	1	US-08-125-746-4
7	311	31.7	401	4	US-09-643-597-261
8	311	31.7	401	4	US-09-480-884A-261
9	311	31.7	401	4	US-09-542-615A-261
10	311	31.7	401	4	US-09-606-421B-261
11	310.8	31.7	2305	3	US-08-526-136-1
12	310.8	31.7	2311	3	US-08-526-136-3
13	134.6	13.7	1793	4	US-09-620-312D-747
14	123.6	12.6	644	3	US-09-328-111-721
15	96.6	9.8	502	3	US-09-328-111-625
16	96.6	9.8	630	3	US-09-328-111-491
17	93.6	9.5	501	3	US-09-328-111-481
18	88.2	9.0	1293	4	US-09-325-932A-17
19	74.8	7.6	643	3	US-09-385-982-306
20	69.6	7.1	543	3	US-09-328-111-428
21	69.4	7.1	704	4	US-09-325-932A-21
22	60.6	6.2	1001	4	US-09-641-638-188
23	59.6	6.1	789	4	US-09-325-932A-20
24	49.4	5.0	7218	1	US-08-232-463-14
25	47.4	4.8	1001	4	US-09-641-638-123
26	44.8	4.6	1001	4	US-09-641-638-106
27	44.8	4.6	1001	4	US-09-641-638-107

c	28	44.6	4.5	215	4	US-09-451-651-24	Sequence 24, Appl
	29	44.2	4.5	212	1	US-08-594-031-156	Sequence 156, App
	30	44	4.5	741	4	US-09-641-638-81	Sequence 81, Appl
	31	41.6	4.2	1001	4	US-09-641-638-202	Sequence 202, App
	32	41.2	4.2	1001	4	US-09-641-638-201	Sequence 201, App
	33	37.8	3.9	640	3	US-08-961-083-33	Sequence 33, Appl
	34	37.8	3.9	640	4	US-09-536-784-33	Sequence 33, Appl
	35	37.8	3.9	11309	4	US-08-961-527-108	Sequence 108, App
	36	37	3.8	278	2	US-08-454-557C-101	Sequence 101, App
	37	37	3.8	278	2	US-08-340-426D-101	Sequence 101, App
	38	37	3.8	278	2	US-08-450-673C-101	Sequence 101, App
	39	37	3.8	278	5	PCT-US95-17111A-101	Sequence 101, App
c	40	36	3.7	2416	4	US-09-016-434-1270	Sequence 1270, Ap
c	41	35.6	3.6	546	4	US-09-252-991A-5395	Sequence 5395, Ap
c	42	35.6	3.6	969	4	US-09-252-991A-5401	Sequence 5401, Ap
c	43	35.6	3.6	1464	4	US-09-252-991A-5409	Sequence 5409, Ap
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c	45	35.4	3.6	1001	4	US-09-641-638-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-09-324-096A-5
; Sequence 5, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(981)
US-09-324-096A-5

Query Match	100.0%	Score 981;	DB 4;	Length 981;
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QY	121	GATGAGGAGAGCATCTGACTCTGTGACATCCGGAAGTAAGTCTCAGCGCCAGGAATC	180	
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QY	241	ACTGAAATTTGAAAAATTAATTTGGCTCTGTATGAAACCCCTCTCGGCTTTATGATGCT	300	
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Db 361 ATTGCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 420
QY 421 GGCTCAAGCCTGGGAAGATGACGTGGTGGGGACACTTCACGGGTACTACCGCGGATGTTG 480
Db 421 GGCTCAAGCCTGGGAAGATGACGTGGTGGGGACACTTCACGGGTACTACCGCGGATGTTG 480
QY 481 GTGTTCTCCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 540
Db 481 GTGTTCTCCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 540
QY 541 CAAGATGCTCAGGCTTATTTCAAGGCTGGAGAACTTAAATGGGGACAGATGAGAGAAAG 600
Db 541 CAAGATGCTCAGGCTTATTTCAAGGCTGGAGAACTTAAATGGGGACAGATGAGAGAAAG 600
QY 601 TTTATCACCCTCTTGGAAACACGAGTGTGCTCATTTGAGAAAGGTTTGTGACAGATAC 660
Db 601 TTTATCACCCTCTTGGAAACACGAGTGTGCTCATTTGAGAAAGGTTTGTGACAGATAC 660
QY 661 ATGACTATATCAGGATTTCAAAATGAGGAAACCACTTGAACCGGAGACTTCTGGCAATTTA 720
Db 661 ATGACTATATCAGGATTTCAAAATGAGGAAACCACTTGAACCGGAGACTTCTGGCAATTTA 720
QY 721 GAGCAACTACTCCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
Db 721 GAGCAACTACTCCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
QY 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATATACCTCATCAGAGTCATG 840
Db 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATATACCTCATCAGAGTCATG 840
QY 841 GTTTCCAGGAGTGAATTTGATCTCTTTAAACATCAGGAAGAGTTTAGGAAGAAATTTGCC 900
Db 841 GTTTCCAGGAGTGAATTTGATCTCTTTAAACATCAGGAAGAGTTTAGGAAGAAATTTGCC 900
QY 901 ACCTCTCTTATTCCTGATTTAAGGAGATACATCTCGGGAGTATAAGAAAGCTCTTCTG 960
Db 901 ACCTCTCTTATTCCTGATTTAAGGAGATACATCTCGGGAGTATAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGAGAGATGAC 981
Db 961 CTGCTCTCCGAGAGATGAC 981
```

RESULT 2

US-09-324-096A-1
; Sequence 1, Application US/09324096A
; Patent No. 6323313

GENERAL INFORMATION:

; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOPW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324.096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 981

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(981)

US-09-324-096A-1

Query Match 99.58; Score 976.2; DB 4; Length 981;

Best Local Similarity 99.74; Pred. No. 1.9e-289;

Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCGATGTGCGGTGATATGGCAGAGTCTCAGAGGCACTGTGACTGACTTCCCT 60

|||||

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Db 1 ATGCGATGTGCGGTGCGCATATGGCAGAGTCTCAGAGGCACTGTGACTGACTTCCCT 60
QY 61 GGATTTGATGAGCGGGCTGATGCGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
Db 61 GGATTTGATGAGCGGGCTGATGCGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
QY 121 GATGAGGAGAGCATCTCTGACTCTGTGTGACATCCCGAAGTAATGCTFCAGCGCCAGGAATC 180
Db 121 GATGAGGAGAGCATCTCTGACTCTGTGTGACATCCCGAAGTAATGCTFCAGCGCCAGGAATC 180
QY 181 TCTCGAGCTTTTAAGACTCTCTTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTA 240
Db 181 TCTCGAGCTTTTAAGACTCTCTTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTA 240
QY 241 ACTGGAATAATTTGAAAAATTAATCTGCTGCTCTGATGAAACCTCTCGGCTTTTATGATGCT 300
Db 241 ACTGGAATAATTTGAAAAATTAATCTGCTGCTCTGATGAAACCTCTCGGCTTTTATGATGCT 300
QY 301 TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAAT 360
Db 301 TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAAT 360
QY 361 ATTGCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 420
Db 361 ATTGCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 420
QY 421 GGCTCAAGCCTGGGAAGATGACGTGGTGGGGACACTTCACGGGTACTACCGGGATGTTG 480
Db 421 GGCTCAAGCCTGGGAAGATGACGTGGTGGGGACACTTCACGGGTACTACCGGGATGTTG 480
QY 481 GTGTTCTCCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 540
Db 481 GTGTTCTCCTTCAAGGACACCTGAGAACTGAGAGCCCATCAAAACAGTTTATGAGAGAGATAT 540
QY 541 CAAGATGCTCAGGCTTATTTCAAGGCTGGAGAACTTAAATGGGGACAGATGAGAGAAAG 600
Db 541 CAAGATGCTCAGGCTTATTTCAAGGCTGGAGAACTTAAATGGGGACAGATGAGAGAAAG 600
QY 601 TTTATCACCCTCTTGGAAACACGAGTGTGCTCATTTGAGAAAGGTTTGTGACAGATAC 660
Db 601 TTTATCACCCTCTTGGAAACACGAGTGTGCTCATTTGAGAAAGGTTTGTGACAGATAC 660
QY 661 ATGACTATATCAGGATTTCAAAATGAGGAAACCACTTGAACCGGAGACTTCTGGCAATTTA 720
Db 661 ATGACTATATCAGGATTTCAAAATGAGGAAACCACTTGAACCGGAGACTTCTGGCAATTTA 720
QY 721 GAGCAACTACTCCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
Db 721 GAGCAACTACTCCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
QY 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATATACCTCATCAGAGTCATG 840
Db 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATATACCTCATCAGAGTCATG 840
QY 841 GTTTCCAGGAGTGAATTTGATCTCTTTAAACATCAGGAAGAGTTTAGGAAGAAATTTGCC 900
Db 841 GTTTCCAGGAGTGAATTTGATCTCTTTAAACATCAGGAAGAGTTTAGGAAGAAATTTGCC 900
QY 901 ACCTCTCTTATTCCTGATTTAAGGAGATACATCTCGGGAGTATAAGAAAGCTCTTCTG 960
Db 901 ACCTCTCTTATTCCTGATTTAAGGAGATACATCTCGGGAGTATAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGAGAGATGAC 981
Db 961 CTGCTCTCCGAGAGATGAC 981
```

RESULT 3

US-09-324-096A-3

; Sequence 3, Application US/09324096A

; Patent No. 6323313

; GENERAL INFORMATION:

; APPLICANT: Tait, Jonathan

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; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(981)
US-09-324-096A-3

Query Match      99.5%; Score 976.2; DB 4; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.9e-289;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCATGTGGCTGGCGTTCATATGCGACAGGCTTCTCAGAGGCACTGTGACTGACTTCCT 60
Db 1 ATGGCAGGTGCTGTGGCCATATGCCACAGGTCTCAGAGGCACTGTGACTGACTTCCT 60
QY 61 GGATTTGATAGCGGGCTGATGCGAAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
Db 61 GGATTTGATAGCGGGCTGATGCGAAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
QY 121 GATGAGGAGAGCACTCTGACTCTGTGACATCCGCACTAATGCTGCAGCGCCAGCAATC 180
Db 121 GATGAGGAGAGCACTCTGACTCTGTGACATCCGCACTAATGCTGCAGCGCCAGCAATC 180
QY 181 TCTGAGCTTTTAAGACTCTCTTTGGCAGGAGTCTTCTGGATGACTGAAATCAGAACTA 240
Db 181 TCTGAGCTTTTAAGACTCTCTTTGGCAGGAGTCTTCTGGATGACTGAAATCAGAACTA 240
QY 241 ACTGGAATTTGAAATTAATTTGTGGCTCTGATGAAACCCCTTCGGCTTTATGATGCT 300
Db 241 ACTGGAATTTGAAATTAATTTGTGGCTCTGATGAAACCCCTTCGGCTTTATGATGCT 300
QY 301 TATGAACCTGAACATGCGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360
Db 301 TATGAACCTGAACATGCGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360
QY 361 ATTGCTTCAAGSACACCTGAAGACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
Db 361 ATTGCTTCAAGSACACCTGAAGACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
QY 421 GCCTCAAGCTGGAAGATGACGTGTGGGGGACACTTCAGGGTACTACAGGGGATGTTG 480
Db 421 GCCTCAAGCTGGAAGATGACGTGTGGGGGACACTTCAGGGTACTACAGGGGATGTTG 480
QY 481 GTGGTTCTCCCTCAGGCTAACAGAGACCTTGATGCTGGAATTTGATGAAGCTCAAGTTCAA 540
Db 481 GTGGTTCTCCCTCAGGCTAACAGAGACCTTGATGCTGGAATTTGATGAAGCTCAAGTTCAA 540
QY 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGAGAACTTAAATGGGGGACAGATGAAGAAAAG 600
Db 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGAGAACTTAAATGGGGGACAGATGAAGAAAAG 600
QY 601 TTTATCACCATCTTTGGACACAGAAAGTGTCTCATTTGAGAAAGGTTTGAACAAGTAC 660
Db 601 TTTATCACCATCTTTGGACACAGAAAGTGTCTCATTTGAGAAAGGTTTGAACAAGTAC 660
QY 661 ATGACTATATCAGGATTTCAATTTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTA 720
Db 661 ATGACTATATCAGGATTTCAATTTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTA 720
QY 721 GAGCAACTACTCTTGTGCTGTAATCTATTTCGAAGTATACCTGCTACCTTCGACAG 780
Db 721 GAGCAACTACTCTTGTGCTGTAATCTATTTCGAAGTATACCTGCTACCTTCGACAG 780
QY 781 ACCCTCTATTATGCTATGAAGGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
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Db 781 ACCCTCTATTATGCTATGAAGGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
QY 841 GTTCCAGAGTGAAGATTGATCTGTTTAAACATCAGGAAGGAGTGTAGGAAGAATTTTGGC 900
Db 841 GTTCCAGAGTGAAGATTGATCTGTTTAAACATCAGGAAGGAGTGTAGGAAGAATTTTGGC 900
QY 901 ACCCTCTTTTATTCATGATTAAAGGAGATACATCTGGGGACTATAAAGAAAGCTCTTCTG 960
Db 901 ACCCTCTTTTATTCATGATTAAAGGAGATACATCTGGGGACTATAAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGAGAGAGATGAC 981
Db 961 CTGCTCTCCGAGAGAGATGAC 981

RESULT 4
5225537-3
; Patent No. 5225537
; APPLICANT: FOSTER, DONALD
; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
; PHOSPHOLIPID-BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,082
; FILING DATE: 29-DEC-1989
; SEQ ID NO: 3
; LENGTH: 1460
5225537-3

Query Match      97.5%; Score 956.8; DB 6; Length 1460;
Best Local Similarity 99.8%; Pred. No. 2.1e-283;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
Db 13 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 72
QY 82 CGAGAACTCTTCGGAAGGCTATGAAAGGCTTTGGGCACAGATGAGGAGAGCATCTCTGACT 141
Db 73 CGAGAACTCTTCGGAAGGCTATGAAAGGCTTTGGGCACAGATGAGGAGAGCATCTCTGACT 132
QY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAAGCTTTTAAAGACTCG 201
Db 133 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAAGCTTTTAAAGACTCG 192
QY 202 TTTGGCAGGATCTTCTGATGACCTGAAATCAGAACTAACTTGGAAATTTTCAAAAATTA 261
Db 193 TTTGGCAGGATCTTCTGATGACCTGAAATCAGAACTAACTTGGAAATTTTCAAAAATTA 252
QY 262 ATTTGGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCTTGG 321
Db 253 ATTTGGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCTTGG 312
QY 322 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 313 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372
QY 382 GAACTGAGAGCCATCAAAACAACTTTATGAAGAGATATGCTCAAGCTTGAAGATGAC 441
Db 373 GAACTGAGAGCCATCAAAACAACTTTATGAAGAGATATGCTCAAGCTTGAAGATGAC 432
QY 442 GTGGTGGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTTCCTCCTCAGGCTAAC 501
Db 433 GTGGTGGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTTCCTCCTCAGGCTAAC 492
QY 502 AGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
Db 493 AGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 552
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCAACATCTTTGGAACA 621
Db 553 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCAACATCTTTGGAACA 612
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QY 922 AAGGAGATACATCTGGGAGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAGATGAC 981
|||||
Db 1036 AAGGAGATACATCTGGGAGACTATAAGAAAGCTCTTCTGCTGCTCTGTGGAGAGATGAC 1095
|||||

RESULT 6

US-08-125-746-4

; Sequence 4, Application US/08125746

; Patent No. 5591633

; GENERAL INFORMATION:

; APPLICANT: SAINO, YUSHI

; APPLICANT: IWASAKI, AKIO

; APPLICANT: IWASAKI, AKIO

; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/125,746

; FILING DATE: 24-SEP-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/807,623

; FILING DATE: 13-DEC-1991

; PRIOR APPLICATION DATA: JP 037227/1987

; FILING DATE: 20-FEB-1987

; PRIOR APPLICATION DATA: JP 184428/1987

; FILING DATE: 23-JUL-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: Odion, No. 5591633man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 80-074-0 DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 957 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

US-08-125-746-4

Query Match

Best Local Similarity 97.2%; Score 953.8; DB 1; Length 957;

Matches 955; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 GCACAGGTTCTCAGAGGCTATGAAGGCTTGGGACAGATGAGGAGCATCTGACTCG 84
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Db 1 GCACAGGTTCTCAGAGGCTATGAAGGCTTGGGACAGATGAGGAGCATCTGACTCG 60
|||||
QY 85 GAACTCTCGGAGGCTATGAAGGCTTGGGACAGATGAGGAGCATCTGACTCG 144
|||||
Db 61 GAACTCTCGGAGGCTATGAAGGCTTGGGACAGATGAGGAGCATCTGACTCG 120
|||||
QY 145 TTGACATCCGAAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTCTGTT 204
|||||
Db 121 TTGACATCCGAAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTCTGTT 180
|||||

QY 205 GCGAGGATCTTCTGATGACCTGAAATCAGAACTAACTGGAAATTTGAAAAATTAATT 264
|||||
Db 181 GCGAGGATCTTCTGATGACCTGAAATCAGAACTAACTGGAAATTTGAAAAATTAATT 240
|||||
QY 265 GTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCCTGAAG 324
|||||
Db 241 GTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCCTGAAG 300
|||||
QY 325 GCGCTGGACAAATGAAAGTACTGACAGAAATTTGCTTCAAGGACACCTGANGAA 384
|||||
Db 301 GCGCTGGACAAATGAAAGTACTGACAGAAATTTGCTTCAAGGACACCTGANGAA 360
|||||
QY 385 CTGAGAGCCATCAAAAGTATTATGAAGAAGTATGGCTCAAGCTTGAAGATGACGCTG 444
|||||
Db 361 CTGAGAGCCATCAAAAGTATTATGAAGAAGTATGGCTCAAGCTTGAAGATGACGCTG 420
|||||
QY 445 GTGGGGGACACTTCAGGGTACTACAGCGGATGTTGGGGTCTCTCTCAGGCTACAGCA 504
|||||
Db 421 GTGGGGGACACTTCAGGGTACTACAGCGGATGTTGGGGTCTCTCTCAGGCTACAGCA 480
|||||
QY 505 GACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTCAG 564
|||||
Db 481 GACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTCAG 540
|||||
QY 565 GCTGGAGAACTTAAATGGGGGACAGATCAAGAAAGTATTATCACCATCTTTTGGAAACGA 624
|||||
Db 541 GCTGGAGAACTTAAATGGGGGACAGATCAAGAAAGTATTATCACCATCTTTTGGAAACGA 600
|||||
QY 625 AGTGTGCTCATTTGAGAAAGTGTGACAAAGTATGACAAAGTATGACAAAGTATGACAAAGT 684
|||||
Db 601 AGTGTGCTCATTTGAGAAAGTGTGACAAAGTATGACAAAGTATGACAAAGTATGACAAAGT 660
|||||
QY 685 GAGGAAACCATTTGACGCGGAGACTTCTGCAATTTAGAGCACTACTCTCTGCTGTG 744
|||||
Db 661 GAGGAAACCATTTGACGCGGAGACTTCTGCAATTTAGAGCACTACTCTCTGCTGTG 720
|||||
QY 745 AAATCTATTTCGAAGTATACCTGCTTACCTTGCAGAGACCCCTTATTTATGCTATGAAGGA 804
|||||
Db 721 AAATCTATTTCGAAGTATACCTGCTTACCTTGCAGAGACCCCTTATTTATGCTATGAAGGA 780
|||||
QY 805 GCTGGACAGATGATCATACCTCATCAGAGTCACTGGTTTCCAGAGTGAGATGATCTG 864
|||||
Db 781 GCTGGACAGATGATCATACCTCATCAGAGTCACTGGTTTCCAGAGTGAGATGATCTG 840
|||||
QY 865 TTTAATCATCAGGAGGAGTTTAGGAGAGTATTTGCCACTCTCTTTATCCATGATTAAG 924
|||||
Db 841 TTTAATCATCAGGAGGAGTTTAGGAGAGTATTTGCCACTCTCTTTATCCATGATTAAG 900
|||||
QY 925 GGAGATACATCTGGGAGCTTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAGATGAC 981
|||||
Db 901 GGAGATACATCTGGGAGCTTATAAGAAAGCTCTTCTGCTGCTCTGTGGAGAGATGAC 957
|||||

RESULT 7

US-09-643-597-261

; Sequence 261, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aljun

; APPLICANT: Skelky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNelli, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
; US-09-970-969-5

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.2e-85;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 22 ATGCGACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTGATGAGCGGCTGAT 81
DB 89 ATGCGACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 208
QY 142 CTGTTGACATCCCGAAGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 201
DB 209 CTGTTGACATCCCGAAGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 268
QY 202 TTTGGCAGGATCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
DB 269 TTTGGCAGGATCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 328
QY 262 ATTGTGCTCTGTATGAAAGGCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 321
DB 329 ATTGTGCTCTGTATGAAAGGCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 388
QY 322 AAGGAGCTGAA 334
DB 389 AAGGAGCTGAA 401

RESULT 8

US-09-480-884A-261
; Sequence 261, Application US/09480884A
; Patent No. 6482597

; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
; US-09-480-884A-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.2e-85;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGCGACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTGATGAGCGGCTGAT 81
DB 89 ATGCGACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 208
QY 142 CTGTTGACATCCCGAAGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 201
DB 209 CTGTTGACATCCCGAAGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 268
QY 202 TTTGGCAGGATCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
DB 269 TTTGGCAGGATCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 328
QY 262 ATTGTGCTCTGTATGAAAGGCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 321
DB 329 ATTGTGCTCTGTATGAAAGGCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 388
QY 322 AAGGAGCTGAA 334
DB 389 AAGGAGCTGAA 401

RESULT 9

US-09-542-615A-261
; Sequence 261, Application US/09542615A
; Patent No. 6518256

; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
; US-09-542-615A-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.2e-85;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGCGACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTGATGAGCGGCTGAT 81
DB 89 ATGCGACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 208
QY 142 CTGTTGACATCCCGAAGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 201
DB 209 CTGTTGACATCCCGAAGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 268
QY 202 TTTGGCAGGATCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
DB 269 TTTGGCAGGATCTTCTGGATGAACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 328

OY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 321
|||||
Db 329 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 388
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OY 322 AAGGAGCTGGAA 334
|||||
Db 389 AAGGAGCTGGAA 401
|||||

RESULT 10

US-09-606-421B-261
; Sequence 261, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-261

Query Match 31.7%; Score 311; DB 4; Length 401;

Best Local Similarity 99.4%; Pred. No. 1.2e-85;

Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 22 ATGGCACAGGTTCTCAGAGCCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCTGACT 81
|||||
Db 89 ATGGCACAGGTTCTCAGAGCCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCTGACT 148
|||||
OY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCTGACT 141
|||||
Db 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCTGACT 208
|||||
OY 142 CTGTGTGATCCGGAAGTAAGTCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201
|||||
Db 209 CTGTGTGATCCGGAAGTAAGTCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 268
|||||
OY 202 TTTGCGAGGATCTCTCGATGACCTGAAATCAGAACTAACTGGAATTTGAAAAATTA 261
|||||
Db 269 TTTGCGAGGATCTCTCGATGACCTGAAATCAGAACTAACTGGAATTTGAAAAATTA 328
|||||
OY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 321
|||||
Db 329 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 388
|||||
OY 322 AAGGAGCTGGAA 334
|||||
Db 389 AAGGAGCTGGAA 401
|||||

RESULT 11

US-08-526-136-1

; Sequence 1, Application US/08526136

; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55sx
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2305
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-526-136-1

Query Match 31.7%; Score 310.8; DB 3; Length 2305;

Best Local Similarity 58.0%; Pred. No. 3.3e-85;

Matches 549; Conservative 0; Mismatches 397; Indels 0; Gaps 0;

OY 36 CAGAGGCACTGTGACTGACTTCCCTCTGGATTTGATGAGCGGGCTGATGAGAACTCTTCG 95
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Db 665 CCGAGGCACCATCACAGATGCATCTGGCTTTGACCCCTCGGAGATGCTGAAGTCTGCG 724
|||||
OY 96 GAAGCCTATGAAGGCTTTGGGCACAGATGAGGAGAGCATCTCTGTTGACATCCGG 155
|||||
Db 725 GAAGCCATGAAGGCTTTGGGACTGACGAGCGCCATCAATTGACTGCCTGGGTAGTCG 784
|||||
OY 156 AAGTAATCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGCTCTGTTTGGCAGGACTCT 215
|||||
Db 785 CTCACAGCAACACAGACAGATCTCTCTGCTTCAAGACAGCATATGGGAAGATT 844
|||||
OY 216 TCTGATGACCTGAAATCAGAACTAACTGGAAAATTTGAAAATTTAATTTGGTCTGAT 275
|||||
Db 845 GATCAAGATCTGAAATCTGAACTGTCAAGAACTTTGAGAAGACAATCTTGGCCCTGAT 904
|||||
OY 276 GAAACCTCTCGGCTTTTATGATGCTTATGAACTGAAACATGCCCTTGAAGGGAGCTGGAAC 335
|||||
Db 905 GAAGACCTCTGCTCTCTTTTGGCTTATGAGATAAAGGAAGCTATCAAGGGGGCGGCAC 964
|||||
OY 336 AAATGAAAAAGTACTGACAGAAAATTTATGCTTCAAGAGCACCTGTAAGAACTGAGAGCCAT 395
|||||
Db 965 TGATGAGGCTGCTGATGCTGAGATCTTGGCTTCCCGCAGACACAGACATCCGGAGCT 1024
|||||
OY 396 CAAACAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGACGTGGTGGGGGACAC 455
|||||

Db	1025	GAACAGAGTCTACAAGACAGAAATTCAAAAGAGCCCTGGAGAGGCCATTTCGGAGCGACAC	1084
Qy	456	TTCAAGGTACTACCACGGGATGTGGTGGTCTCTCTTCAGCGCTAACAGAGACCCTGATGC	515
Db	1085	TTCAAGGCACCTCCAGCGGCTCTCATCTCTCTCAGGGAACCGGATGAAGACAC	1144
Qy	516	TGGNATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACT	575
Db	1145	AAACGTGGACATGACCCCTTCTCAGAGAGATGTGCAGGAGCTCTATGCATCGGGAGAA	1204
Qy	576	TAAATGGGGACAGATGAACAAAAGTTATCACCATCTTTTGGAAACAGGAAGTGTGTCTCA	635
Db	1205	CCGCTTGGGAACAGATGAGTCCAAGTCAATGCGATTCTGCTCCGGAGCGGGGCCA	1264
Qy	636	TTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAAATTCAGGAACCCAT	695
Db	1265	CCTGGTGGCAAGTTTTAAACGAGTATCAGAGGATGACAGGACGTGACATTCAGAAGAGCAT	1324
Qy	696	TGACCGCGACACTTCGGCAATTTAGAGCAACTACTCCTTTCCTGTTGTGGAATCTATTTCG	755
Db	1325	CTCCGGGAGATGTCCGGGACCTGGAGCAGGGATGCTGGCGTGTGGTGAATGTCTTAA	1384
Qy	756	AAGTATACCTGCCTACCTTTCAGAGAGCCCTCTATTATGCTATGAAGGGAGCTGGGACAGA	815
Db	1385	GAATACCCAGCCTTCTTTCGTAAGGCTCAACAAGGCCATCAGGGGAGCCGGAACCA	1444
Qy	816	TGATCATACCTCATCAGATCTATGTTTCCAGGAGTGAGATTGATCTGTTTAAACATCAG	875
Db	1445	AGACCGACCCCTCATCCGCATCATGTTGTCTCGACGGAGATCGACTCCTCGTGACATCAG	1504
Qy	876	GAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTTCCATGATTAAAGGGAGATACATC	935
Db	1505	AGCAGAGTATAAGCGCTGTATGCAAGTGCCTGCTACCAGGACATCAGGGAGACACTTC	1564
Qy	936	TGGGGACTATAAGAAAGCTTCTTCTGCTGCTCTCCGGAGAGATGAC	981
Db	1565	AGGGGATTACCGGAAGATTTCTGCTGAAGATCTCTGGTGGCAATGAC	1610

RESULT 12

US-08-526-136-3

; Sequence 3, Application US/08526136

; Patent No. 6107089

GENERAL INFORMATION:

APPLICANT: Towle, Christine A. et al.

TITLE OF INVENTION: ANNEXIN XI

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

; SOFTWARE: WordPerfect (

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/526,136

FILING DATE:

CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/214,036

; FILING DATE: 10/10/2007

APPLICATION NUMBER: 07/837,775

FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/354,455

APPLICATION NUMBER: 07/764,465
FILING DATE: September 22, 1991

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ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul T

NAME: CLARK, PAUL J.

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 721
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(644)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-721

Query Match 12.6%; Score 123.6; DB 3; Length 644;
Best Local Similarity 52.8%; Pred. No. 4.3e-28;
Matches 267; Conservative 0; Mismatches 241; Indels 0; Gaps 0;
YQ 356 AAATTTATGCTTCAAGGACACCTGAAGAATCTGAGAGCCATCAACAAAGTTTATGAAGAAG 415
DB 511 AGATTTTGGCNCAGACCAATCAGGAATCCGAGAAATGTCAGATGTTATCACTCAG 452
YQ 416 AATATGGCTCAGCCCTGGAAGATGAGTGGTGGGGGACACCTTCAGGGTACTACACGCGGA 475
DB 451 AATTTGGACGAGACCTTGAAGAGNCATTAGGTTCAGATACATCAGGACATTTTGAACGTT 392
YQ 476 TGTGTGTTCTTCCCTTCAGGCTAACAGAGACCCCTGATGCTGGAATTGATGAAGCTCAAG 535
DB 391 TACTTGTCCATGTGCCAGGAAATCGTATGAGAACCCAGAGTATATAACCCACCAATGG 332
YQ 536 TTCAACAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAG 595
DB 331 CTCAGGAAGATGCTCAGGCTCTCTATCAAGCTGGTGGGGGACACTAGGACCGATGAAT 272
YQ 596 AAAAGTTTATCACCATCTTTGGACACAGAGTGTCTCATTTGAGAAAGGTGTTTGACA 655
DB 271 CTTGCTTTAATGATGCTTGGACACAGAGCTTCTCAGCTGAGAGCTACCATCGAGG 212
YQ 656 AGTACATGATATATCAGGATTTCAAAATGAGGAACCAATTTGACCCGAGACTTTCTGGCA 715
DB 211 CTTATTTCTAGGATGGCTTAATCGAGACTTGTAAAGCAGTGTGAGCCGTGAGTTTCCGGAT 152
YQ 716 ATTTAGAGCAACTACTCTTCTGCTGTGTGTAATCTATTGAAATCTATTGAACTGCTACTTGG 775
DB 151 ATGTGAAGATGTTTGAAGACCATCTTGACGTGCTCCCTGAAACCCCTGCTCTTTG 92
YQ 776 CAGAGACCTCTATTATGCTATGAAGGAGCTGGGACAGATGATCATACCCCTCATCAGAG 835
DB 91 CTCAGAGGCTCTACTATGCTATGAAGGTCGTGGCAGAGTCACTCCACCCCTGCTCTTTG 32
YQ 836 TCATGGTTTCCAGGAGTGAATGATCT 863
DB 31 TTGTGCTCACTCGAAGTGAATGACCT 4

RESULT 15

US-09-328-111-625/C
; Sequence 625, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111

; CURRENT FILING DATE: 1999-06-08
; EARLIER FILING NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 625
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-625

Query Match 9.8%; Score 96.6; DB 3; Length 502;
Best Local Similarity 53.6%; Pred. No. 7.2e-20;
Matches 201; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
YQ 40 GGCACTGTGACTGACTTCCCTGATTTGATGACGGCTGATCGACAAACTCTTCGGAAG 99
DB 379 GGTCTGTCAAGCCCTATATACTTTGATGCTGAGGGGATGCTTTGAACATTGAACA 330
YQ 100 GCTATGAAAGGCTTTGGGCACAGATGAGGAGAGTCTCTGACTCTGTTGACATCCCGAAGT 159
DB 319 GCATCAAGACCAAGGTGTGGATGAGTCAACCATTTGACCAACCGCAGC 260
YQ 160 AATGCTCAGCGCCGAGAAATCTCTGAGCTTTTAAAGACTCTGTTGGCAGGGATCTTCG 219
DB 259 AATGCACAGAGACAGGATATTGCTTTCGCTTACGAGAGAGGACCAAAAAGAACTTGCA 200
YQ 220 GATGACCTGAAATCAGAACTAACTGGAAATTTGAAAATTAATTTGCTCTCTGATGAA 279
DB 199 TCAGCACTGAAAGTCAGCCCTTATCTGGCCACCTGGAGACGGTGATTTTGGGCCCTATTGAAG 140
YQ 280 CCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTGAAGGGAGCTGGAACAAAT 339
DB 139 ACACCTGCTCAGTATCAGCCCTCTGAGCTAAAGCTTTCCATGAAGGGGCTGGGACCGAC 80
YQ 340 GAAAAAGTACTGACAGAAATTAATGCTTCAAGGACACCTGGAAGAACTGAGAGCCATCAA 399
DB 79 GAGGACTCTCTCATTGAGATCATCTGCTCCAGAACCAACCGAGCTGCAGGAAATTAAC 20
YQ 400 CAAGTTTATGAAGAA 414
DB 19 AGAGTCTACAAGGAA 5

Search completed: August 28, 2003, 19:41:19
Job time : 57.3333 sec

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:49:00 ; Search time 55.3333 Seconds
(without alignments)
7825.244 Million cell updates/sec

Title: US-09-970-969-1

Perfect score: 981

Sequence: 1 atggcatgtggcggtggcca.....tgctctccggagaagatgac 981

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	978.8	99.7	981	4	US-09-324-096A-3
3	976.2	99.5	981	4	US-09-324-096A-5
4	956.8	97.5	1460	6	5225537-3
5	956.8	97.5	1567	1	US-08-125-746-2
6	953.8	97.2	957	1	US-08-125-746-4
7	311	31.7	401	4	US-09-643-597-261
8	311	31.7	401	4	US-09-480-884A-261
9	311	31.7	401	4	US-09-542-615A-261
10	311	31.7	401	4	US-09-606-421B-261
11	310.8	31.7	2305	3	US-08-526-136-1
12	310.8	31.7	2311	3	US-08-526-136-3
13	134.6	13.7	1793	4	US-09-620-312D-747
14	123.6	12.6	644	3	US-09-328-111-721
15	96.6	9.8	502	3	US-09-328-111-625
16	96.6	9.8	630	3	US-09-328-111-491
17	93.6	9.5	501	3	US-09-328-111-481
18	88.2	9.0	1293	4	US-09-325-932A-17
19	74.8	7.6	643	3	US-09-385-982-306
20	69.6	7.1	543	3	US-09-328-111-428
21	69.4	7.1	704	4	US-09-325-932A-21
22	60.6	6.2	1001	4	US-09-641-638-188
23	59.6	6.1	789	4	US-09-325-932A-20
24	49.4	5.0	7218	1	US-08-232-463-14
25	47.4	4.8	1001	4	US-09-641-638-123
26	44.8	4.6	1001	4	US-09-641-638-106
27	44.8	4.6	1001	4	US-09-641-638-107

Sequence 24, Appl
Sequence 156, App
Sequence 81, Appl
Sequence 202, App
Sequence 201, App
Sequence 33, Appl
Sequence 108, App
Sequence 101, App
Sequence 101, App
Sequence 101, App
Sequence 101, App
Sequence 1270, Ap
Sequence 5395, Ap
Sequence 5401, Ap
Sequence 5409, Ap
Sequence 5404, Ap
Sequence 186, App

US-09-451-651-24
US-08-594-031-156
US-09-641-638-81
US-09-641-638-202
US-09-641-638-201
US-08-961-083-33
US-09-536-784-33
US-08-961-527-108
US-08-454-557C-101
US-08-340-426D-101
US-08-450-673C-101
PCT-US95-17111A-101
US-09-016-434-1270
US-09-252-991A-5395
US-09-252-991A-5401
US-09-252-991A-5409
US-08-252-991A-5404
US-09-641-638-186

ALIGNMENTS

RESULT 1

US-09-324-096A-1
Sequence 1, Application US/09324096A.
Patent No. 6323313

GENERAL INFORMATION:

APPLICANT: Tait, Jonathan

APPLICANT: Brown, David

TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES

FILE REFERENCE: UOFW-1-13841

CURRENT APPLICATION NUMBER: US/09/324.096A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 981

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(981)

US-09-324-096A-1

Query Match 100.0%; Score 981; DB 4; Length 981;

Best Local Similarity 100.0%; Pred. No. 8.3e-284; Mismatches 0; Indels 0; Gaps 0;

Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCATGTGCGGTGGCCCATATGGCACAGGTTCTCAGAGGCACTGTGACTGCTTCCT 60

Db 1 ATGGCATGTGCGGTGGCCCATATGGCACAGGTTCTCAGAGGCACTGTGACTGCTTCCT 60

Qy 61 GGATTTGATGAGCGGCTGATGCAAACTCTCGGAAGGCTATGAAGGCTTGGGCACA 120

Db 61 GGATTTGATGAGCGGCTGATGCAAACTCTCGGAAGGCTATGAAGGCTTGGGCACA 120

Qy 121 GATCAGGAGCATCTTGACTCTCTGACATCCCGAAGTATGCTCAGCGCCAGGAATC 180

Db 121 GATCAGGAGCATCTTGACTCTCTGACATCCCGAAGTATGCTCAGCGCCAGGAATC 180

Qy 181 TCTCAGCTTTTAAGACTCTGTTGGCAGGATCTTCTGGATGATGATGATGATGATGATGAT 240

Db 181 TCTCAGCTTTTAAGACTCTGTTGGCAGGATCTTCTGGATGATGATGATGATGATGATGAT 240

Qy 241 ACTGGAATAATTGAAAAATTAATTTGCTGCTCTGATGAACCCCTCTCGGCTTTATGATGCT 300

Db 241 ACTGGAATAATTGAAAAATTAATTTGCTGCTCTGATGAACCCCTCTCGGCTTTATGATGCT 300

Qy 301 TATCACTGAACATGCTTGAAGGAGCTTGAACAAATGAAAAAGTACTACAGAAAT 360

Db 301 TATCACTGAACATGCTTGAAGGAGCTTGAACAAATGAAAAAGTACTACAGAAAT 360

Db	1	ATGGCAGGTGGCTGTGGCCCATATGGCACAGGTTCTCAGAGGACCTGTGACTGACTTCCCT	60
Qy	61	GGATTTGATGAGCGGCTGATGCAGAAACTCTTCGSAAGGCTATGAAAGGCTTGGGCACA	120
Db	61	GGATTTGATGAGCGGCTGATGCAGAAACTCTTCGSAAGGCTATGAAAGGCTTGGGCACA	120
Qy	121	GATGAGGAGACATCCTGACTCTGTGTGGACATCCGAAGTAAATGCTCAGCGCAGGAATC	180
Db	121	GATGAGGAGACATCCTGACTCTGTGTGACATCCGAAGTAAATGCTCAGCGCAGGAATC	180
Qy	181	TCCTGCAGCTTTTAAGACTCTGTGTGGCAGGGATCTCTGGATGACCTGAAATCAGAAGTA	240
Db	181	TCGCGAGCTTTTAAGACTCTGTGTGGCAGGGATCTCTGGATGACCTGAAATCAGAAGTA	240
Qy	241	ACTGGAAATTTTCAAAAATTAATGTGGTCTCATGAAACCCCTCTCGGCTTTATGATGCT	300
Db	241	ACTGGAAATTTTCAAAAATTAATGTGGTCTCATGAAACCCCTCTCGGCTTTATGATGCT	300
Qy	301	TATGAATGAACATGCCCTTGAGGGAGCTGGAAACAATGAAAAAGTACTGACAGAAAT	360
Db	301	TATGAATGAACATGCCCTTGAGGGAGCTGGAAACAATGAAAAAGTACTGACAGAAAT	360
Qy	361	ATTGCTTCAGGACACCTGAGAACTGAGAGCACTCAACACAGTTTATGAAAGAAATAT	420
Db	361	ATTGCTTCAGGACACCTGAGAACTGAGAGCACTCAACACAGTTTATGAAAGAAATAT	420
Qy	421	GGCTCAAGCCTGGAAGTACGCTGTGGGGGACACTTCAGGGTACTACACGGGATGTTG	480
Db	421	GGCTCAAGCCTGGAAGTACGCTGTGGGGGACACTTCAGGGTACTACACGGGATGTTG	480
Qy	481	GTGGTCTCCTTCAGGCTAACAGAGACCCGTGATGCTGGAATTGATGAGCTCAAGTTGAA	540
Db	481	GTGGTCTCCTTCAGGCTAACAGAGACCCGTGATGCTGGAATTGATGAGCTCAAGTTGAA	540
Qy	541	CAAGATGCTCAGGCTTTATTTCCAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAG	600
Db	541	CAAGATGCTCAGGCTTTATTTCCAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAG	600
Qy	601	TTTATCACCATCTTTGGAACACGAACTGTCTCATTTGAGAAAGTGTGTTGACAACTAC	660
Db	601	TTTATCACCATCTTTGGAACACGAACTGTCTCATTTGAGAAAGTGTGTTGACAACTAC	660
Qy	661	ATGACTATATCAGATTTCAAAATGAGGAAACCATTTGACCGGAGACTTCTGGCAATTTA	720
Db	661	ATGACTATATCAGATTTCAAAATGAGGAAACCATTTGACCGGAGACTTCTGGCAATTTA	720
Qy	721	GAGCAACTACTCTCTGCTGTGTGAAATCTATTTCGAAGTATACCTGCGCTACCTTCGACAG	780
Db	721	GAGCAACTACTCTCTGCTGTGTGAAATCTATTTCGAAGTATACCTGCGCTACCTTCGACAG	780
Qy	781	ACCCCTCTATTATGCTATGAGGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCAATG	840
Db	781	ACCCCTCTATTATGCTATGAGGGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCAATG	840
Qy	841	GTGTTCCAGGAGTCAGATTGATCTGTTTACATCAGGAAGGAGTTTAGGAAGAAATTTTCCC	900
Db	841	GTGTTCCAGGAGTCAGATTGATCTGTTTAAATCAGGAAGGAGTTTAGGAAGAAATTTTCCC	900
Qy	901	ACCTCTCTTTATTTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTG	960
Db	901	ACCTCTCTTTATTTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTG	960
Qy	961	CTGCTCTCCGGAGAAGATGAC 981	
Db	961	CTGCTCTCCGGAGAAGATGAC 981	

of

Oy	721	GAGCACTACTCCTCGCTGTTGTGGAAATCTATTTCAGAGTATACCTGCCTACCTTGCAGAG	781
Dδ	721	GAGCACTACTCCTCGCTGTTGTGGAAATCTATTTCGAAGTATACCTGCCCTACCTTGCAGAG	781
Oy	781	ACCCTCTATTATCTCTATGAAGSGAGCTGGGACAGATGATCACCCCTCATCAGAGTCA TG	841
Dδ	781	ACCCTCTATTATCTCTATGAAGSGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCA TG	841
Oy	841	GT TTC CAG GAG T GAG AT T GAT CT GT TT AA CAT CAG GA AG G AT TT TAG GA A GA AT TT T GCC	901
Dδ	841	GT TTC CAG GAG T GAG AT T GAT CT GT TT AA CAT CAG SA AG G AG TT TAG GA A GA AT TT T GCC	901
Oy	901	ACCTCTCTTTATTCCTCATGATTAA GG S GAG AT AC AT CTGGGG ACTATAAGAAAGCTCTCTTG	961
Dδ	901	ACCTCTCTTTATTCCTCATGATTAA GG S GAG AT AC AT CTGGGG ACTATAAGAAAGCTCTCTTG	961
Oy	961	CTGCTCTCCGGAGAAGATGAC	981
Dδ	961	CTGCTCTCCGGAGAAGATGAC	981

RESULT 3
US-09-324-096A-5
; Sequence 5, Application US/09324096A

; Patent NO. 6323313
 ; GENERAL INFORMATION:
 ; APPLICANT: Tait, Jonathan

APPLICANT: Brown, David
: TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
: FILE REFERENCE: UOFW-1-13841
: CURRENT APPLICATION NUMBER: US/09/324.096A
: CURRENT FILING DATE: 1999-06-01
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 981
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(981)
US-09-324-096A-5

Query Match 99.5%; Score 976.2; DB 4; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.3e-282;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCGATGTGGCGTGGCCATATGCGACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCT 60
Db 1 ATGCGATGTGGCTCGGCTCATATGCGACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCT 60

Qy 61 GGATTTGATGAGCGGCTGATGCGAAGCTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
Db 61 GGATTTGATGAGCGGCTGATGCGAAGCTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120

Qy 121 GATGAGGAGCATCTGACTCTGTTGCGAGGATCTTCTGATGACCTGAAATGCTCAGCGCCAGGAATC 180
Db 121 GATGAGGAGCATCTGACTCTGTTGCGAGGATCTTCTGATGACCTGAAATGCTCAGCGCCAGGAATC 180

Qy 181 TCTGAGCTTTTAAAGACTCTGTTTGGCAGGATCTTCTGATGACCTGAAATGCTCAGCGCCAGGAATC 240
Db 181 TCTGAGCTTTTAAAGACTCTGTTTGGCAGGATCTTCTGATGACCTGAAATGCTCAGCGCCAGGAATC 240

Qy 241 ACTGGAATTTGAAATTAATTTGCGCTCTGATGAAACCTCTCGGCTTTATGATGCT 300
Db 241 ACTGGAATTTGAAATTAATTTGCGCTCTGATGAAACCTCTCGGCTTTATGATGCT 300

Qy 301 TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360
Db 301 TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360

Qy 361 ATTGCTTCAAGGACACCTGGAAGACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
Db 361 ATTGCTTCAAGGACACCTGGAAGACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420

Qy 421 GGCTCAAGCTTGAAGATGAGCTGTTGGGGACACCTTCAGGGTACTACCAGCGGATGTTG 480
Db 421 GGCTCAAGCTTGAAGATGAGCTGTTGGGGACACCTTCAGGGTACTACCAGCGGATGTTG 480

Qy 481 GTGGTTCTCTCAGGCTTAACAGAGACCTCTGATGCTGGAATTTGATGAGCTCAAGTTGAA 540
Db 481 GTGGTTCTCTCAGGCTTAACAGAGACCTCTGATGCTGGAATTTGATGAGCTCAAGTTGAA 540

Qy 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAATTTAAATGGGGACAGATGAAGAAAG 600
Db 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAATTTAAATGGGGACAGATGAAGAAAG 600

Qy 601 TTTATCACCATTCTTGGACACAGAGTGTCTCATTTTGAGAAAGGTTTGGACAAGTAC 660
Db 601 TTTATCACCATTCTTGGACACAGAGTGTCTCATTTTGAGAAAGGTTTGGACAAGTAC 660

Qy 661 ATGACTATCAGGATTTCAATTTGAGAAACCAATGACCCGAGACTTCTGGCAATTTA 720
Db 661 ATGACTATCAGGATTTCAATTTGAGAAACCAATGACCCGAGACTTCTGGCAATTTA 720

Qy 721 GAGCACTACTCTCTGTTGTTGAAATCTATTTCGAAGTATACCTGCTACTCTGCAGAG 780
Db 721 GAGCACTACTCTCTGTTGTTGAAATCTATTTCGAAGTATACCTGCTACTCTGCAGAG 780

Qy 781 ACCCTCTATTATGCTATGAAGGGAGCTGGGACAGATGATCATACCTCATCAGAGTCA 840

Db 781 ACCCTCTATTATGCTATGAAGGAGCTGGGACAGATGATCATACCTCATCAGAGTCA 840
Qy 841 GTTTCAGGAGTGAAGTGTCTTTAAACATCAGGAGGAGTTTAGGAAGATTTTCC 900
Db 841 GTTTCAGGAGTGAAGTGTCTTTAAACATCAGGAGGAGTTTAGGAAGATTTTCC 900
Qy 901 ACCTCTCTTTATCCATGATTAAAGGAGATACATCTGGGAGTATTAAGAAAGCTCTTCTG 960
Db 901 ACCTCTCTTTATCCATGATTAAAGGAGATACATCTGGGAGTATTAAGAAAGCTCTTCTG 960
Qy 961 CTGCTCTCCGGAGAGATGAC 981
Db 961 CTGCTCTCCGGAGAGATGAC 981

RESULT 4
522537-3
: Patent No. 522537
: APPLICANT: FOSTER, DONALD
: TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
: PHOSPHOLIPID-BINDING PROTEINS
: NUMBER OF SEQUENCES: 14
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/459.082
: FILING DATE: 29-DEC-1989
: SEQ ID NO: 3
: LENGTH: 1460
522537-3

Query Match 97.5%; Score 956.8; DB 6; Length 1460;
Best Local Similarity 99.8%; Pred. No. 1.8e-276;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 22 ATGCGACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
Db 13 ATGCGACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 72

Qy 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCTCGACT 141
Db 73 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCTCGACT 132

Qy 142 CTGTTGACATCCGGAAGTAAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTCTG 201
Db 133 CTGTTGACATCCGGAAGTAAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTCTG 192

Qy 202 TTTGCGAGGATCTCTGATGACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
Db 193 TTTGCGAGGATCTCTGATGACTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 252

Qy 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATCGCTTG 321
Db 253 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATCGCTTG 312

Qy 322 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTTCTTCAAGGACACCTGAA 381
Db 313 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTTCTTCAAGGACACCTGAA 372

Qy 382 GAATGAGAGCATCAAAAGTTTATGAAGAAGTATGGCTCAAGCTTGAAGATGAC 441
Db 373 GAATGAGAGCATCAAAAGTTTATGAAGAAGTATGGCTCAAGCTTGAAGATGAC 432

Qy 442 GTGTGGGGGACACTTCCAGGCTACTACCAGCGGATGTTGGTGGTCTCTCAGGCTAAC 501
Db 433 GTGTGGGGGACACTTCCAGGCTACTACCAGCGGATGTTGGTGGTCTCTCAGGCTAAC 492

Qy 502 AGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTTATTT 561
Db 493 AGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTTATTT 552

Qy 562 CAGCTGAGAACTTAAATGGGGGACAGATGAAAGAAAGTTTATCACCATCTTTGGAACA 621
Db 553 CAGCTGAGAACTTAAATGGGGGACAGATGAAAGAAAGTTTATCACCATCTTTGGAACA 612

QY 622 CGAAGTGTCTCATTTGAGAAAGTCTTTGACAAGTACATGACTATATCAGGATTCAA 681
DB 613 CGAAGTGTCTCATTTGAGAAAGTCTTTGACAAGTACATGACTATATCAGGATTCAA 672
QY 682 ATTGAGAAACCAATTGACCGGAGACTCTGGCAATTTAGAGCAACTACTCCTTGTGTT 741
DB 673 ATTGAGAAACCAATTGACCGGAGACTCTGGCAATTTAGAGCAACTACTCCTTGTGTT 732
QY 742 GTCAATCTATTGCAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATCAAG 801
DB 733 GTCAATCTATTGCAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATCAAG 792
QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCAATGTTTCCAGGAGTGAATGAT 861
DB 793 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCAATGTTTCCAGGAGTGAATGAT 852
QY 862 CTGTTTAACATCAGGAGGAGTTTAGAAGAAATTTTGGCCACCTCTCTTTATTCATGATT 921
DB 853 CTGTTTAACATCAGGAGGAGTTTAGAAGAAATTTTGGCCACCTCTCTTTATTCATGATT 912
QY 922 AAGGGAGATACATCTGGGAGTATAAGAAAGCTCTTCTGCTGCTCCCGGAGAGATGAC 981
DB 913 AAGGGAGATACATCTGGGAGTATAAGAAAGCTCTTCTGCTGCTCTGTGGAGAGATGAC 972

RESULT 5
US-08-125-746-2
; Sequence 2, Application US/08125746
; Patent No. 5591633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IWASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 037227/1987
; FILING DATE: 20-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184428/1987
; FILING DATE: 23-JUL-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5591633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELETEXT: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 136..1095
; US-08-125-746-2

Query Match 97.5%; Score 956.8; DB 1; Length 1567;
Best Local Similarity 99.8%; Pred. No. 1.8e-276;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
DB 136 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 135
QY 82 GCAGAACTCTTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141
DB 196 GCAGAACTCTTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 255
QY 142 CTGTTGACATCCCGAAGTATGCTCAGCGCCAGCAATCTCTGCAGCTTTTAAGACTCTG 201
DB 256 CTGTTGACATCCCGAAGTATGCTCAGCGCCAGCAATCTCTGCAGCTTTTAAGACTCTG 315
QY 202 TTTGGCAGGAGTCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 261
DB 316 TTTGGCAGGAGTCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 375
QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAAACATGCTTG 321
DB 376 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAAACATGCTTG 435
QY 322 AAGGGAGCTGGAAACAAATGAAGAAGTACTCAGCAAGAAATTTATGCTTCAAGGACACCTGAA 381
DB 436 AAGGGAGCTGGAAACAAATGAAGAAGTACTCAGCAAGAAATTTATGCTTCAAGGACACCTGAA 495
QY 382 GAACTCAGAGGCCATCAACAAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGAC 441
DB 496 GAACTCAGAGGCCATCAACAAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGAC 555
QY 442 GTGGTGGGGACACTTTCAGGGTACTACACGCGGATCTTGGTGGTCTTCTCCTTCAGGCTAAC 501
DB 556 GTGGTGGGGACACTTTCAGGGTACTACACGCGGATCTTGGTGGTCTTCTCCTTCAGGCTAAC 615
QY 502 AGAGACCCCTGATGCTGCAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
DB 616 AGAGACCCCTGATGCTGCAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 675
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA 621
DB 676 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGAAACA 735
QY 622 CNAAGTGTCTCTCATTTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTCAA 681
DB 736 CNAAGTGTCTCTCATTTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTCAA 795
QY 682 ATTGAGAAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGTGTT 741
DB 796 ATTGAGAAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGTGTT 855
QY 742 GTGAAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 801
DB 856 GTGAAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG 915
QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCAATGTTTCCAGGAGTGAATGAT 861
DB 916 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCAATGTTTCCAGGAGTGAATGAT 975
QY 862 CTGTTTAAACATCAGGAGGAGTTTAGAAGAAATTTTGGCCACCTCTCTTTATTCATGATT 921
DB 976 CTGTTTAAACATCAGGAGGAGTTTAGAAGAAATTTTGGCCACCTCTCTTTATTCATGATT 1035

Qy	922	AAGGGAGATACATCTGGGGACTATAGAAAGCTCTTCTGCTCTCCGGGAGAAGATGAC	981
D _b	1036	AAGGGAGATACATCTGGGGACTATAGAAAGCTCTTCTGCTCTGTGGAGAAGATGAC	1095

RESULT 6

US-08-125-746-4
Sequence 4, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: IWASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-125-746-4

Qy	205	GGCAGGATCTTCGGATGACCTGAAATCGAAGCTAACCTGGAAAAATTGTGAATAATTAATT	264
Dd	181	GGCAGGATCTTCGGATGACCTGAAATCGAAGCTAACCTGGAAAAATTGTGAATAATTAATT	240
Qy	265	GTGGCTCTGATGAACCCTCTCGGCTTTTATGATGCTTATGAACCTGAACATGCCCTTGAG	324
Dd	241	GTGGCTCTGATGAACCCTCTCGGCTTTTATGATGCTTATGAACCTGAACATGCCCTTGAG	300
Qy	325	GGAGCTGGACAATAATGAAAAAGTAGCTGCACAGAAAATTATTGCTTCAAGGACACCTCGAAGAA	384
Dd	301	GGAGCTGGACAATAATGAAAAAGTAGCTGCACAGAAAATTATTGCTTCAAGGACACCTCGAAGAA	360
Qy	385	CTGAGAGCCATCAACAAGTTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGACGTG	444
Dd	361	CTGAGAGCCATCAACAAGTTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGACGTG	420
Qy	445	GTGGGGACACTTCAGGTACTACCAGCGATGTTGGTGGTTCTCTTCAGGCTAACAGA	504
Dd	421	GTGGGGACACTTCAGGTACTACCAGCGATGTTGGTGGTTCTCTTCAGGCTAACAGA	480
Qy	505	GACCTCATGCTGGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTTCAG	564
Dd	481	GACCTCATGCTGGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTTCAG	540
Qy	565	GCTGGAGAACTTAATGGGGACAGATGAAGAAAAGTTTATCACCATCTTTTGGACACGA	624
Dd	541	GCTGGAGAACTTAATGGGGACAGATGAAGAAAAGTTTATCACCATCTTTTGGACACGA	600
Qy	625	AGTGTGTCATTTGAGAAAGTGTTTCACAGTACATGACTATATCAGGATTCGAAATT	684
Dd	601	AGTGTGTCATTTGAGAAAGTGTTTCACAGTACATGACTATATCAGGATTCGAAATT	660
Qy	685	GAGAAACCAATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCTGCTGTTGTG	744
Dd	661	GAGAAACCAATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCTGCTGTTGTG	720
Qy	745	AAATCTATTCGAAGTATACCTGCTTACCTTCGAGAGACCTCTATTATGCTATGAAGGA	804
Dd	721	AAATCTATTCGAAGTATACCTGCTTACCTTCGAGAGACCTCTATTATGCTATGAAGGA	780
Qy	805	GCTGGACAGATGATCATACCTCATCAGATCATGTTTCGAGGAGTCAGATTGATCTG	864
Dd	781	GCTGGACAGATGATCATACCTCATCAGATCATGTTTCGAGGAGTCAGATTGATCTG	840
Qy	865	TTTAAATCATCAGGAGGCTTTAGGAAGAATTTTGGCACCTCTCTTATTTCCATGATTAAG	924
Dd	841	TTTAAATCATCAGGAGGCTTTAGGAAGAATTTTGGCACCTCTCTTATTTCCATGATTAAG	900
Qy	925	GGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCGGGAGAGATGAC	981
Dd	901	GGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTGTTGGAGAAATGAC	957

RESULT 7

RES-091 /
US09-643-597-261
Sequence 261, Application US/09643597
Patent NO. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: AND DIAGNOSIS O
FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.8e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 81
DB 89 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 208
QY 142 CTGTTGACATCCCGAAGTAACTGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAAGACTCTG 201
DB 209 CTGTTGACATCCCGAAGTAACTGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAAGACTCTG 268
QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAACTCAGAACTAAGTGGAAAAATTTGAAAAATTA 261
DB 269 TTTGGCAGGGATCTTCTGGATGACCTGAACTCAGAACTAAGTGGAAAAATTTGAAAAATTA 328
QY 262 ATGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTTG 321
DB 329 ATGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTTG 388
QY 322 AAGGGAGCTGGAA 334
DB 389 AAGGGAGCTGGAA 401

RESULT 8

US-09-480-884A-261
; Sequence 261, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.8e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 81
DB 89 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 208
QY 142 CTGTTGACATCCCGAAGTAACTGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAAGACTCTG 201
DB 209 CTGTTGACATCCCGAAGTAACTGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAAGACTCTG 268
QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAACTCAGAACTAAGTGGAAAAATTTGAAAAATTA 261
DB 269 TTTGGCAGGGATCTTCTGGATGACCTGAACTCAGAACTAAGTGGAAAAATTTGAAAAATTA 328
QY 262 ATGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTTG 321
DB 329 ATGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTTG 388
QY 322 AAGGGAGCTGGAA 334
DB 389 AAGGGAGCTGGAA 401

RESULT 9

US-09-542-615A-261
; Sequence 261, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.8e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 81
DB 89 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 208
QY 142 CTGTTGACATCCCGAAGTAACTGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAAGACTCTG 201
DB 209 CTGTTGACATCCCGAAGTAACTGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAAGACTCTG 268
QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAACTCAGAACTAAGTGGAAAAATTTGAAAAATTA 261
DB 269 TTTGGCAGGGATCTTCTGGATGACCTGAACTCAGAACTAAGTGGAAAAATTTGAAAAATTA 328

QY 262 ATTGTGGCTCTGATGAACACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 321
|||||
Db 329 ATTGTGGCTCTGATGAACACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 388
|||||
QY 322 AAGGAGCTGGAA 334
|||||
Db 389 AAGGAGCTGGAA 401
|||||

RESULT 10

US-09-606-421B-261
; Sequence 261, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasar A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 1.8e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGATGAGCGGGCTGAT 81
|||||
Db 89 ATGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGATGAGCGGGCTGAT 148
|||||
QY 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGGATCCTGACT 141
|||||
Db 149 GCANAACTCTTCGGAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGGATCCTGACT 208
|||||
QY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAAGACTGTG 201
|||||
Db 209 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAAGACTGTG 268
|||||
QY 202 TTTCGAGGAGTCTCTGGATGACTGAAATCAGAACTAACTGGAAAATTTGAAAATTA 261
|||||
Db 269 TTTCGAGGAGTCTCTGGATGACTGAAATCAGAACTAACTGGAAAATTTGAAAATTA 328
|||||
QY 262 ATTGTGGCTCTGATGAACACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 321
|||||
Db 329 ATTGTGGCTCTGATGAACACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTTG 388
|||||
QY 322 AAGGAGCTGGAA 334
|||||
Db 389 AAGGAGCTGGAA 401
|||||

RESULT 11

US-08-526-136-1
; Sequence 1, Application US/08526136

; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2305
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-526-136-1

Query Match 31.7%; Score 310.8; DB 3; Length 2305;
Best Local Similarity 58.0%; Pred. No. 4.7e-83;
Matches 549; Conservative 0; Mismatches 397; Indels 0; Gaps 0;

QY 36 CAGAGGCACTGTGACTGACTTCCCTGGATTGTGATGAGCGGGCTGATGAGAACTCTTTCG 95
|||||
Db 665 CCGAGGCACCATCACAGATGCATCTGGCTTTTGACCCCTCGCAGATGCTGAAGTCTGCG 724
|||||
QY 96 GAAGGCTATGAAGGCTTGGCCACAGATGAGGAGAGATCCTGACTCTGTTGACATCCGG 155
|||||
Db 725 GAAGGCCATGAAGGCTTTGGGACTGAGCAGCAGGCCATCATTTGACTCCCTGGTAGTCG 784
|||||
QY 156 AAGTAATCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTGTTTGGCAGGATCT 215
|||||
Db 785 CTCCACACAGCAGCAGCAGATGCTCTGCTGTTCAAGCAGCATATGGGAAGATTT 844
|||||
QY 216 TCTGGATGACCTGAAATCAGAACTAACTGGAAAATTTGAAAATTTAATTTGGCTCTGAT 275
|||||
Db 845 GATCAAGACTGTAATCTGAATCTGAACTGTCAGGAACTTTGAGAAGACAACTTTGGCCCTGAT 904
|||||
QY 276 GAAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAAACATGCTTGAAGGAGCTGGAAC 335
|||||
Db 905 GAAGACCCCTCTCTCTTTGAGCGCTTATGAGTAAGGAAGCTATCAAGGGGGCGGGCAC 964
|||||
QY 336 AAATGAAAAAGTACTGACAGAAATTTATGCTTTCAGGACACCTGTAAGAACTGAGAGCCAT 395
|||||
Db 965 TGATGAAGCCCTGCTGATGATGATGCTTGGCCCTCCCGCAGCAGCAGCATCCGGGAGCT 1024
|||||
QY 396 CAAACAAGTTTATGAAGAAATATGCTCAAGCCTGGAAGATGACGTGGTGGGGGACAC 455
|||||

1025 GAACAGAGTCTACAGACAGAAATTCAAAAGAGCCCTGGAGGAGCCATTCGGAGCGACAC 1084
456 TTCAGGGTACTACACAGCGGATGTTGGTGTCTCTCCTTACAGGCTTAAACAGAGACCCCTGATGC 515
1085 TTCAGGGCACTTCAGGGGCTCTCTCTCTCCTCAGGGAACCGGGATGAAGACAC 1144
516 TGAATTTGATGAAGCTCAAGTTCAACAAGATGCTCAGGCTTATTTTCAGGCTGGAAGACT 575
1145 AACGTGGACATGACCCCTTGTCCAGAGAGATGTGCAGGAGCTCTATGCAGCTGGGAGAA 1204
576 TAAATGGGGACAGATGAAGAAAGTTTATACACCTTTTGGAAACAGAGTGTGTCTCA 635
1205 CCCTCTGGGAACAGATGAGTCCAAAGTTCAATGGGATTTCTGTCTCCGGAGCGGGCCCA 1264
636 TTTGAAAGAGTCTTGGACAGTACATGACTATATCAGGATTTCAAAATGAGGAACCAT 695
1265 CTTGGTGGGAGTTTAAACAGATATCAGAGGATGACAGGACGTGACATTTGAGAAGACAT 1324
696 TGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGTCTGTGTGCTGAAATCTATTGC 755
1325 CTGCGGGAGATCTCGGGGACCTGGAGCAGGCGCATGCTGGCTGTGTGTAATGTCTTAA 1384
756 AAGTATACCTGCTACTCTGCAGAGACCCCTCTATTATGCTATGAAGGAGCTGGGACAG 815
1385 GAATACCCCGAGCTCTTTGCTGAAAGGCTCAACAAGGCGCATGAGGGAGCCCGGAACCA 1444
816 TGATCATACCTCATCAGAGTCAATGTTCCAGAGTGTGATGATGCTGTGTTAAACATCAG 875
1445 AGACCGGACCTGATCGGATCATGTTGCTCCAGGAGTGTCTCCAGGAGTGCAGCTCTGCAATCAG 1504
876 GAAGGAGTTTGAAGAAATTTTCCACCTCTCTTTTATTCATGATTAAAGGAGATACATC 935
1505 AGCAGAGTAAAGCGCTGTATGGCAAGTGTGTACAGGACATCAGCGGACACACTTC 1564
936 TGGGGACTATAAGAAAGCTTCTTCTGCTCTCCGGAGAGATGAC 981
1565 AGGGGATACCGGAAGATTCTGCTGAAGATCTGTGTGGCAATGAC 1610

RESULT 12

US-08-526-136-3

; Sequence 3, Application US/08526136

; Patent No. 6107089

; GENERAL INFORMATION:

; APPLICANT: Towle, Christine A. et al.

; TITLE OF INVENTION: ANNEXIN XI

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX

; SOFTWARE: Wordperfect (Version 3.30)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/526,136

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION NUMBER: US/08/214,036

; FILING DATE:

; APPLICATION NUMBER: 07/837,775

; FILING DATE: February 13, 1992

; APPLICATION NUMBER: 07/764,465

; FILING DATE: September 23, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-526-136-3

Query Match 31.7%; Score 310.8; DB 3; Length 2311;
Best Local Similarity 58.0%; Pred. No. 4.8e-83;
Matches 549; Conservative 0; Mismatches 397; Indels 0; Gaps 0;
36 CAGAGGACATGTGACTGACTTCCCTGGATTTGATGAGCGGCTGTATGTCAGAAAACCTTCG 95
671 CCAGGACCACTACAGATGCATCTGGCTTTGACCCCTCGAGATGCTGAAGTCTCTCG 730
96 GAAGGCTATGAAGGCTTGGCACAGATGAGGAGAGATCCTGACTCTGTGACATCCCG 155
731 GAAGGCTATGAAGGCTTGGGACTGACGAGCAGGCGCATCATTTGACTGCCCTGGTAGTCG 790
156 AAGTAAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTCTTTGGCAGGGATCT 215
791 CTCCAACAGCAACGACAGCAGATCCTCTGCTGCTTCAACAGACAGCATATGGGAAGGATTT 850
216 TCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAATTAATTTGGCTCTGAT 275
851 GATCAAGATCTGAAATCTGAACTGTCAAGAAACTTTTGAAGAGACAATCTTTGCCCTGAT 910
276 GAACCTCTCGGCTTATGATGCTTATGAATGAAACATGCTTGAAGGAGCTGGAAC 335
911 GAAGCCCTCTCTCTTTGACCTTATGAGATGAAGAGAGCTATCAAGGGGGCGGCAC 970
336 AATGAAAGTACTGACAGAAATTTATGCTTCAAGAGACACCTGAAGAACTGAGAGCAT 395
971 TGATGAAGCTGCTGATGATGATGCTTGGCTTCCCGCAGCAACGAGCAGCATCCGGAGCT 1030
396 CAACAAAGTTTATGAAGAAGAAATGCTCAAGCTGGAAGATGACGTGTGGGGGACAC 455
1031 GAACAGAGTCTACAAGACAGAAATTCAAAAGACCTCGAGGAGGCCATTCGGAGCGAC 1090
456 TTCAGGCTACTACGAGGATGTTGGTGTCTCTTCAAGCTTAACAGAGACCTGATGC 515
1091 TTCAGGCACTTCCAGGCTCTCTATCTCTCTCTCTCAGGGAACCGGGATGAAGCAC 1150
516 TGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTTCAGGCTGAGAACT 575
1151 AACGTGGACATGACCTTGTCCAGAGAGATGTGCAGGAGCTCTATGCAGCTGGGAGAA 1210
576 TAAATGGGGACAGATGAAGAAAGTTTATCACATCTTTTGAACAGAGAGTGTGTCTCA 635
1211 CCCTCTGGGAAACAGATGAGTCCAAAGTTCAATGCGATTTCTGTCTCCCGGAGCGGGCCA 1270
636 TTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAAAATTCAGGAACCAT 695
1271 CCTGGTGGCAGTTTAAACAGATATCAGAGGATGACAGGACGTGACATTTGAGAAGACAT 1330
696 TGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTGTGTAATCTATTTCG 755
1331 CTCCCGGAGATGTCCGGGACCTCGAGAGGCGATGCTGCTGTGTGTAATCTATTTCG 1390
756 AAGTATACCTGCTACCTTTCAGAGACCCCTCTATTATGCTATGAAGGAGCTGGGACAGA 815
1391 GAATACCCAGCTCTCTTCTGTAAGGCTCAACAAGGCCATGAGGGGAGCCCGGAACCA 1450
816 TGATCATACCTCATCAGAGTCAATGTTTCCAGAGTGAATGATGATCTGTTTAACTACAG 875
1451 AGACCGGACCTGTATCGCATCATGTTGTTCTCGAGGAGATGAGCTCTCTGAGACATCAG 1510

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 721
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(644)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-721

Query Match 12.6%; Score 123.6; DB 3; Length 644;
Best Local Similarity 52.6%; Pred. No. 2.7e-27;
Matches 267; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

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QY 356 AAATTTATGCTTCAAGGACACCTGAAGAAGCTGAGAGCCATCAACAAGTTTATGAAGAAG 415
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 511 AGATTTTGTGTCNCAAGACCAATCAAGGAATCCGAGAAATGTCAGATGTTATCAGTCAG 452
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 416 AATATGGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACACGCGGA 475
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 451 AATTTGGACGAGACCTTGAAGAGNCATTAAGGTACAGATACATCAGGACATTTTGAACGTT 392
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 476 TGTGGTGGTTCCTTCAGGCTAACAGAGACCCCTGATGCTGGAATGATGAAGCTCAAG 535
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 391 TACTTGTGTCATGTGCCAGGGAATCGTGATGAGAACCCAGAGATATAAACCCACCAATGG 332
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 536 TTCAACAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAATTAATGGGGGACAGATGAAG 595
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 331 CTCAGGAAGATGCTCAGGCTCTCTATCAAGCTGGTGAAGGGGAGCTAGGACCCGATGAAT 272
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 596 AIAAGTTTATCACCATCTTTTGAACACGAGTGTCTCATTTGAGAAAGGTGTTTGACA 655
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 271 CTTCGCTTAAATGATCTCTTGGCACAGAAGCTTCTCAGCTGAGAGCTACCATGGAGG 212
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 656 AGTACATGACTATACAGATTTCAAAATGAGAGAAACCATTTACCCGGAGACTTCTGGCA 715
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 CTTATTCTAGGATGGTAAATCGAGACTTGTAAAGCAGTGTGAGCCGTGAGTTTCCGGAT 152
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 716 ATTTAGGACCACTACCTCTGCTGTTGTGAAATCTATTGAAATATACCTGCTACTCTTG 775
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 ATGTAGAAGTGGTTTGAAGACCATCTTCAGTGTGCCCTGMAACCCCTGCTCTCTTTG 92
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 776 CAGAGACCCCTCTATTATGCTATGAAGGAGCTGGGACAGATCATACCTCATCAGAG 835
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QY 836 TCATGCTTTCCAGGAGTGAGATTGATCT 863
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RESULT 15

US-09-328-111-625/c
; Sequence 625, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111

; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 625
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-625

Query Match 9.8%; Score 96.6; DB 3; Length 502;
Best Local Similarity 53.6%; Pred. No. 2.9e-19;
Matches 201; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

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Db 259 -AATGCACAGAGACAGGATATTGCTTTCGCTTACCCAGAGAGGACCAAAAAGGAATTTGCA 200
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 GATGACTGANAATCAGAACTAACTGGAAAATTTGAAAATTAATTTGGCTCTGATGAA 279
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QY 280 CCCTCTCGGCTTTATGATGCTTATGAACATGAACATGCCCTTGAAGGAGCTGGAACAAAT 339
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QY 400 CAAGTTTATGAAGAA 414
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Search completed: August 28, 2003, 19:41:15
Job time : 57.3333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:49:00 ; Search time 55.3333 Seconds
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7825.244 Million cell updates/sec

Title: US-09-970-969-3

Perfect score: 981

Sequence: 1 atggcagggtgtgtggcca.....tgctctccggagaagatgac 981

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	977.8	99.7	981	4	US-09-324-096A-1
3	976.2	99.5	981	4	US-09-324-096A-5
4	956.8	97.5	1460	6	5225537-3
5	956.8	97.5	1567	1	US-08-125-746-2
6	953.8	97.2	957	1	US-08-125-746-4
7	311	31.7	401	4	US-09-643-597-261
8	311	31.7	401	4	US-09-480-884A-261
9	311	31.7	401	4	US-09-542-615A-261
10	311	31.7	401	4	US-09-606-421B-261
11	310.8	31.7	2305	3	US-08-526-136-1
12	310.8	31.7	2311	3	US-08-526-136-3
13	134.6	13.7	1793	4	US-09-620-312D-747
14	123.6	12.6	644	3	US-09-328-111-721
15	96.6	9.8	502	3	US-09-328-111-625
16	96.6	9.8	630	3	US-09-328-111-491
17	93.6	9.5	501	3	US-09-328-111-481
18	88.2	9.0	1293	4	US-09-325-932A-17
19	74.8	7.6	643	3	US-09-385-982-306
20	69.6	7.1	543	3	US-09-328-111-428
21	69.4	7.1	704	4	US-09-325-932A-21
22	60.6	6.2	1001	4	US-09-641-638-188
23	59.6	6.1	789	4	US-09-325-932A-20
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25	47.4	4.8	1001	4	US-09-641-638-123
26	44.8	4.6	1001	4	US-09-641-638-106
27	44.8	4.6	1001	4	US-09-641-638-107

c	28	44.6	4.5	215	4	US-09-451-651-24	Sequence 24, Appl
	29	44.2	4.5	212	1	US-08-594-031-156	Sequence 156, App
	30	44	4.5	741	4	US-09-641-638-81	Sequence 81, Appl
	31	41.6	4.2	1001	4	US-09-641-638-202	Sequence 202, App
	32	41.2	4.2	1001	4	US-09-641-638-201	Sequence 201, App
	33	37.8	3.9	640	3	US-08-961-083-33	Sequence 33, Appl
	34	37.8	3.9	640	4	US-09-536-784-33	Sequence 33, Appl
	35	37.8	3.9	11309	4	US-08-961-527-108	Sequence 108, App
	36	37	3.8	278	2	US-08-454-557C-101	Sequence 101, App
	37	37	3.8	278	2	US-08-340-426D-101	Sequence 101, App
	38	37	3.8	278	2	US-08-450-673C-101	Sequence 101, App
	39	37	3.8	278	5	PCT-US95-17111A-101	Sequence 101, App
c	40	36	3.7	2416	4	US-09-016-434-1270	Sequence 1270, Ap
c	41	35.6	3.6	546	4	US-09-252-991A-5395	Sequence 5395, Ap
c	42	35.6	3.6	969	4	US-09-252-991A-5401	Sequence 5401, Ap
c	43	35.6	3.6	1464	4	US-09-252-991A-5409	Sequence 5409, Ap
c	44	35.6	3.6	2403	4	US-09-252-991A-5404	Sequence 5404, Ap
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ALIGNMENTS

RESULT 1

US-09-324-096A-3

; Sequence 3, Application US/09324096A

; Patent No. 6323313

; GENERAL INFORMATION:

; APPLICANT: Tait, Jonathan

; APPLICANT: Brown, David

; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES

; FILE REFERENCE: DOFW-1-13841

; CURRENT APPLICATION NUMBER: US/09/324.096A

; CURRENT FILING DATE: 1999-06-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 981

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(981)

; US-09-324-096A-3

Query Match 100.0%; Score 981; DB 4; Length 981;

Best Local Similarity 100.0%; Pred. No. 1.4e-283;

Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCGAGTGGCTGTGGCCATATGGCACAGTTCTCAGAGGCACCTGTGACTTGCTTCCT	60
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Qy	61	GGATTTGATGAGCGGGCTGATGCAGAAACTTTTCGGAAGGCTATGAAAGGCTTGGGCACA	120
Db	61	GGATTTGATGAGCGGGCTGATGCAGAAACTTTTCGGAAGGCTATGAAAGGCTTGGGCACA	120
Qy	121	GATGAGGAGACATCTGACTCTGTTGCATCCGGAAGTAACTGCTCAGCGCCAGGAATC	180
Db	121	GATGAGGAGACATCTGACTCTGTTGACATCCGGAAGTAACTGCTCAGCGCCAGGAATC	180
Qy	181	TCGTCAGCTTTTAAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTA	240
Db	181	TCGTCAGCTTTTAAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTA	240
Qy	241	ACTGGAAATTTGAAATTAATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCT	300
Db	241	ACTGGAAATTTGAAATTAATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCT	300
Qy	301	TATGAACCTGAACATGCTTTGAAGGAGCTTGGAAACAATAAAGTACTGACAGAAAT	360
Db	301	TATGAACCTGAACATGCTTTGAAGGAGCTTGGAAACAATAAAGTACTGACAGAAAT	360

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QY 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
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Db 421 GGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGCTACTACACGGGATGTTG 480
QY 481 GTGGTCTCTTCAGGCTAACAGAGACACCTGATGCTGGATGATGAAGCTCAAGTTGAA 540
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Db 721 GAGCAACTACTCTTCTGCTGTTGAAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAG 780
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QY 841 GTTTCAGAGGTGAGATGATCTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGCC 900
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Db 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGGACTATAAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGGAGAGATGAC 981
Db 961 CTGCTCTCCGGAGAGATGAC 981

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RESULT 2

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US-09-324-096A-1
; Sequence 1, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(981)
US-09-324-096A-1

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Query Match 99.7%; Score 977.8; DB 4; Length 981;
Best Local Similarity 99.8%; Pred. No. 1.3e-282;
Matches 979; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCAGGTGGCTGTGGCCATATGCCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCT 60
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Db 1 ATGGCATGTGGCGGTGGCCATATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCT 60
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Db 61 GGATTTGATGACGGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
QY 121 GATGAGGAGAGCATCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAAATC 180
Db 121 GATGAGGAGAGCATCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAAATC 180
QY 181 TCTGAGCTTTTAAAGACTCTGTTTGGCAGGATCTTCGGATGACCTGAATTCAGAACTA 240
Db 181 TCTGAGCTTTTAAAGACTCTGTTTGGCAGGATCTTCGGATGACCTGAATTCAGAACTA 240
QY 241 ACTGCAAAATTTGAAAATTAATCTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCT 300
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QY 301 TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAGTACTGACAGAAAT 360
Db 301 TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAGTACTGACAGAAAT 360
QY 361 ATTGCTTCAAGGACACCTGAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
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QY 421 GGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGCTACTACACGGGATGTTG 480
Db 421 GGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGCTACTACACGGGATGTTG 480
QY 481 GTGGTCTCTTCAGGCTAACAGAGACCCCTGATGCTGGAATTTGATGAAGTCTCAAGTTGAA 540
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QY 541 CAAGATGCTCAGGCTTTATTTTCAAGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
Db 541 CAAGATGCTCAGGCTTTATTTTCAAGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
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Db 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
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Db 841 GTTTCAGAGGTGAGATGATCTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGCC 900
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Db 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGGACTATAAAGAAAGCTCTTCTG 960
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RESULT 3
US-09-324-096A-5
; Sequence 5, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan

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APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES.
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324.096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(981)
US-09-324-096A-5

Query Match 99.5%; Score 976.2; DB 4; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.9e-282;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGCGAGTGGCTGTGGCCATATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCCT 60
Db 1 ATGCGAGTGGCTGTGGCCATATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCCT 60
Qy 61 GGATTTGATGAGCGGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
Db 61 GGATTTGATGAGCGGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120
Qy 121 GATGAGGAGCATCTTGAAGTCTTGTGACATCCCGAAGTATGCTCAGCGCCAGGAATC 180
Db 121 GATGAGGAGCATCTTGAAGTCTTGTGACATCCCGAAGTATGCTCAGCGCCAGGAATC 180
Qy 181 TCTCAGCTTTAAGACTCTTTTGGCAGGAGTCTTCTGATGATGACCTGAAATCAGAACTA 240
Db 181 TCTCAGCTTTAAGACTCTTTTGGCAGGAGTCTTCTGATGATGACCTGAAATCAGAACTA 240
Qy 241 ACTGGAAATTTGAAATTAATTTGGCTGTGATGAAACCTCTCGGCTTTATGATGCT 300
Db 241 ACTGGAAATTTGAAATTAATTTGGCTGTGATGAAACCTCTCGGCTTTATGATGCT 300
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Db 301 TATCACTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT 360
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Db 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAGATAT 420
Qy 421 GGCTCAAGCTTGAAGATGAGCTGGTGGGAGACACTTCAAGGTACTACAGCGGATGTTG 480
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Db 781 ACCCTCTATTATGCTATGAGGGAGCTGGGACAGATGATCATACCTCATCAGAGTCATG 840
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Qy 961 CTGCTCTCCGAGAGATGAC 981
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RESULT 4
522537-3
; Patent No. 522537
; APPLICANT: FOSTER, DONALD
; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
; PHOSPHOLIPID-BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459.082
; FILING DATE: 29-DEC-1989
; SEQ ID NO: 3
; LENGTH: 1460
522537-3
Query Match 97.5%; Score 956.8; DB 6; Length 1460;
Best Local Similarity 99.8%; Pred. No. 3e-276;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 22 ATGCACAGTTCAGAGGCACTGTGACTGACTTCCCTGGATTGTAGCGGGCTGAT 81
Db 13 ATGCACAGTTCAGAGGCACTGTGACTGACTTCCCTGGATTGTAGCGGGCTGAT 72
Qy 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGACAGATGAGGAGCATCTGACT 141
Db 73 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGACAGATGAGGAGCATCTGACT 132
Qy 142 CTGTTGATATCCCGAAGTAAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAAGACTG 201
Db 133 CTGTTGATATCCCGAAGTAAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAAGACTG 192
Qy 202 TTTCGAGGATCTCTCGGATGACCTGAAATCAGAACTAACTGGAAATTTGAAAAATTA 261
Db 193 TTTCGAGGATCTCTCGGATGACCTGAAATCAGAACTAACTGGAAATTTGAAAAATTA 252
Qy 262 ATTGCTGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTG 321
Db 253 ATTGCTGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCCCTG 312
Qy 322 AAGGAGCTGGAACAAATGAAAGAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 313 AAGGAGCTGGAACAAATGAAAGAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372
Qy 382 GAATGAGAGCATCAACAAAGTTTATGAAAGAAATATGCTCAAGCTTGGAGATGAC 441
Db 373 GAATGAGAGCATCAACAAAGTTTATGAAAGAAATATGCTCAAGCTTGGAGATGAC 432
Qy 442 GTGCTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 501
Db 433 GTGCTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 492
Qy 502 AGAGACCTTGATGCTGGAATTTGATGAAGCTCAAGTGTGAACAAAGTGTCTCAGGCTTATTT 561
Db 493 AGAGACCTTGATGCTGGAATTTGATGAAGCTCAAGTGTGAACAAAGTGTCTCAGGCTTATTT 552
Qy 562 CAGCTGGAGAACTTAAATGGGGACAGATGAAAGAAATTTATCACCATCTTTGGAAACA 621
Db 553 CAGCTGGAGAACTTAAATGGGGACAGATGAAAGAAATTTATCACCATCTTTGGAAACA 612

```

QY 622 CGAAGTGTCTCTATTGAGAAAGGTGTTTGACAAAGTACATGACTATATCAGGATTCAA 681
Db 613 CGAAGTGTCTCTATTGAGAAAGGTGTTTGACAAAGTACATGACTATATCAGGATTCAA 672
QY 682 ATTGAGAAACCAATTCACCGGAGACTTCTGGCAATTTAGAGAACTACTCTTGTCTGTT 741
Db 673 ATTGAGAAACCAATTCACCGGAGACTTCTGGCAATTTAGAGAACTACTCTTGTCTGTT 732
QY 742 GTGAATCTATTGGAAGTATACCTGCTACCTTGACAGAGCCCTCTATTATGCTATGAAG 801
Db 733 GTGAATCTATTGGAAGTATACCTGCTACCTTGACAGAGCCCTCTATTATGCTATGAAG 792
QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCTGTTTCCAGGAGTGAATGAT 861
Db 793 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCTGTTTCCAGGAGTGAATGAT 852
QY 862 CTGTTTAAACATCAGGAAGGAGTTAGGAAGATTTTGGCACCCTCTCTTTATCCATGATT 921
Db 853 CTGTTTAAACATCAGGAAGGAGTTAGGAAGATTTTGGCACCCTCTCTTTATCCATGATT 912
QY 922 AAGGAGATACATCTCGGGACTATAAGAAAGCTCTTCTGCTCTCCCGGAGAGATGAC 981
Db 913 AAGGAGATACATCTCGGGACTATAAGAAAGCTCTTCTGCTCTCTGAGAGATGAC 972

```

RESULT 5

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US-08-125-746-2
; Sequence 2, Application US/08125746
; Patent No. 5591633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IMASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 037227/1987
; FILING DATE: 20-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184428/1987
; FILING DATE: 23-JUL-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5591633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 136..1095
; US-08-125-746-2

Query Match          97.5%; Score 956.8; DB 1; Length 1567;
Best Local Similarity 99.8%; Pred. No. 3.1e-276;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACGTGTGACTGACTTCCCTGGATTTTATGAGCGGCTGAT 81
Db 136 ATGGCACAGGTTCTCAGAGGCACGTGTGACTGACTTCCCTGGATTTTATGAGCGGCTGAT 195
QY 82 GCNAGAACTCTTCGCGAAGGCTATGAAAGGCTTGGGCACAGATGAGAGAGCATCCTGACT 141
Db 196 GCNAGAACTCTTCGCGAAGGCTATGAAAGGCTTGGGCACAGATGAGAGAGCATCCTGACT 255
QY 142 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201
Db 256 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 315
QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 261
Db 316 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 375
QY 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTTATGAACTGAACATGCTTG 321
Db 376 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTTATGAACTGAACATGCTTG 435
QY 322 AAGGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 436 AAGGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 495
QY 382 GAACTGAGAGCCATCAACAAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGAC 441
Db 496 GAACTGAGAGCCATCAACAAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGAC 555
QY 442 GTGGTGGGGGACATTCAGGGTACTACACCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 501
Db 556 GTGGTGGGGGACATTCAGGGTACTACACCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 615
QY 502 AGAGACCTGTGCTGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
Db 616 AGAGACCTGTGCTGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 675
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAAGTTTATACCATCTTTTGAACA 621
Db 676 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAAGTTTATACCATCTTTTGAACA 735
QY 622 CGAAGTGTCTCTCATTTGAGAAAGGTGTTTGACAAAGTACATGACTATATCAGGATTCAA 681
Db 736 CGAAGTGTCTCTCATTTGAGAAAGGTGTTTGACAAAGTACATGACTATATCAGGATTCAA 795
QY 682 ATTGAGAAACCAATTCACCGGAGACTTCTGGCAATTTAGAGAACTACTCTTGTCTGTT 741
Db 796 ATTGAGAAACCAATTCACCGGAGACTTCTGGCAATTTAGAGAACTACTCTTGTCTGTT 855
QY 742 GTGAATCTATTGGAAGTATACCTGCTACCTTGACAGAGCCCTCTATTATGCTATGAAG 801
Db 856 GTGAATCTATTGGAAGTATACCTGCTACCTTGACAGAGCCCTCTATTATGCTATGAAG 915
QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCTGTTTCCAGGAGTGAATGAT 861
Db 916 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTCTGTTTCCAGGAGTGAATGAT 975
QY 862 CTGTTTAAACATCAGGAAGGAGTTTAGGAAGATTTTGGCACCCTCTCTTTATCCATGATT 921
Db 976 CTGTTTAAACATCAGGAAGGAGTTTAGGAAGATTTTGGCACCCTCTCTTTATCCATGATT 1035

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Qy 922 AAGGAGATACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTCCGGAGAGATGAC 981
Db 1036 AAGGAGATACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTGGAGAGATGAC 1095

RESULT 6

US-08-125-746-4
; Sequence 4, Application US/08125746
; Patent No. 5591633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IWASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991
; APPLICATION DATA:
; FILING DATE: 20-FEB-1987
; APPLICATION NUMBER: JP 037227/1987
; FILING DATE: 20-FEB-1987
; APPLICATION DATA:
; FILING DATE: 23-JUL-1987
; APPLICATION NUMBER: JP 184428/1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5591633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-125-746-4

Query Match 97.28; Score 953.8; DB 1; Length 957;
Best Local Similarity 99.88; Pred. No. 1.9e-275;
Matches 955; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 25 GCACAGTTCTCAGAGGCTGTGACTGCTCCCTGGATTGATGAGCGGCTGATGCA 84
Db 1 GCACAGTTCTCAGAGGCTGTGACTGCTCCCTGGATTGATGAGCGGCTGATGCA 60
Qy 85 GAAACTCTCGAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGCATCTCTGACRTG 144
Db 61 GAAACTCTCGAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGCATCTCTGACRTG 120
Qy 145 TTGACATCCCGAAGTATGCTCAGCGCCAGGAATCTCTGACGCTTTTAAGACTCTGTT 204
Db 121 TTGACATCCCGAAGTATGCTCAGCGCCAGGAATCTCTGACGCTTTTAAGACTCTGTT 180

RESULT 7

US-09-643-597-261
; Sequence 261, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lijun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11

Qy 205 GGAGGATCTCTGGATGACCTGAAATCAGAACTAACTGAAAAATTTGAAAAATTAATT 264
Db 181 GGAGGATCTCTGGATGACCTGAAATCAGAACTAACTGAAAAATTTGAAAAATTAATT 240
Qy 265 GTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACATGAACATGCTTGAAG 324
Db 241 GTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACATGAACATGCTTGAAG 300
Qy 325 GGAGCTGGAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAAGAA 384
Db 301 GGAGCTGGAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAAGAA 360
Qy 385 CTGAGAGCCATCAACCAAGTTTATGAAGAAGATATGGCTCAAGCCCTGGAAGATGAGCTG 444
Db 361 CTGAGAGCCATCAACCAAGTTTATGAAGAAGATATGGCTCAAGCCCTGGAAGATGAGCTG 420
Qy 445 GTGGGGACACTTACAGGGTACTACACGGGATGTTGGTTCCTTCAGGCTAACAGAA 504
Db 421 GTGGGGACACTTACAGGGTACTACACGGGATGTTGGTTCCTTCAGGCTAACAGAA 480
Qy 505 GACCCCTGATGCTGAATGATGAGCTCAAGTTCAGCAAGATGCTCAGGGCTTTATTTCAG 564
Db 481 GACCCCTGATGCTGAATGATGAGCTCAAGTTCAGCAAGATGCTCAGGGCTTTATTTCAG 540
Qy 565 GCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCACCTTTTGGAAACAGA 624
Db 541 GCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCACCTTTTGGAAACAGA 600
Qy 625 AGTGTGCTCATTTGAGAAAGGTTTGGACAAGTACATGACTATATCAGGATTTCAAAT 684
Db 601 AGTGTGCTCATTTGAGAAAGGTTTGGACAAGTACATGACTATATCAGGATTTCAAAT 660
Qy 685 GAGGAACCATTTGACCGGAGACTCTGGCAATTTAGACCACTACTCTCTGCTGCTG 744
Db 661 GAGGAACCATTTGACCGGAGACTCTGGCAATTTAGACCACTACTCTCTGCTGCTG 720
Qy 745 AAATCTATTGGAAGTATACCTGCTTGCAGAGACCCCTCTATTTATGCTATGAAGGA 804
Db 721 AAATCTATTGGAAGTATACCTGCTTGCAGAGACCCCTCTATTTATGCTATGAAGGA 780
Qy 805 GCTGGGACAGATGATACCTCATCAGAGTCTAGTTTCCAGAGGATGAGATGATCTG 864
Db 781 GCTGGGACAGATGATACCTCATCAGAGTCTAGTTTCCAGAGGATGAGATGATCTG 840
Qy 865 TTTAAACATCAGGAAGGATTTAGGAAGAAATTTCCACCTCTCTTTTATCCATGATTAAG 924
Db 841 TTTAAACATCAGGAAGGATTTAGGAAGAAATTTCCACCTCTCTTTTATCCATGATTAAG 900
Qy 925 GGAGATACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTCCGGAGAAAGATGAC 981
Db 901 GGAGATACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTCGGAGAAAGATGAC 957

; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-261

Query Match 31.7%; Score 311; DB 4; Length 401;

Best Local Similarity 99.4%; Pred. No. 2,1e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 22 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
DB 89 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 148
QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 208
QY 142 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGAAATCTCTGCAGCTTTTAAGACTCTG 201
DB 209 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGAAATCTCTGCAGCTTTTAAGACTCTG 268
QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG 321
DB 329 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG 388
QY 322 AAGGAGCTGGAA 334
DB 389 AAGGAGCTGGAA 401

RESULT 8

US-09-480-884A-261
; Sequence 261, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-261

Query Match 31.7%; Score 311; DB 4; Length 401;

Best Local Similarity 99.4%; Pred. No. 2,1e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
DB 89 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 148
QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 208
QY 142 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGAAATCTCTGCAGCTTTTAAGACTCTG 201
DB 209 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGAAATCTCTGCAGCTTTTAAGACTCTG 268
QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG 321
DB 329 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG 388
QY 322 AAGGAGCTGGAA 334
DB 389 AAGGAGCTGGAA 401

RESULT 9

US-09-542-615A-261
; Sequence 261, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-261

Query Match 31.7%; Score 311; DB 4; Length 401;

Best Local Similarity 99.4%; Pred. No. 2,1e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
DB 89 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 148
QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
DB 149 GCANAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 208
QY 142 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGAAATCTCTGCAGCTTTTAAGACTCTG 201
DB 209 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGAAATCTCTGCAGCTTTTAAGACTCTG 268
QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG 321
DB 269 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG 388

QY 262 ATTGTGGCTCTGATGAACCCCTCTGGCTTTATGATGCTTATGAACCTGAACATGCTG 321
|||||
Db 329 ATTGTGGCTCTGATGAACCCCTCTGGCTTTATGATGCTTATGAACCTGAACATGCTG 388
|||||
QY 322 AAGGAGCTGGAA 334
|||||
Db 389 AAGGAGCTGGAA 401
|||||

RESULT 10

US-09-606-421B-261
; Sequence 261, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-261

Query Match 31.7%; Score 311; DB 4; Length 401;
Best Local Similarity 99.4%; Pred. No. 2.1e-83;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGCGACAGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 81
|||||
Db 89 ATGCGACAGTTCTCAGAGCACTGNGACTGACTTCCCTGGATTGATGAGCGGCTGAT 148
|||||
QY 82 GCAGAACTCTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
|||||
Db 149 GCANAACTCTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 208
|||||
QY 142 CTGTTGACATCCCGAAGTATGCTCAGCGCAGGAAATCTCGAGCTTTAGACTCTG 201
|||||
Db 209 CTGTTGACATCCCGAAGTATGCTCAGCGCAGGAAATCTCGAGCTTTAGACTCTG 268
|||||
QY 202 TTTGGCAGGATCTTCTGGATGACCTGAATACAGAACTAACTGAAATTTGAAAATTA 261
|||||
Db 269 TTTGGCAGGATCTTCTGGATGACCTGAATACAGAACTAACTGAAATTTGAAAATTA 328
|||||
QY 262 ATTGTGGCTCTGATGAACCCCTCTGGCTTTATGATGCTTATGAACCTGAACATGCTG 321
|||||
Db 329 ATTGTGGCTCTGATGAACCCCTCTGGCTTTATGATGCTTATGAACCTGAACATGCTG 388
|||||
QY 322 AAGGAGCTGGAA 334
|||||
Db 389 AAGGAGCTGGAA 401
|||||

RESULT 11

US-08-526-136-1
; Sequence 1, Application US/08526136

; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526.136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214.036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2305
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-526-136-1

Query Match 31.7%; Score 310.8; DB 3; Length 2305;
Best Local Similarity 58.0%; Pred. No. 5.6e-83;
Matches 549; Conservative 0; Mismatches 397; Indels 0; Gaps 0;

QY 36 CAGAGGCACGTGTGACTGACTTCCCTGGATTGATGAGCGGCTGATGAGAACTCTTCG 95
|||||
Db 665 CCGAGGCACCATCACATGCTGCTTTGACCCCTCGAGATGCTGAAGTCTCGG 724
|||||
QY 96 GAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCTGACTCTGTTGACATCCG 155
|||||
Db 725 GAAGGCTATGAAGGCTTGGGACTGACGAGCGCATCATTTGACTGCTTGGTAGTCG 784
|||||
QY 156 AAGTAACTGCTCAGCGCCAGGAAATCTCTGCGAGCTTTTAAAGACTCTGTTGSCAGGATCT 215
|||||
Db 785 CTCCAACAACGACGACGACGATCCCTGCTCTCAAGACACATATGGAAGGATTT 844
|||||
QY 216 TCTGGATGACTGAAATCAGAACTAACTGGAATAATTTGAAAATTTAATTTGGCTCTGAT 275
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1565 AGGGGATTACCGGAAGATTCTGCTGAAGATCTGTGTGGCAATGAC 1610
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RESULT 12

US-08-526-136-3

Sequence 3, Application US/08526136

Patent No. 6107089

GENERAL INFORMATION:

APPLICANT: Towle, Christine A. et al.

TITLE OF INVENTION: ANNEXIN XI

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55sx

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/526,136

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/214,036

FILING DATE:

APPLICATION NUMBER: 07/837,775

FILING DATE: February 13, 1992

APPLICATION NUMBER: 07/764,465

FILING DATE: September 23, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

```

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-526-136-3
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Query Match 31.7%; Score 310.8; DB 3; Length 2311;

Best Local Similarity 58.0%; Pred. No. 5.6e-83;

Matches 549; Conservative 0; Mismatches 397; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:43:40 ; Search time 216.333 seconds
(without alignments)
12241.057 Million cell updates/sec

Title: US-09-970-969-5

Perfect score: 981

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	976.2	99.5	981	22 AAC91368	Modified human ann
3	976.2	99.5	981	22 AAC91369	Modified human ann
4	957.8	97.6	1466	9 AAN91353	Vascular anti-coag
5	956.8	97.5	1567	9 AAN81113	Plasamid contg. pla
6	956.8	97.5	1578	25 ABX63162	human cDNA #162 di
7	956.8	97.5	1605	10 AAN91821	Endonexin II compl
8	956.2	97.5	1575	10 AAN90112	Anticoagulant PP4

9	955.6	97.4	1803	21	AAAL1241	Annexin V/uokinas
10	955.2	97.4	1454	9	AAN82107	PAP-I cDNA from hu
11	955.2	97.4	1460	12	AAQ12679	PAP-I. Homo sapie
12	954.6	97.3	1466	9	AAN80801	Sequence encoding
13	953.6	97.2	963	9	AAN80873	Sequence encoding
14	952	97.0	1574	10	AAN90599	Human lipocortin-v
15	943.8	96.2	1637	21	AAF18269	Lung cancer associ
16	882	89.9	1024	25	AB283344	Toxicologically re
17	749.4	76.4	1480	24	ABI99289	Mouse ischaemic co
18	727	74.1	1417	24	ABK63699	Rat sequence diffe
19	518.4	52.8	960	25	AB221925	Human annexin V pr
20	517.8	52.8	2016	25	AB221926	Modified annexin p
21	495.8	50.5	847	25	ABX05088	Human novel polynu
22	412.2	42.0	438	12	AAQ12681	PAP-I-protein C fu
23	412.2	42.0	1529	12	AAQ12680	PAP-I-protein C fu
24	365	37.2	422	25	ABX47939	Bovine EST associa
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29	349.4	35.6	2155	21	AAC77826	Human cancer assoc
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31	349.4	35.6	2213	20	AAZ77514	Human ovarian tumo
32	349.4	35.6	2300	25	ABX63220	Human cDNA #220 di
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35	348.2	35.5	2468	24	ABK84730	Human cDNA differe
36	348.2	35.5	2468	24	ABN97346	Gene #3844 used to
37	346.6	35.3	2016	11	AAQ02887	cDNA of human plac
38	346.6	35.3	2056	25	ABX72249	Human NOVX polynu
39	319.8	32.6	529	24	ABQ59306	Human colon cancer
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ALIGNMENTS

RESULT 1
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ID AAC91370 standard; DNA; 981 BP.
XX AAC91370;
AC AAC91370;
XX
DT 16-MAR-2001 (first entry)
XX Modified human annexin nucleotide sequence, SEQ ID NO: 5.
DE Human: annexin; chelation site; nuclear imaging; apoptosis;
KW transplacental rejection; ds.
XX Homo sapiens.
XX WO200073332-A1.
XX PD 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US14324.
XX PR 01-JUN-1999; 95US-0324096.
XX (UNIW) UNIV WASHINGTON.
XX Tait JF, Brown DS;
XX WPI; 2001-080465/09.
XX P-PSDB; AAB50865.
XX Novel modified annexin useful for imaging vascular thrombi and

PT apoptosis, has N-terminal chelation site comprising amino acid
PT extension which comprises a glycine and a cysteine residue -
XX
PS
XX
PS
XX
CC The present sequence encodes a modified annexin having an N-terminal
CC chelation site, which comprises an amino acid extension including a
CC glycine and a cysteine residue. The modified annexin is useful for
CC imaging vascular thrombi or apoptosis which is associated with response
CC to a chemotherapeutic agent or with rejection as a result of
CC transplantation. The modified annexin can effectively chelate a
CC radionuclide and retain annexin bioactivity. It can be readily prepared
CC in high radiochemical yield and with high radiochemical purity. In
CC contrast to conventional conjugation chemistries that provide a
CC distribution of conjugation products, the modified annexin has a single
CC chelation site remote from the site of biological activity.
XX
SQ Sequence 981 BP; 286 A; 187 C; 250 G; 258 T; 0 other;
Query Match 100.0%; Score 981; DB 22; Length 981;
Best Local Similarity 100.0%; Pred. No. 1.3e-274;
Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCATGGCTGCGGTCTATATGCGACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCT 60
DB 1 ATGGCATGGCTGCGGTCTATATGCGACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCT 60
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DT 16-MAR-2001 (first entry)
XX
DE Modified human annexin nucleotide sequence, SEQ ID NO: 1.
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KW Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplant rejection; ds.
XX
OS Homo sapiens.
XX
PN NC020073332-A1.
XX
PD 07-DEC-2000.
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PE 25-MAY-2000; 2000WO-US14324.
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PR 01-JUN-1999; 99US-0324096.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Tait JF, Brown DS;
XX
DR WPI; 2001-080465/09.
DR P-PSDB; AAB50863.
XX
PT Novel modified annexin useful for imaging vascular thrombi and
PT apoptosis, has N-terminal chelation site comprising amino acid
PT extension which comprises a glycine and a cysteine residue -
XX
PS Claim 25; Page 28-30; 39pp; English.
XX
CC The present sequence encodes a modified annexin having an N-terminal
CC chelation site, which comprises an amino acid extension including a
CC glycine and a cysteine residue. The modified annexin is useful for
CC imaging vascular thrombi or apoptosis which is associated with response
CC to a chemotherapeutic agent or with rejection as a result of
CC transplantation. The modified annexin can effectively chelate a
CC radionuclide and retain annexin bioactivity. It can be readily prepared
CC in high radiochemical yield and with high radiochemical purity. In
CC contrast to conventional conjugation chemistries that provide a
CC distribution of conjugation products, the modified annexin has a single
CC chelation site remote from the site of biological activity.
XX
SQ Sequence 981 BP; 286 A; 187 C; 251 G; 257 T; 0 other;
Query Match 99.5%; Score 976.2; DB 22; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.3e-273;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCATGTGCTCGCTCATATGACACAGGTTCTCAGAGGACACTGTGACTTCCCT 60
 Db 1 ATGCATGTGCTCGCTCATATGACACAGGTTCTCAGAGGACACTGTGACTTCCCT 60
 Qy 61 GGATTTGATGAGCGGCTGATGCGAAGACTCTTCGGAAGCTATGAAGCTTGGGCACA 120
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 Qy 121 GATGAGGAGACATCCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAATC 180
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AAC91369;
 16-MAR-2001 (first entry)
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 Human; annexin; chelation site; nuclear imaging; apoptosis;
 transplant rejection; ds.
 Homo sapiens.
 WO200073332-A1.
 07-DEC-2000.
 25-MAY-2000; 2000WO-US14324.
 01-JUN-1999; 99US-0324096.
 (UNIW) UNIV WASHINGTON.
 Tait JF, Brown DS;
 WPI; 2001-080465/09.
 P-PSDB; AAB50864.
 Novel modified annexin useful for imaging vascular thrombi and
 apoptosis, has N-terminal chelation site comprising amino acid
 extension which comprises a glycine and a cysteine residue -
 Claim 26; Page 31-33; 39pp; English.
 The present sequence encodes a modified annexin having an N-terminal
 chelation site, which comprises an amino acid extension including a
 glycine and a cysteine residue. The modified annexin is useful for
 imaging vascular thrombi or apoptosis which is associated with response
 to a chemotherapeutic agent or with rejection as a result of
 transplantation. The modified annexin can effectively chelate a
 radionuclide and retain annexin bioactivity. It can be readily prepared
 in high radiochemical yield and with high radiochemical purity. In
 contrast to conventional conjugation chemistries that provide a
 distribution of conjugation products, the modified annexin has a single
 chelation site remote from the site of biological activity.
 Sequence 981 BP; 286 A; 187 C; 251 G; 257 T; 0 other;
 Query Match 99.5%; Score 976.2; DB 22; Length 981;
 Best Local Similarity 99.7%; Pred. No. 3.3e-273;
 Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ATGGCATGTGCTGCGGTCATATGGCACAGGTTCTCAGAGGACACTGTGACTTCCCT 60
 Db 1 ATGGCATGTGCTGCGGTCATATGGCACAGGTTCTCAGAGGACACTGTGACTTCCCT 60
 Qy 61 GGATTTGATGAGCGGCTGATGCGAAGACTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
 Db 61 GGATTTGATGAGCGGCTGATGCGAAGACTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
 Qy 121 GATGAGGAGACATCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAATC 180
 Db 121 GATGAGGAGACATCCTGACTCTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAATC 180
 Qy 181 TCTCAGCTTTAAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTA 240
 Db 181 TCTCAGCTTTAAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTA 240
 Qy 241 ACTGGAATTTGAAAAATTAATTTGGCTCTGATGAACCTCTCGGCTTTATGATGCT 300
 Db 241 ACTGGAATTTGAAAAATTAATTTGGCTCTGATGAACCTCTCGGCTTTATGATGCT 300
 Qy 301 TATGAATGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAGTACTCAGCAAAAT 360
 Db 301 TATGAATGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAGTACTCAGCAAAAT 360

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QY 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAAACAGTTTATGAAGAAGATAT 420
DB 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAAACAGTTTATGAAGAAGATAT 420
QY 421 GGCTCAAGGCTGGAAGATGACGTGGTGGGGGACACTTACAGGTAATGATGAAGCTCAAGTTG 480
DB 421 GGCTCAAGGCTGGAAGATGACGTGGTGGGGGACACTTACAGGTAATGATGAAGCTCAAGTTG 480
QY 481 GTGGTTCTCTTCAGGCTTACAGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAA 540
DB 481 GTGGTTCTCTTCAGGCTTACAGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAA 540
QY 541 CRAAGTGTCTCAGGCTTATTTTCAAGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
DB 541 CRAAGTGTCTCAGGCTTATTTTCAAGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600
QY 601 TTTATCAGCATCTTTGGACACAGTGTGCTCATTTTGAGAAAGGTGTTTGACAAGTAC 660
DB 601 TTTATCAGCATCTTTGGACACAGTGTGCTCATTTTGAGAAAGGTGTTTGACAAGTAC 660
QY 661 ATGACTATATCAGGATTTCAAAATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTA 720
DB 661 ATGACTATATCAGGATTTCAAAATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTA 720
QY 721 GAGCAACTACTCTCTGCTGTGTGAAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAG 780
DB 721 GAGCAACTACTCTCTGCTGTGTGAAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAG 780
QY 781 ACCCTCTATATGCTATGAAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
DB 781 ACCCTCTATATGCTATGAAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
QY 841 GTTTCAGGAGTGAAGATGATCTGTTTAACTCAGGAAGAGTTTATAGGAAGATTTTGGC 900
DB 841 GTTTCAGGAGTGAAGATGATCTGTTTAACTCAGGAAGAGTTTATAGGAAGATTTTGGC 900
QY 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGACTATTAAGAAAGCTCTTCTG 960
DB 901 ACCTCTCTTTATTCATGATTAAGGAGATACATCTGGGACTATTAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGGAGAGATGAC 981
DB 961 CTGCTCTCCGGAGAGATGAC 981

RESULT 4
AAN91353
ID AAN91353 standard; DNA; 1466 BP.
AC AAN91353;
XX
XX
XX 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 30-JUL-1989 (first entry)
XX
XX Vascular anti-coagulating protein-alpha cDNA.
DE
XX Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas; ss.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Mus musculus.
XX
XX Key Location/Qualifiers
FH CDS 35..996
FT /*tag- a
FT /label=VAC-alpha cDNA
XX
XX DE3810331-A.
XX
XX 05-OCT-1989.
XX
XX 26-MAR-1988; 88DE-3810331.

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XX
XX 26-MAR-1988; 88DE-3810331.
XX (BOEH ) BOEHRINGER INGELHEIM.
XX
XX Gunther A;
XX
XX WPI; 1989-293724/41.
XX P-PSDB; AAP91953.
XX
XX Monoclonal antibodies to vascular anti-coagulating proteins - and
XX hybridomas producing such antibodies.
XX
XX Disclosure; fig 1; 11pp; German.
XX
XX The vascular anti-coagulating protein (VAC)-alpha encoded by this cDNA
XX is used in the preparation of monoclonal antibodies (Mabs). The
XX VAC-alpha is injected into a host animal, in conjugation with eg keyhole
XX limpet haemocyanin, and the B-cells from the immunised hosts are then
XX fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9)
XX produce Abs specific to VAC-alpha. The Abs can be used as immunosay
XX reagents to detect VAC proteins, as affinity ligands for purific. of
XX VACs and as medicaments for binding and/or neutralising VAC proteins in
XX vivo. See also AAN91354 and Ep-181465.
XX (Updated on 10-MAR-2003 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 1466 BP; 423 A; 291 C; 327 G; 425 T; 0 other;

Query Match 97.6%; Score 957.8; DB 10; Length 1466;
Best Local Similarity 99.8%; Pred. No. 9e-268;
Matches 959; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGAGCGGGCTGA 80
DB 21 TATGGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGAGCGGGCTGA 93
QY 81 TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGAC 140
DB 81 TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGAC 153
QY 141 TCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGCGAGCTTTTAAAGACTCT 200
DB 141 TCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGCGAGCTTTTAAAGACTCT 213
QY 201 GTTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATT 260
DB 201 GTTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATT 273
QY 261 AATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCCT 320
DB 261 AATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCCT 333
QY 321 GAAGGAGCTGGAAACAATGAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGA 380
DB 321 GAAGGAGCTGGAAACAATGAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGA 393
QY 381 AGAACTGAGAGCCATCAAAACAGTTTATGAAGAAGATATGCTCAAGCTGGAAGATGA 440
DB 381 AGAACTGAGAGCCATCAAAACAGTTTATGAAGAAGATATGCTCAAGCTGGAAGATGA 453
QY 441 CGTGTGGGGGACACTTACAGGGTACTACCGCGGATGTTGGTGGTTCTCCTTCAGGCTAA 500
DB 441 CGTGTGGGGGACACTTACAGGGTACTACCGCGGATGTTGGTGGTTCTCCTTCAGGCTAA 513
QY 501 CAGAGACCTGATGCTGGAAATGATGAAGTCAAGTTGAACAGATGCTCAGGCTTTATT 560
DB 501 CAGAGACCTGATGCTGGAAATGATGAAGTCAAGTTGAACAGATGCTCAGGCTTTATT 573
QY 561 TCAGGCTGGAGAACTTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAC 620
DB 561 TCAGGCTGGAGAACTTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAC 633
QY 574 TCAGGCTGGAGAACTTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAC 633
DB 574 TCAGGCTGGAGAACTTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAC 633

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QY 621 ACAGAGTGTCTCATTTGAGAAAGGTTGTCAGCAAGTACATGACTATATCAGGATTTC 680
 DB 634 ACAGAGTGTCTCATTTGAGAAAGGTTGTCAGCAAGTACATGACTATATCAGGATTTC 693
 QY 681 AATTGAGAAACCAATTGACCCGAGACTTCTGGCAATTTAGAGCAACTACTCTTGGCTGT 740
 DB 694 AATTGAGAAACCAATTGACCCGAGACTTCTGGCAATTTAGAGCAACTACTCTTGGCTGT 753
 QY 741 TGTGAATCTATTCGAAGTATACCTGGCTACCTTGCAGAGACCCTCTATTATGCTATGAA 800
 DB 754 TGTGAATCTATTCGAAGTATACCTGGCTACCTTGCAGAGACCCTCTATTATGCTATGAA 813
 QY 801 GGGAGCTGGGACATGATCATACCTCATCAGAGTATGCTTCCAGGAGTATGAGATGA 860
 DB 814 GGGAGCTGGGACATGATCATACCTCATCAGAGTATGCTTCCAGGAGTATGAGATGA 873
 QY 861 TCTGTTTAACATCAGGAGGAGTTTAGCAAAATTTGCCACCTCTCTTTATTCATCATGAT 920
 DB 874 TCTGTTTAACATCAGGAGGAGTTTAGCAAAATTTGCCACCTCTCTTTATTCATCATGAT 933
 QY 921 TAAGGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCCGAGAGATGA 980
 DB 934 TAAGGGAGATACATCTGGGACTATAAGAAAGCTCTTCTGCTGCTCTGCTGCTGAGAGATGA 993
 QY 981 C 981
 DB 994 C 994

RESULT 5
 ID AAN81113 standard; DNA; 1567 BP.
 XX AAN81113;
 AC
 XX
 DT 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 12-NOV-1990 (first entry)
 XX
 XX
 DE Plasmid contg. placental coagulation inhibitor gene.
 XX
 KW Placental coagulation inhibitor; disseminated vascular coagulation;
 KW thrombosis; ss.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 136..1098
 FT /*tag= a
 FT /label=placental coagulation inhibitor
 FT 1568
 FT /*tag= b
 XX
 XX EP279459-A.
 FN JP03219875-A.
 XX
 XX 24-AUG-1988.
 XX
 XX 19-FEB-1988; 88EP-0102468.
 XX
 XX 20-FEB-1987; 87JP-0037227.
 XX 23-JUL-1987; 87JP-0184428.
 XX
 XX (KOWA) KOWA CO LTD.
 XX
 XX Saino Y, Iwasaki A, Suda M;
 XX
 XX WPI; 1988-236733/34.
 XX WPI; 1991-329110/45.
 XX P-PSDB; AAP80511.
 XX
 XX Recombinant placental coagulation inhibitor - useful for the prevention
 XX and treatment of thromboses or disseminated intra-vascular coagulation.
 XX

XX Disclosure: Page ?; p: English.

CC This recombinant DNA sequence comprises a promoter region, ribosome
 CC binding site, initiation sequence, termination codon and a trans-
 CC cription terminator in addition to the placental coagulation inhibitor
 CC gene. The polypeptide produced on culturing of transformed host cells
 CC exhibits strong anticoagulant activities and is useful for the treat-
 CC ment and prevention of eg thrombosis or disseminated intravascular
 CC coagulation in the brain, heart and peripheral blood vessels.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 1567 BP; 430 A; 332 C; 358 G; 447 T; 0 other;

Query Match 97.5%; Score 956.8; DB 9; Length 1567;
 Best Local Similarity 99.8%; Pred. No. 1.8e-267;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 ATGSCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATCAGCGGCTGAT 81
 DB 136 ATGSCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATCAGCGGCTGAT 195
 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGATCCTGACT 141
 DB 196 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGATCCTGACT 255
 QY 142 CTGTTGACATCCCGAAGTAAATGCTAGCGCCAGGAAATCTCTGCACTTTTAAAGACTCTG 201
 DB 256 CTGTTGACATCCCGAAGTAAATGCTAGCGCCAGGAAATCTCTGCACTTTTAAAGACTCTG 315
 QY 202 TTTGGCAGGATCTTCGGATGACCTGAAATCAGAACTACTGGAATTTGAAAAATTA 261
 DB 316 TTTGGCAGGATCTTCGGATGACCTGAAATCAGAACTACTGGAATTTGAAAAATTA 375
 QY 262 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCCTTG 321
 DB 376 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCCTTG 435
 QY 322 AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 DB 436 AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 495
 QY 382 GAAGTGAGAGCCATCAACAAAGTTTATGAAAGAAATATGCTCAAGCCTGGAAGATGAC 441
 DB 496 GAAGTGAGAGCCATCAACAAAGTTTATGAAAGAAATATGCTCAAGCCTGGAAGATGAC 555
 QY 442 GTGGTGGGGACACTTTCAGGCTACTTACCAGCGGATTTTGGTGGTCTCTCCTTCAGGCTAAC 501
 DB 556 GTGGTGGGGACACTTTCAGGCTACTTACCAGCGGATTTTGGTGGTCTCTCCTTCAGGCTAAC 615
 QY 502 AGAGACCTGATGCTGGAATTTGATGAAGTCAAGTTGAACAAAGTATGCTCAGGCTTTATTT 561
 DB 616 AGAGACCTGATGCTGGAATTTGATGAAGTCAAGTTGAACAAAGTATGCTCAGGCTTTATTT 675
 QY 562 CAGGCTGGGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGGAACA 621
 DB 676 CAGGCTGGGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGGAACA 735
 QY 622 CGAAGTGTCTCATTTGAGAAAGGTTTTCACAAAGTACATGACTATATCAGGATTTCAA 681
 DB 736 CGAAGTGTCTCATTTGAGAAAGGTTTTCACAAAGTACATGACTATATCAGGATTTCAA 795
 QY 682 ATTGAGGAAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGT 741
 DB 796 ATTGAGGAAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGT 855
 QY 742 GTGAATCTATTCGAAGTATACCTGCCCTACCTTGCAGAGACCCTCTATTATGCTATGAG 801
 DB 856 GTGAATCTATTCGAAGTATACCTGCCCTACCTTGCAGAGACCCTCTATTATGCTATGAG 915

QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGATGTTTCCAGGAGTGAGATTGAT 861
 Db 916 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGATGTTTCCAGGAGTGAGATTGAT 975
 QY 862 CTCTTTAAATCAGGAGGAGTTAGGAAGATTTTCCACCTCTCTTTATTCATGATT 921
 Db 976 CTCTTTAAATCAGGAGGAGTTAGGAAGATTTTCCACCTCTCTTTATTCATGATT 1035
 QY 922 AAGGAGATACATCTGGGAGCTATAAGAAAGCTTCTGCTGCTCTCCGGAGAGATGAC 981
 Db 1036 AAGGAGATACATCTGGGAGCTATAAGAAAGCTTCTGCTGCTCTGGAGAGATGAC 1095

RESULT 6
 ABX63162
 ID ABX63162 standard; cDNA; 1578 BP.
 AC ABX63162;
 XX
 DT 25-FEB-2003 (first entry)
 DE Human cDNA #162 differentially expressed in activated vascular tissue.
 DE Human: gene; ss: vascular tissue; cytostatic; atherosclerosis;
 KW cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke;
 XX
 OS Homo sapiens.
 XX
 PN US2002137081-A1.
 XX
 XX 26-SEP-2002.
 XX
 XX 08-JAN-2002; 2002US-0044090.
 XX
 XX 28-JUL-2000; 2000US-222469P.
 PR 08-JAN-2001; 2001US-260483P.
 XX
 XX (BAND/) BANDMAN O.
 XX
 XX Bandman O.
 XX
 DR WPI; 2003-110597/10.
 XX
 PT Combination for diagnosing, staging, treating, or monitoring the
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several cDNAs that are differentially expressed in activated
 PT vascular tissue -
 XX
 PS Claim 1; Page -; 18pp; English.

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiatherosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new

CC nucleic acid molecules. Antibodies to the proteins encoded by the
 CC cDNAs are useful for diagnosing pre-pathological disorders, and chronic
 CC or acute diseases associated with abnormalities in the expression,
 CC amount or distribution of the protein. The present sequence
 CC represents a cDNA of the invention that is differentially expressed in
 CC activated vascular tissue.
 CC Note: The sequence data for this patent did not form part of the
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>.
 XX
 SQ Sequence 1578 BP; 432 A; 335 C; 360 G; 451 T; 0 other;
 Query Match 97.5%; Score 956.8; DB 25; Length 1578;
 Best Local Similarity 99.8%; Pred. No. 1.8e-267;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 22 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
 Db 142 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 201
 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 141
 Db 202 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 261
 QY 142 CTCTTGACATCCCGAAGTAAATGCTCAGCCAGGAAATCTCTCGAGCTTTTAAGACTCTG 201
 Db 262 CTCTTGACATCCCGAAGTAAATGCTCAGCCAGGAAATCTCTCGAGCTTTTAAGACTCTG 321
 QY 202 TTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAATCTGGAATTTGAAAAATTA 261
 Db 322 TTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAATCTGGAATTTGAAAAATTA 381
 QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACATGACCTTG 321
 Db 382 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACATGACCTTG 441
 QY 322 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATATGCTTCAAGGACACCTGAA 381
 Db 442 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATATGCTTCAAGGACACCTGAA 501
 QY 382 GAACTGAGAGCCCATCAACAAAGTTTATGAGAGAAATATGGCTCAAGCCTGGAAGTAC 441
 Db 502 GAACTGAGAGCCCATCAACAAAGTTTATGAGAGAAATATGGCTCAAGCCTGGAAGTAC 561
 QY 442 GTGGTGGGGACACATTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 501
 Db 562 GTGGTGGGGACACATTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 621
 QY 502 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 561
 Db 622 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 681
 QY 562 CAGGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGANCA 621
 Db 682 CAGGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGANCA 741
 QY 622 CGAAGTGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 681
 Db 742 CGAAGTGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 801
 QY 682 ATTGAGAAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTT 741
 Db 802 ATTGAGAAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTT 861
 QY 742 GTGAAATCTATTGGAAGTATACCTGCTTGCAGAGACCCCTCTATTATGCTATGAAG 801
 Db 862 GTGAAATCTATTGGAAGTATACCTGCTTGCAGAGACCCCTCTATTATGCTATGAAG 921
 QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGATGTTTCCAGGAGTGAGATTGAT 861
 Db 922 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTATGATGTTTCCAGGAGTGAGATTGAT 981
 QY 862 CTCTTTAAATCAGGAGGAGTTAGGAAGATTTTCCACCTCTCTTTATTCATGATT 921


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Db 982 CTGTTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTCATGATT 1041
QY 922 AAGGAGACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTCCGAGAGATGAC 981
Db 1042 AAGGAGATACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTGTGGAGAAGATGAC 1101

RESULT 7
AAN91821
ID AAN91821 standard; DNA; 1605 BP.
XX AC AAN91821;
XX DT 25-MAR-2003 (updated)
XX DT 16-MAR-1990 (first entry)
XX DE Endonexin II complete cDNA.
XX KW Placenta; blood coagulation
XX OS Homo sapiens (human).
XX FH Key Location/Qualifiers
XX FT CDS 160..1119
XX FT /*tag= a
XX PN EP339285-A.
XX PD 02-NOV-1989.
XX PF 30-MAR-1989; 89EP-0105626.
XX PR 31-MAR-1988; 88US-0176802.
XX PA (RORE ) RORER INT OVERSEAS INC.
XX PI Kaplan R, Jaye M;
XX DR WPI; 1989-317181/44.
XX DR P-PSDB; AAP91021.
XX PT Recombinant human endonexin II - which inhibits blood coagulation
XX FT and phospholipase A2 and is used as an antiinflammatory agent
XX PS Claim 1; fig. 1; 13pp; English.
XX CC HENII is a calcium and phospholipid binding protein.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 1605 BP; 447 A; 337 C; 366 G; 455 T; 0 other;

Query Match 97.5%; Score 956.8; DB 10; Length 1605;
Best Local Similarity 99.8%; Pred. No. 1.8e-267;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 22 ATGCACAGGTTCTCAGAGGACATGTGACTGACTTCCTGCTGATTGTGATGAGCGGCTGAT 81
Db 160 ATGCACAGGTTCTCAGAGGACATGTGACTGACTTCCTGCTGATTGTGATGAGCGGCTGAT 219
QY 82 GCAGAAACTCTTCGGAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGACT 141
Db 220 GCAGAAACTCTTCGGAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGACT 279
QY 142 CTGTTGACATCCCAAGTAATGCTCAGCGCAGGAAATCTGACGCTTTTAAACACTG 201
Db 280 CTGTTGACATCCCAAGTAATGCTCAGCGCAGGAAATCTGACGCTTTTAAACACTG 339
QY 202 TTTGGCAGGATCTCTCGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
Db 340 TTTGGCAGGATCTCTCGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 399
QY 262 ATTGCTGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACATGACATGCTG 321

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Db 400 ATTGCTGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGAACATGCGCTTG 459
QY 322 AAGGAGCTGGAACAATAATGAAAGTACTGACAGAAATATTGCTTCAAGACACCTGAA 381
Db 460 AAGGAGCTGGAACAATAATGAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA 519
QY 382 GAACTGAGAGCATCAACAAGTTTATGAAGAAATATGGCTCAAGCTCGAAGATGAC 441
Db 520 GAACTGAGAGCATCAACAAGTTTATGAAGAAATATGGCTCAAGCTCGAAGATGAC 579
QY 442 GTGTTGGGGACACTTCCAGGCTACTACAGCGGATGTTGGTGGTCTCTCCCTCAGGCTAAC 501
Db 580 GTGTTGGGGACACTTCCAGGCTACTACAGCGGATGTTGGTGGTCTCTCCCTCAGGCTAAC 639
QY 502 AGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 561
Db 640 AGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 699
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAACA 621
Db 700 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAACA 759
QY 622 CGAAGTGTGCTCATTTTGAAGAAAGTTTGTGACAAAGTACATGACTATATCAGGATTTCAA 681
Db 760 CGAAGTGTGCTCATTTTGAAGAAAGTTTGTGACAAAGTACATGACTATATCAGGATTTCAA 819
QY 682 ATTGAGGAACCATTTGACCGGACACTTCGGCAATTTAGAGCAACTACTCTTCTGCTGTT 741
Db 820 ATTGAGGAACCATTTGACCGGACACTTCGGCAATTTAGAGCAACTACTCTTCTGCTGTT 879
QY 742 GTGAAATCTATTGCAAGTATACCTGCTTACCTTCAGAGACCCCTCTATTATGCTATGAAG 801
Db 880 GTGAAATCTATTGCAAGTATACCTGCTTACCTTCAGAGACCCCTCTATTATGCTATGAAG 939
QY 802 GGAGCTGGACAGATGATACCTCATCAGAGCTCATGTTTCCAGAGGTGAGATTGAT 861
Db 940 GGAGCTGGACAGATGATACCTCATCAGAGCTCATGTTTCCAGAGGTGAGATTGAT 999
QY 862 CTGTTTAACTCAGAGAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTCATGATT 921
Db 1000 CTGTTTAACTCAGAGAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTCATGATT 1059
QY 922 AAGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAAGATGAC 981
Db 1060 AAGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTGCGAGAGATGAC 1119

RESULT 8
AAN90112
ID AAN90112 standard; DNA; 1575 BP.
XX AC AAN90112;
XX DT 25-MAR-2003 (updated)
XX DT 01-NOV-1989 (first entry)
XX DE Anticoagulant P4 DNA.
XX KW Anticoagulant; P4 protein; thromboplastin.
XX OS Homo sapiens (human).
XX FH Key Location/Qualifiers
XX FT polyA_signal 1539..1575
XX FT /*tag= a
XX FT CDS 107..1066
XX FT /*tag= b
XX PN EP318703-A.
XX PD 07-JUN-1989.
XX XX

```

PF 29-OCT-1988; 88EP-0118039.

XX PR 03-NOV-1987; 87DE-3737239.

XX (BEHW) BEHRINGERWERKE AG.

XX Grundmann U., Abel KJ., Kupper H;

XX WPI; 1989-166767/23.

XX New DNA sequence encoding anticoagulant PP4 protein
inhibits blood coagulation at the thromboplastin stage.
The derived protein is 320 amino acids.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX

PS Claim 1; table 1; 14pp; German.

XX DNA sequence encoding anticoagulant PP4 protein. This
inhibits blood coagulation at the thromboplastin stage.
The derived protein is 320 amino acids.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX

XX Sequence 1575 BP; 461 A; 322 C; 351 G; 441 T; 0 other;

Query Match 97.5%; Score 956.2; DB 10; Length 1575;
Best Local Similarity 99.7%; Pred. No. 2.7e-267;
Matches 958; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 21 TATGGCAGAGTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGGGGCTGA 80
DB |||||
QY 81 TGCAGAACTCTTCGGAAGCTATGAAAGCTTGGGCACAGATGAGGAGATCTCTGAC 140
DB |||||
QY 166 TGCAGAACTCTTCGGAAGCTATGAAAGCTTGGGCACAGATGAGGAGATCTCTGAC 225
DB |||||
QY 141 TCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAAGCTTTTAAAGACTCT 200
DB |||||
QY 226 TCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAAGCTTTTAAAGACTCT 285
QY 201 GTTTGGCAGGATCTCTGGATGACCTGAATCAGAACTAACTGGGAAATTTGAAAAATTT 260
DB |||||
QY 286 GTTTGGCAGGATCTCTGGATGACCTGAATCAGAACTAACTGGGAAATTTGAAAAATTT 345
QY 261 AATTGGGCTCTGATCAAAACCTCTCGGCTTTATGATGCTTATGAACCTCAAAACATCCCTT 320
DB |||||
QY 346 AATTGGGCTCTGATCAAAACCTCTCGGCTTTATGATGCTTATGAACCTCAAAACATCCCTT 405
QY 321 GAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGA 380
DB |||||
QY 406 GAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGA 465
QY 381 AGAAGTCAAGGATCAAAAGATTTATGAAGAGATATGCTCAAGCTGGAAGATGA 440
DB |||||
QY 466 AGAAGTCAAGGATCAAAAGATTTATGAAGAGATATGCTCAAGCTGGAAGATGA 525
QY 441 CTTGTTGGGGGACACTTCAAGGCTACTACAGCGGATTTGGTGGTCTCTCCCTCAGGCTAA 500
DB |||||
QY 526 CTTGTTGGGGGACACTTCAAGGCTACTACAGCGGATTTGGTGGTCTCTCCCTCAGGCTAA 585
QY 501 CAGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAGATGCTTCAGGCTTTATT 560
DB |||||
QY 586 CAGAGACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAGATGCTTCAGGCTTTATT 645
QY 561 TCAGGCTGAGAACTTAATGTTGGGACAGATGAAGAAAGTTTATCACCCTTTTGGAC 620
DB |||||
QY 646 TCAGGCTGAGAACTTAATGTTGGGACAGATGAAGAAAGTTTATCACCCTTTTGGAC 705
QY 621 ACGAAGTGTCTCATTTTGAAGAGTGTTCACAAAGTACATGACTATATCAGGATTTCA 680
DB |||||
QY 706 ACGAAGTGTCTCATTTTGAAGAGTGTTCACAAAGTACATGACTATATCAGGATTTCA 765

QY 681 AATTGAGGAACCAATTGACGGGAGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGT 740
DB |||||
QY 766 AATTGAGGAACCAATTGACGGGAGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGT 825
DB |||||
QY 741 TGTGAANTCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGA 800
DB |||||
QY 826 TGTGAANTCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGA 885
QY 801 GGGAGCTGGACAGATGATCATACCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA 860
DB |||||
QY 886 GGGAGCTGGACAGATGATCATACCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA 945
QY 861 TCTGTTTAAATCAGGAAGAGGTTTAGGAAGAAATTTTGGCACCTCTCTTTATTTCCATGAT 920
DB |||||
QY 946 TCTGTTTAAATCAGGAAGAGGTTTAGGAAGAAATTTTGGCACCTCTCTTTATTTCCATGAT 1005
QY 921 TAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTGCTCTCCGGAGAACATGA 980
DB |||||
QY 1006 TAAGGAGATACATCTGGGAGCTATTAAGAAAGCTCTTCTGCTGCTCTGTGGAGAACATGA 1065
QY 981 C 981
DB 1066 C 1066

RESULT 9

AAAL1241

ID AAAL1241 standard; DNA; 1803 BP.

XX AC AAAL1241;

XX DT 25-OCT-2000 (first entry)

XX DE Annexin V/urokinase fusion construct.

XX DE Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;

XX KW urokinase; insect cell; fibrinolysis; ss.

XX OS Unidentified.

XX PH Key Location/Qualifiers

XX FT 1..1803

XX FT /tag= a

XX FT /product= "annexin V/urokinase fusion protein"

XX FT /note= "no start or stop codons are given at the 5'

XX FT or 3' ends of the sequence"

XX PN CN1247195-A.

XX PD 15-MAR-2000.

XX PF 12-MAR-1999; 99CN-0113524.

XX PR 12-MAR-1999; 99CN-0113524.

XX PA (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.

XX PI Wu X., Sun J., Yang G;

XX DR WPI; 2000-413098/36.

XX DR P-PSDB; AAY92930.

XX PT New thrombolytic fusion protein for targeting thrombus - comprises

XX PT fusion of Annexin V and urokinase

XX PS Claim 2; Page 2-4; 20pp; Chinese.

XX CC Annexin V, which has high affinity for active thrombocytes, is used

XX CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion

XX CC protein. The protein is the result of expression of a fusion gene

XX CC (this sequence) comprising the Annexin V gene and a low-molecular

XX CC urokinase gene, in insect cells. The Annexin V-scu-PA-32 fusion protein,

XX CC expressed in insect cell strain Tn-5B1-4, has high affinity for active

CC thrombocytes and has the fibrinolytic activity of urokinase.

XX Sequence 1803 BP; 495 A; 415 C; 462 G; 431 T; 0 other;

Query Match	97.4%	Score 955.6;	DB 21;	Length 1803;
Best Local Similarity	99.6%	Pred. No. 4.3e-267;		
Matches 958;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	20	ATATGGCACAGGTTCTTCAGAGCCACTGTGACTGCTCCCTGGATTTGATGAGGGGCTG	79	
DB	839	AGATGGCACAGGTTCTTCAGAGCCACTGTGACTGCTCCCTGGATTTGATGAGGGGCTG	898	
QY	80	ATGCAGAACTCTTCGGAAGGCTATGAAGGCTTTGGCCACAGATGAGGAGCATCTCTGA	139	
DB	899	ATGCAGAACTCTTCGGAAGGCTATGAAGGCTTTGGCCACAGATGAGGAGCATCTCTGA	958	
QY	140	CTCTGTTCACATCCGGAAGTATGCTCAGCCGAGGAAATCTCTGCAGCTTTTAAAGACTC	199	
DB	959	CTCTGTTCACATCCGGAAGTATGCTCAGCCGAGGAAATCTCTGCAGCTTTTAAAGACTC	1018	
QY	200	TGTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAAT	259	
DB	1019	TGTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAAT	1078	
QY	260	TAATTTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAATGAACATGCTC	319	
DB	1079	TAATTTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAATGAACATGCTC	1138	
QY	320	TGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTG	379	
DB	1139	TGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTG	1198	
QY	380	AAGAACTCAGAGCCATCAAAAGTTTATGAAGAAATATGGCTCAAGCTCGGAAGATG	439	
DB	1199	AAGAACTCAGAGCCATCAAAAGTTTATGAAGAAATATGGCTCAAGCTCGGAAGATG	1258	
QY	440	ACGTGGTGGGGACACCTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCCATCAGGTA	499	
DB	1259	ACGTGGTGGGGACACCTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCCATCAGGTA	1318	
QY	500	ACAGAGACCTTGATGCTGGAATGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTAT	559	
DB	1319	ACAGAGACCTTGATGCTGGAATGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTAT	1378	
QY	560	TTCAGCTGGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGAA	619	
DB	1379	TTCAGCTGGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGAA	1438	
QY	620	CACGAAGTGTCTCATTTGAGAAAGTGTGTTGACAACTAGATGATATCAGGATTC	679	
DB	1439	CACGAAGTGTCTCATTTGAGAAAGTGTGTTGACAACTAGATGATATCAGGATTC	1498	
QY	680	AAATTTGAGAAACCATTCACCGGAGACTTCTGGCAATTTAGACAACTACTCCTGCTG	739	
DB	1499	AAATTTGAGAAACCATTCACCGGAGACTTCTGGCAATTTAGACAACTACTCCTGCTG	1558	
QY	740	TTGTGAATCTATTTCGAAGTATACCTGCTTACCTTGCAGAGACCTCTATTATGCTATGA	799	
DB	1559	TTGTGAATCTATTTCGAAGTATACCTGCTTACCTTGCAGAGACCTCTATTATGCTATGA	1618	
QY	800	AGGAGCTGGGACAGATGATACCTCTCATCAGAGTCAATGTTTCCAGGAGTGAATG	859	
DB	1619	AGGAGCTGGGACAGATGATACCTCTCATCAGAGTCAATGTTTCCAGGAGTGAATG	1678	
QY	860	ATCTGTTTAAACATCAGGAGGAGTTTAGAAGAAATTTTCCACCTCTCTTTATTCATGA	919	
DB	1679	ATCTGTTTAAACATCAGGAGGAGTTTAGAAGAAATTTTCCACCTCTCTTTATTCATGA	1738	
QY	920	TTAAGGAGATACATCTGGGACTATAAGAAGCTCTTCTGCTGCTCTCCGAGAGATG	979	
DB	1739	TTAAGGAGATACATCTGGGACTATAAGAAGCTCTTCTGCTGCTCTCCGAGAGATG	1798	
QY	980	AC 981		

DB 1799 AC 1800

RESULT 10
AA82107
ID AA82107 standard; cDNA; 1454 BP.

XX AC AA82107;
XX AC AA82107;
DT 25-MAR-2003 (updated)
DT 13-NOV-1990 (first entry)

XX PAP-I cDNA from human placenta, used for anticoagulant production.

XX PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;
KW phospholipase A2; disseminated intravascular coagulation; human placenta;
KW deep vein thrombosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 13..972
FT /*tag= a
FT /product=PAP-I

PN WO8805659-A.

XX PD 11-AUG-1988.

XX PF 05-FEB-1988; 88WO-US00340.

XX PR 06-FEB-1987; 87US-0011782.

XX PR 05-JUN-1987; 87US-0059355.

XX (ZYMO) ZYMOGENETICS INC.

PA (UNIW) UNIV WASHINGTON.

XX Fujikawa K, Iraní MH, Carter BLA;

XX WPI; 1988-235049/33.

DR P-PSDB; AAP82317.

XX Human proteins having anticoagulant and antiinflammatory activity -
isolated from biological fluid by anion-exchange chromatograph media.

PS Disclosure; Page ?; p; English.

XX A human placenta cDNA library (Clontech) was screened to obtain
this sequence. The cDNA does not contain a leader peptide sequence,
indicating that PAP-I is probably not constitutively secreted.
CC The product binds to phospholipid and inhibits phospholipase A2.
CC The protein can substitute heparin or other anticoagulants in
the treatment of disseminated intravascular coagulation, deep vein
thrombosis, or other disorders. It also has antiinflammatory
properties.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1454 BP; 434 A; 280 C; 324 G; 416 T; 0 other;

Query Match 97.4%; Score 955.2; DB 9; Length 1454;
Best Local Similarity 99.7%; Pred. No. 5.1e-267;
Matches 957; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGGGGCTGAT 81

DB 13 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGGGGCTGAT 72

QY 82 CGAGAACTCTTCGGAAGGCTATGAAGGCTTTGGCCACAGATGAGGAGCATCTCTGACT 141

DB 73 CGAGAACTCTTCGGAAGGCTATGAAGGCTTTGGCCACAGATGAGGAGCATCTCTGACT 132

QY 142 CTGTTGACATCCGGAAGTAATGCTCAGGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201

133 CTGTTGACATCCCGAAGTAATGCTCAGCGCAGGAATCTCTGCAGCTTTTAAGACTCTG 192
 202 TTTGGCAGGAGTCTCTGGATGACCTGAATCAGAATACTGAAATTTGAAAAATTA 261
 193 TTTGGCAGGAGTCTCTGGATGACCTGAATCAGAATACTGAAATTTGAAAAATTA 252
 262 ATTGTGGCTCTGATGAACACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCTCTG 321
 253 ATTGTGGCTCTGATGAACACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCTCTG 312
 322 AAGGAGCTGGAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 313 AAGGAGCTGGAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372
 382 GAACTGAGAGCCATCAACAAGTTTATGAAGAGAAATATGGCTCAAGCCTGGAGATGAC 441
 373 GAACTGAGAGCCATCAACAAGTTTATGAAGAGAAATATGGCTCAAGCCTGGAGATGAC 432
 442 GTGGTGGGGACACTTCAGGCTACTACACGGGATGTTGGTGTCTCTCTTCAGGCTAAC 501
 433 GTGGTGGGGACACTTCAGGCTACTACACGGGATGTTGGTGTCTCTCTTCAGGCTAAC 492
 502 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 493 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 552
 562 CAGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGAACA 621
 553 CAGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGAACA 612
 622 CGAAGTGTCTCTCATTTGAAAGAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 681
 613 CGAAGTGTCTCTCATTTGAAAGAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 672
 682 ATTGAGAAACCATGACCGGAGACTTCTGGCAATTTAGACAACTACTCTTCTGCTGT 741
 673 ATTGAGAAACCATGACCGGAGACTTCTGGCAATTTAGACAACTACTCTTCTGCTGT 732
 742 GTGAAATCTATTGAAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAG 801
 733 GTGAAATCTATTGAAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAG 792
 802 GGAGCTGGGACAGATGATCATACCTCTCATCAGAGTATGTTTCCAGGAGTGAGATTGAT 861
 793 GGAGCTGGGACAGATGATCATACCTCTCATCAGAGTATGTTTCCAGGAGTGAGATTGAT 852
 862 CTGTTTAAACATCAGGAGGAGTTTAGAAGAAATTTGCCACCTCTCTTTATCCATGATT 921
 853 CTGTTTAAACATCAGGAGGAGTTTAGAAGAAATTTGCCACCTCTCTTTATCCATGATT 912
 922 AAGGAGATACATCTGGGAGTATAAGAAAGCTCTTCTGCTGCTCTCCGAGAGATGAC 981
 913 AAGGAGATACATCTGGGAGTATAAGAAAGCTCTTCTGCTGCTCTGTGAGAGATGAC 972

RESULT 11

AAQ12679
 ID AAQ12679 standard; cDNA; 1460 BP.
 XX
 AC AAQ12679;
 XX
 DT 25-MAR-2003 (updated)
 DT 30-SEP-1991 (first entry)
 XX
 DE PAP-I.
 XX
 KW Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;
 KW gla-domain; VKDP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

CDS 13..972
 /*tag= a
 /product= PAP-I
 WO9109953-A.
 11-JUL-1991.
 13-DEC-1990; 90WO-US07335.
 29-DEC-1989; 89US-0459082.
 (ZYMO) ZYMOGENETICS INC.
 Foster DC;
 WPI; 1991-222905/30.
 P-PSDB; AARI3082.
 Recombinant prodn. of hybrid phospholipid-binding proteins -
 comprising lipocortin phospholipid-binding domain and
 vitamin K-dependent protein
 Disclosure; Fig 7; 57pp; English.
 This sequence, or a fragment of it, is used in the construction of
 DNA sequences encoding hybrid phospholipid-binding proteins (PBP)
 comprising at least one lipocortin phospholipid binding domain (PBD),
 e.g. of PAP-I, joined to a gla-domainless vitamin K-dependent
 protein, e.g. protein C or activated protein C.
 See AAQ12680-81 for such examples.
 CC A human placenta cDNA library was screened using affinity-
 purified antibody against PAP-I in order to obtain this cDNA.
 CC See also AAQ12678-81.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1460 BP; 436 A; 280 C; 323 G; 421 T; 0 other;

Query Match 97.4%; Score 955.2; DB 12; Length 1460;
 Best Local Similarity 99.7%; Pred. No. 5; 1e-267;
 Matches 957; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 22 ATGCGACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
 DB 13 ATGCGACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 72
 QY 82 GCAGAAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 141
 DB 73 GCAGAAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTGACT 132
 QY 142 CTCTTCACATCCGAAAGTATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 201
 DB 133 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 192
 QY 202 TTTGGCAGGAGTCTCTGATGACCTGAAATCAGAATACTGAAATTTGAAAAATTA 261
 DB 193 TTTGGCAGGAGTCTCTGATGACCTGAAATCAGAATACTGAAATTTGAAAAATTA 252
 QY 262 ATTGTGGCTCTGATGAACACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCTCTG 321
 DB 253 ATTGTGGCTCTTATGAACACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCTCTG 312
 QY 322 AAGGAGCTGGAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 DB 313 AAGGAGCTGGAACAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 372
 QY 382 GAACTGAGAGCCATCAACAAGTTTATGAAGAGAAATATGGCTCAAGCCTGGAGATGAC 441
 DB 373 GAACTGAGAGCCATCAACAAGTTTATGAAGAGAAATATGGCTCAAGCCTGGAGATGAC 432
 QY 442 GTGGTGGGGACACTTCAGGCTACTACACGGGATGTTGGTGTCTCTCTTCAGGCTAAC 501
 DB 433 GTGGTGGGGACACTTCAGGCTACTACACGGGATGTTGGTGTCTCTCTTCAGGCTAAC 492

Qy	502	AGAGACCTGATGCTGGAAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	561
Db	493	AGAGACCTGATGCTGGAAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	552
Qy	562	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAGTTTATCACCATTCTTTGGAACA	621
Db	553	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAGTTTATCACCATTCTTTGGAACA	612
Qy	622	CGAAGTGTGCTCAATTTGAGAAAAGTGTTCACAAGTACATGACTATATCAGGATTTCAA	681
Db	613	CGAAGTGTGCTCAATTTGAGAAAAGTGTTCACAAGTACATGACTATATCAGGATTTCAA	672
Qy	682	ATTGAGAAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCACTACTCCTTGCTGTT	741
Db	673	ATTGAGAAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCACTACTCCTTGCTGTT	732
Qy	742	GTGAAATCTATTTCGAAGTATACCTGCCTACCTTCGAGAGACCTCTATTATGCTATGAAG	801
Db	733	GTGAAATCTATTTCGAAGTATACCTGCCTACCTTCGAGAGACCTCTATTATGCTATGAAG	792
Qy	802	GGAGCTGGACAGATGATCATCCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT	861
Db	793	GGAGCTGGACAGATGATCATCCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT	852
Qy	862	CTGTTTAAACATCAGGAAGGAGCTTTAGGAAGAATTTTGGCACCTCTCTTTATTTCCATGATT	921
Db	853	CTGTTTAAACATCAGGAAGGAGCTTTAGGAAGAATTTTGGCACCTCTCTTTATTTCCATGATT	912
Qy	922	AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTCTCCGGAGAGATGAC	981
Db	913	AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTCTCCGGAGAGATGAC	972

RESULT 12

AAN80801
ID AAN80801 standard; DNA; 1466 BP.

XX	
AC	AAN80801;
XX	
DT	25-MAR-2003 (updated)
DT	12-SEP-1990 (first entry)

Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha (Glu22).

KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant;
antiinflammatory; phospholipase inhibitory.
KW

xx Homo sapiens.

aa	Key	Location/Qualifiers
FT	mat_peptide	35..997
FT		/*tag= a
FT		/note="claimed in c

PN W08807576-A.

06-OCT-1988.

26-MAR-1988: 88WO-EP00266.

XX
PR 2A-MAR-1987. 87DE-3710309

PR 28-MAR-1987; 87DE-3710364.
PR 28-MAR-1987; 87DE-3710430

PR 04-NOV-1987; 87DE-3737367.

PA (BOEH) BOEHRINGER INGELHEIM

PI Hauptmann R, Maurer-Fogy I, Bodo G,

XX XX
DR WPI; 1988-292861/41.

Db 694 AATTGAGAAACCAATTGACCGGAGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGT 753
 QY 741 TGTGAAATCTATTGGAAGTATACCTGCTTACCTTGCAGAGACCTCTATTATGCTATGAA 800
 Db 754 TGTGAAATCTATTGGAAGTATACCTGCTTACCTTGCAGAGACCTCTATTATGCTATGAA 813
 QY 801 GGGAGCTGGGACAGATGATCATACCTCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA 860
 Db 814 GGGAGCTGGGACAGATGATCATACCTCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA 873
 QY 861 TCTGTTTAACATCAGGAGAGGTTTAGGAAGAATTTGGCCACCTCTCTTTATTCATGAT 920
 Db 874 TCTGTTTAACATCAGGAGAGGTTTAGGAAGAATTTGGCCACCTCTCTTTATTCATGAT 933
 QY 921 TAAGGAGATACATCTGCGGACTATAGAAAGCTCTTCTGCTGCTCTCTCCGAGAGATGA 980
 Db 934 TAAGGAGATACATCTGCGGACTATAGAAAGCTCTTCTGCTGCTCTCTGCGAGAGATGA 993
 QY 981 C 981
 Db 994 C 994

RESULT 13

AA080873
 ID AA080873 standard; DNA; 963 BP.

XX AA080873;
 XX 25-MAR-2003 (updated)
 DT 12-SEP-1990 (first entry)
 XX Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
 DE (Asp22).
 XX Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
 KW antiinflammatory; phospholipase inhibitory.
 XX Homo sapiens.

Key	Location/Qualifiers
mat_peptide	35..963
FT	/*tag= a
PN	WO807576-A.
PD	06-OCT-1988.
PF	26-MAR-1988; 88WO-EP00266.
PR	28-MAR-1987; 87DE-3710309.
PR	28-MAR-1987; 87DE-3710364.
PR	28-MAR-1987; 87DE-3710430.
PR	04-NOV-1987; 87DE-3737367.
XX	(BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX	Hauptmann R, Maurer-Fogy I, Bodo G, Swetly P, Stratowa C, Falkner E; Adolf G, Reutlingsperger CMP; WPI: 1988-292861/41. P-PSDB: AAP80242.
XX	New vascular anti-coagulating proteins - useful as thrombin inhibitors, antiinflammatory agents, etc
PS	Claim 2; Page 160-161; 183pp; German.

The DNA is produced by determining the amino acid sequence of isolated
 CC and highly purified VAPs, constructing DNA probes on the basis of this
 CC sequence, using the probes to search through suitable cDNA libraries,
 CC isolating cDNA that hybridises with the probes, by inserting the cDNA
 CC into a suitable vector, and using the vector to transform a host

CC organism. VAC-alpha has anticoagulant activity under certain
 CC conditions, but loses this activity in the event of severe bleeding.
 CC It acts by inhibiting conversion of factor X to factor Xa and conversion
 CC of prothrombin to thrombin. It is structurally related to lipocortin I
 CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
 CC has similar antiinflammatory and phospholipase inhibitory activity.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 963 BP; 284 A; 183 C; 242 G; 254 T; 0 other;

Query Match 97.2%; Score 953.6; DB 9; Length 963;
 Best Local Similarity 99.6%; Pred. No. 1.2e-266;
 Matches 956; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	22	ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGGATTTGATGAGCGGGCTGAT	81
Db	1	ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGGATTTGATGAGCGGGCTGAT	60
QY	82	GCAGAAACTCTTCGGGAAGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCTGACT	141
Db	61	GCAGACACTCTTCGGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCTGACT	120
QY	142	CTGTTGACATCCCGAAGTAATGCTCAGCCCGCAGGAAATCTCTSCAGCTTTTAAAGACTCTG	201
Db	121	CTGTTGACATCCCGAAGTAATGCTCAGCCCGCAGGAAATCTCTSCAGCTTTTAAAGACTCTG	180
QY	202	TTTGGCAGGATCTTCTGGTGAACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	261
Db	181	TTTGGCAGGATCTTCTGGTGAACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	240
QY	262	ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG	321
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Db	361	GAACTCAGAGCCATCAACAAAGTTTATGAAGAAGATATGGCTCAAGCCCTGGAAGATGAC	420
QY	442	GTGGTGGGGGACACTTCAGGGTACTACACGCGSATGTGGTGGTTCCTCTCAGGCTAAC	501
Db	421	GTGGTGGGGGACACTTCAGGGTACTACACGCGSATGTGGTGGTTCCTCTCAGGCTAAC	480
QY	502	AGAGACCCCTGATGCTGGGAATTTGATGAAGCTCAAGTTGAAACAAGATGCTCAGGCTTAT	561
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QY	562	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCACATCTTTGGAACA	621
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Db	781	GGAGCTGGGACAGATGATCATACCTCTCATCAGAGTCATGGTTTCCAGGAGTCAGATTGAT	840
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PF 08-MAR-2000; 2000WO-US05918.
XX
PR 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Ruben SM;
PI
XX
XX WPI: 2000-587514/55.
DR P-PSDB; AAB58393.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX
XX Claim 1; Page 746; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnery; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
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Query Match 96.2%; Score 943.8; DB 21; Length 1637;
Best Local Similarity 99.6%; Pred. No. 1.1e-263;
Matches 956; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 22 ATGGCACAGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTTGATGAGCGGGCTGAT 81
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QY 82 GCAGAACTCTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 233 GCAGAACTCTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 292
QY 142 CTGTTGACATCCGAAAGTAATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 201
DB 293 CTGTTGACATCCGAAAGTAATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 352
QY 202 TTGGCAGGGATCTCTCGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAATAATTA 261
DB 353 TTGGCAGGGATCTCTCGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAATAATTA 412
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DB 413 ATTGTGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTTGAACTGAAACATGCTTGG 472
QY 322 AAGGGAGCTGGAAACAATGAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA 381
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DB 1011

DB 593 GTGCTGGGGACACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 652
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DB 653 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTTGAACAAGATGCTCAGGCTTTATTT 712
QY 562 CAGGCTCGAAGACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGANCA 621
DB 713 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGANCA 772
QY 622 CGAAGTGTGCTCATTTTGAAGAAAGGTTTGAACAAGTACATGACTATATCAGATTTCAA 681
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DB 892 GTGAAATCTATTTCGAAAGTATACCTGGCTACCTTTCAGAGACCCCTCTTATTATGCTATGAAG 951
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DB 952 GGAGCTGGGACACATGATCATACCCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTTGAT 1011
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DB 1072 AAGGGAGATACATCTCGGGACTATAAAGAGCTTCTGCTGCTCTCTGTGGAGAGATGAC 1131

Search completed: August 28, 2003, 16:03:37
Job time : 218.333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:43:40 ; Search time 2602.33 Seconds
(without alignments)
15421.677 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 31: em_htg_pln:*
- 32: em_htg_rtd:*
- 33: em_htg_sy:*
- 34: em_htg_vrt:*
- 35: em_htg_hum:*
- 36: em_htgo_hum:*
- 37: em_htgo_inv:*
- 38: em_htgo_mus:*
- 39: em_htgo_pln:*
- 40: em_htgo_rtd:*
- 41: em_htgo_sy:*
- 42: em_htgo_vrt:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	981	100.0	981	6	AR262471	Sequence
2	976.2	99.5	981	6	AR262469	Sequence
3	976.2	99.5	981	6	AR262470	Sequence
4	957.8	97.6	1486	6	A07367	M.musculus
5	957.8	97.6	1536	9	BC004993	Homo sapi
6	957.8	97.6	1539	9	BC012804	Homo sapi
7	957.8	97.6	1539	9	BC012822	Homo sapi
8	957.8	97.6	1582	9	HUMPAP4	Human place
9	956.8	97.5	963	6	A01769	DNA sequence
10	956.8	97.5	1432	6	I07345	Sequence 21
11	956.8	97.5	1444	9	HUMATC	Human place
12	956.8	97.5	1454	6	I08832	Sequence 3
13	956.8	97.5	1538	9	BC001429	Homo sapi
14	956.8	97.5	1560	9	HSVAC	Human mRNA
15	956.8	97.5	1566	6	E01816	cDNA encodi
16	956.8	97.5	1566	6	E03096	DNA encodin
17	956.8	97.5	1586	9	HUMBCI	Homo sapien
18	956.8	97.5	1567	6	I33410	Sequence 2
19	956.8	97.5	1574	9	HUMLC5	Human lipoc
20	956.8	97.5	1592	9	HUMENN	Human endon
21	956.8	97.5	1605	6	I07181	Sequence 12
22	956.2	97.5	1575	6	A13845	H.sapiens p
23	955.2	97.4	983	6	A01770	DNA sequence
24	955.2	97.4	1566	6	E14351	cDNA encodi
25	953.8	97.2	957	6	I33411	Sequence 4
26	953.6	97.2	1574	6	I07344	Sequence 20
27	953.6	97.2	1619	9	BC018671	Homo sapi
28	749.4	76.4	1415	10	MUSANXV	Mouse mRNA
29	749.4	76.4	1480	6	AX305384	Sequence
30	749.4	76.4	1480	10	MM029396	Mus musculu
31	747.8	76.2	1522	10	BC003716	Mus muscu
32	727	74.1	1417	6	AX401930	Sequence
33	727	74.1	1417	10	RAVLC5	Rat lipocor
34	695	70.8	1028	10	AF051895	Rattus no
35	573	58.4	1229	5	CHKANCC2A	Chicken anc
36	535.4	54.6	1477	5	BC043882	Xenopus l
37	494.4	50.4	1579	5	D64134	Newt mRNA f
38	483	49.2	483	6	A01772	DNA sequenc
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40	473.8	48.3	480	6	A01774	DNA sequenc
41	384.4	39.2	1417	5	OLANNEXM2	O.latices m
42	359	36.6	2055	4	BOVENDNX	Bovine endo
43	359	36.6	2055	4	BTCHRA	Bovine mRNA
44	357.4	36.4	1508	4	BOVP1341	Bovine mRNA
45	354.6	36.1	1074	5	AY178799	Danio rer

ALIGNMENTS

RESULT 1
LOCUS AR262471
DEFINITION Sequence 5 from patent US 6323313.
ACCESSION AR262471
VERSION AR262471.1 GI:28073915
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Tait,J.F. and Brown,D.S.
TITLE Annexin derivative with endogenous chelation sites
JOURNAL Patent: US 6323313-A 5 27-NOV-2001;
FEATURES Location/Qualifiers

981 bp DNA linear PAT 29-JAN-2003

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source 1..981
BASE COUNT 286 a 187 c 250 g 258 t
ORIGIN

Query Match 100.0%; Score 981; DB 6; Length 981;
Best Local Similarity 100.0%; Pred. No. 4.4e-248;
Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGATTTGATGAGCGGCTGATCAGAACTCTTCGGAAGCTATGAAAGCTTTGGGCACA 120
Db 61 GGATTTGATGAGCGGCTGATCAGAACTCTTCGGAAGCTATGAAAGCTTTGGGCACA 120
QY 121 GATGAGGAGCATCTGACTCTGTGATGCCGAAGTAATGTCAGAGCCAGGAAATC 180
Db 121 GATGAGGAGCATCTGACTCTGTGATGCCGAAGTAATGTCAGAGCCAGGAAATC 180
QY 181 TCTGCAGCTTTTAAGACTCTGTTTGGCAGGATCTCTGGATGACCTGAAATCAGAACTA 240
Db 181 TCTGCAGCTTTTAAGACTCTGTTTGGCAGGATCTCTGGATGACCTGAAATCAGAACTA 240
QY 241 ACTGGAATTTGAAAAATTAATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCT 300
Db 241 ACTGGAATTTGAAAAATTAATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCT 300
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Query Match 99.5%; Score 976.2; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 8.1e-247;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
AR262469
LOCUS
DEFINITION
Sequence 1 from patent US 6323313.
ACCESSION
AR262469
VERSION
AR262469.1 GI:28073913
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 981)
AUTHORS
Tait,J.F. and Brown,D.S.
TITLE
Annexin derivative with endogenous chelation sites
JOURNAL
Patent: US 6323313-A 1 27-NOV-2001;
FEATURES
Location/Qualifiers
1..981
source
BASE COUNT 286 a 187 c 251 g 257 t
ORIGIN

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RESULT 3
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DEFINITION Sequence 3 from patent US 6323313.
ACCESSION AR262470
VERSION AR262470.1 GI:28073914
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Tait, J.F. and Brown, D.S.
TITLE Annexin derivative with endogenous chelation sites
JOURNAL Patent: US 6323313-A 3 27-NOV-2001;
FEATURES
SOURCE 1..981
BASE COUNT 286 a 187 c 251 g 257 t
ORIGIN

Query Match 99.5%; Score 976.2; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 8.1e-247;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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D 841 GTTTCAGGAGCTGAGATGATCTGTTTAACTACAGAGAGGAGTTTAGGAAGAAATTTGCC 900
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D 961 CTGCTCTCCGAGAGATGAC 981

RESULT 4
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DEFINITION M.musculus VAC-alpha cDNA.
ACCESSION A07367
VERSION A07367.1 GI:412270
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1466)
AUTHORS Patent: DE 3810331-A 3 05-OCT-1989;
JOURNAL Location/Qualifiers
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DB 994 C 994

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

BC004993 1536 bp mRNA linear PRI 06-JUN-2003
Homo sapiens annexin A5, mRNA (cDNA clone MGC:4402 IMAGE:2906015),
complete cds.
BC004993
BC004993.1 GI:13436442
MGC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1536)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932

2 (bases 1 to 1536)
Strausberg, R.
Direct Submission

Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2990,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

Info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Tan Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Scott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL plate: 9 Row: 1 Column: 8

This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4809273.

Location/Qualifiers

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COMMENT

Contact: MGC help desk
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 http://www.systemsbio.org
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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CDS

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 ORIGIN

Query Match 97.6%; Score 957.8; DB 9; Length 1539;
 Best Local Similarity 99.8%; Pred. No. 5.9e-242;
 Matches 959; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 7

BC012822

LOCUS

BC012822

DEFINITION

Homo sapiens annexin A5, mRNA (cdna clone MGC:4465 IMAGE:2961097), complete cds.

ACCESSION

BC012822

VERSION

BC012822.1 GI:15215458

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1539)

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCES

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 MEDLINE
 PUBMED
 12477932
 REFERENCE
 2 (bases 1 to 1539)
 TITLE
 Direct Submission
 Strausberg, R.
 JOURNAL
 Submitted (15-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps@email.nih.gov
 Tissue procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadans@systemsbiology.org
 Anup Madan, Jessica Fahney, Brin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 BASE COUNT 432 a 320 c 355 g 432 t
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 Query Match 97.6%; Score 957.8; DB 9; Length 1539;
 Best Local Similarity 99.8%; Pred. No. 5.9e-242;
 Matches 959; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 21 TATGGCAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGATGAGCGGGCTGA 80
 Db 126 TATGGCAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGATGAGCGGGCTGA 185
 QY 81 TGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCCTGAC 140
 Db 186 TGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCCTGAC 245
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Db 246 TCTGTTGACATCCCGAAGTAATGCTCGACGCCAGGAATCTCTGCAGCTTTTAAGACTCT 305
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 Db 426 GAAGGAGCTGGAAACAATAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGA 485
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 Db 546 CGTGGTGGGGACACTTTCAGGCTACTACCGCGGATGTTGGTGGTCTTCTTCCAGGCTAA 605
 QY 501 CAGAGACCCCTGATGCTGGAAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTAT 560
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 Db 666 TCAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCCTCTTGGAAAC 725
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 Db 726 ACGAAGTGTCTCTCATTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCA 785
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 QY 981 C 981
 Db 1086 C 1086
 RESULT 8
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 LOCUS
 DEFINITION Human placenta anticoagulant protein PP4 mRNA, complete cds.
 ACCESSION M19384 J03264
 VERSION M19384.1 GI:189614
 KEYWORDS anticoagulant protein; thromboplastin inhibitor.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1582)
 Grundmann, U., Abel, K.J., Bohn, H., Lobermann, H., Lottspeich, F. and
 Kupper, H.

Db	530	CAGNAGCCCTGATGCTGGAA	TTGATGAAGCTCAAGTTGAA	CACAAAGATGCTCAGGCTTTAT	568
Qy	561	TCAGGCTGGAGAACTTTAA	TGGGGGGACAGATGAAGAA	AGTTTATCACCATCTTTGGAA	520
Db	690	TCAGGCTGGAGAACTTTAA	TGGGGGGACAGATGAAGAA	AGTTTATCACCATCTTTGGAA	749
Qy	621	ACGAAGTGTGCTCATTTTG	AGAAAGGTTTTCAGCAAGT	TACATGACTATATCAGGATTTCA	580
Db	750	ACGAAGTGTGCTCATTTTG	AGAAAGGTTTTCAGCAAGT	TACATGACTATATCAGGATTTCA	809

681	QY	AAATTGAGGAACCAATTGACCGGAGACCTTCTGGCAATTTTAGAGCAACTACTCCTTCGCTGT	740
810	Db	AAATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTCGCTGT	869
741	QY	TGTGCAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCCCTCTATTATGCTATGAA	800
870	Db	TGTGCAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCCCTCTATTATGCTATGAA	929
801	QY	GGGAGCTGGGACACATGATCATACCCCTCATCAGAGTCAATGGTTTCCAGAGTGAGATGA	860
930	Db	GGGAGCTGGGACACATGATCATACCCCTCATCAGAGTCAATGGTTTCCAGAGTGAGATGA	989
861	QY	TCTGTTTAAACATCAGGAGGAGTTTAGSAGAAATTTTGCCACCTCTCTTTTATTCATGAT	920
990	Db	TCTGTTTAAACATCAGGAGGAGTTTAGSAGAAATTTTGCCACCTCTCTTTTATTCATGAT	104
921	QY	TAAGGGAGATACATCTGGGGACTATAGAAAAGCTCTTCTGCTGCTCTCCGGAGAGAAGATGA	980
1050	Db	TAAGGGAGATACATCTGGGGACTATAGAAAAGCTCTTCTGCTGCTCTCTGGAGAAAGATGA	1105
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1110	Db	C 1110	

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RESULT 9
LOCUS A01769 963 bp DNA linear PAT 01-SEP-1999
DEFINITION DNA sequence (gaa) for vascular anticoagulating protein.
ACCESSION A01769
VERSION A01769.1 GI:410787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 963)
AUTHORS
TITLE VASCULAR ANTICOAGULANT PROTEINS, DNAs WHICH CODE FOR THEM,
MANUFACTURE AND APPLICATION THEREOF
JOURNAL Patent: WO 8807576-A 1 06-OCT-1988;
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BASE COUNT 285 a 181 c 243 g 254 t
ORIGIN
Query Match 97.5%; Score 956.8; DB 6; Length 963;
Best Local Similarity 99.8%; Pred. No. 1.1e-241;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY	22	ATGCACAGGTTCTCAGAGGACCTGTGACTGACTTCCTCGATTTGATGAGCGGCTGAT	81
Db	1	ATGCACAGGTTCTCAGAGGACCTGTGACTGACTTCCTCGATTTGATGAGCGGCTGAT	60
QY	82	GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGCCACAGATGAGGAGACATCCTGACT	141
Db	61	GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGCCACAGATGAGGAGACATCCTGACT	120
QY	142	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAGACTCTG	201
Db	121	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAGACTCTG	180
QY	202	TTTGGCAGGGATCTTCGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	261
Db	181	TTTGGCAGGGATCTTCGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	240
QY	262	ATTGTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTCTG	321
Db	241	ATTGTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTCTG	300
QY	322	AAGGAGCTGCAACAAATGAAGAACTGCTGACGAAATATGCTTCAAGGCTGGAAGATGAC	381
Db	301	AAGGAGCTGCAACAAATGAAGAACTGCTGACGAAATATGCTTCAAGGCTGGAAGATGAC	360
QY	382	GAAGTGAAGCCATCAACAAAGTTTATGAAGAAATATGCTTCAAGGCTGGAAGATGAC	441
Db	361	GAAGTGAAGCCATCAACAAAGTTTATGAAGAAATATGCTTCAAGGCTGGAAGATGAC	420
QY	442	GTGTTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTCTTCAGGCTAAC	501
Db	421	GTGTTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTCTTCAGGCTAAC	480
QY	502	AGAGACCTGATGCTGGAATTTGATCAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT	561
Db	481	AGAGACCTGATGCTGGAATTTGATCAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT	540
QY	562	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCCTTTTGGAAACA	621
Db	541	CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCCTTTTGGAAACA	600
QY	622	CGAAGTGTCTCATTTGAGAAAGGTTTGTGACAAAGTACATGACATATATCAGGATTTCAA	681
Db	601	CGAAGTGTCTCATTTGAGAAAGGTTTGTGACAAAGTACATGACATATATCAGGATTTCAA	660
QY	682	ATTGAGGAAACATTGACCGGAGACTTCTGCGCAATTTAGAGCAACTACTCCTTGCTGTT	741
Db	661	ATTGAGGAAACATTGACCGGAGACTTCTGCGCAATTTAGAGCAACTACTCCTTGCTGTT	720
QY	742	GTGAAATCTATTGGAAGTATACCTGCCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG	801
Db	721	GTGAAATCTATTGGAAGTATACCTGCCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG	780
QY	802	GGAGCTGGGACAGATGATACACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT	861
Db	781	GGAGCTGGGACAGATGATACACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT	840
QY	862	CTGTTTAACATCAGGAGGACTTTAGGAAGATTTTGGCCACTCTCTTTATTCATGATT	921
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QY	922	AAGGAGATACATCTGGGACTATAAGAAAGCTTCTGCTGCTCTCCGGAGAGATGAC	981
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 DEFINITION Sequence 21 from Patent EP 0330396.
 ACCESSION I07345
 VERSION I07345.1
 KEYWORDS GI:590053

SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1432)		
TITLE	Wallner, B.P., Pepinsky, R.B. and Browning, J.L.		
	DNA sequences, recombinant DNA molecules and processes for		
	producing lipocortins III, IV, V & VI		
JOURNAL	Patent: Ep 0330396-A2 21 30-AUG-1989;		
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ORIGIN	/organism="unknown"		
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Best Local Similarity	99.8%: Pred. No. 1.1e-241;		
Matches	958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
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Db	1	ATGCACAGGTTCTCAGAGGACCTGTGACTGACTTCCTCGATTTGATGAGCGGCTGAT	60
Qy	82	GCAGAAACTCTTCGGAAGGCTATCAAAAGGCTTGGCCACAGATGAGGAGACATCCTGACT	141
Db	61	GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGCCACAGATGAGGAGACATCCTGACT	120
Qy	142	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAGACTCTG	201
Db	121	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAGACTCTG	180
Qy	202	TTTGGCAGGGATCTTTCGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	261
Db	181	TTTGGCAGGGATCTTTCGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA	240
Qy	262	ATTGTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG	321
Db	241	ATTGTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCGCTTG	300
Qy	322	AAGGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA	381
Db	301	AAGGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA	360
Qy	382	GAAGTGAAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCCTGGAAGATGAC	441
Db	361	GAAGTGAAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCCTGGAAGATGAC	420
Qy	442	GTGGTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC	501
Db	421	GTGGTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC	480
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Qy	622	CGAAGTGTGCTCATTTTGAGAAAGGTTGTTGACAAAGTACATGACATATATCAGGATTTCAA	681
Db	601	CGAAGTGTGCTCATTTTGAGAAAGGTTGTTGACAAAGTACATGACATATATCAGGATTTCAA	660
Qy	682	ATTGAGGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT	741
Db	661	ATTGAGGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT	720
Qy	742	GTGAAATCTATTGGAAGTATACCTTGCCCTACTCTGCAGAGACCCCTCTATTATGCTATGAAG	801
Db	721	GTGAAATCTATTGGAAGTATACCTTGCCCTACTCTGCAGAGACCCCTCTATTATGCTATGAAG	780
Qy	802	GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT	861
Db	781	GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGAT	840

QY 862 CTGTTTAAATCATCAGGAGGAGTTAGGAAGAATTTTGGCCACCTCTCTTATTCATGATT 921
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 QY 922 AAGGGAGATACATCTGGGAGCTATAGAAGCTCTTCTGCTGCTCCGGAGAGATGAC 981
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RESULT 11
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 DEFINITION Human placental anticoagulant protein (PAP) mRNA, complete cds.
 ACCESSION M18366
 VERSION M18366.1 GI:179131
 KEYWORDS anticoagulant.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1444)
 Funakoshi, T., Hendrickson, L.E., McMullen, B.A. and Fujikawa, K.
 TITLE Primary structure of human placental anticoagulant protein
 JOURNAL Biochemistry 26 (25), 8087-8092 (1987)
 MEDLINE 88163463
 PUBMED 2964863
 COMMENT Original source text: Human placenta, cdna to mRNA, clones
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 Best Local Similarity 99.8%; Pred. No. 1.1e-241;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 ACCESSION I08832
 VERSION I08832.1 GI:588459
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES Unclassified.
 1 (bases 1 to 1454)
 Fujikawa, K., Irani, M.H. and Carter, B.L.A.
 TITLE HUMAN PROTEINS HAVING ANTICOAGULANT AND ANTI-INFLAMMATORY ACTIVITY
 JOURNAL Patent: WO 8805659-A 3 11-AUG-1988;
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 BASE COUNT 434 a 279 c 325 g 416 t
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QY 22 ATGGCACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGACGGGCTGAT 81
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 Best Local Similarity 99.8%; Pred. No. 1.1e-241;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	142	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGACGCTTTTAAGACCTG	201
Db	133	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGACGCTTTTAAGACCTG	192
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Qy	262	ATTGTCGCTCTGATGAACCTCTCGGCTTATGATGCTTATGATGCTTATGATGCTTATG	321
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Db	313	AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTAATGCTTCAAGGACACCTGAA	372
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Qy	442	GTGCTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTTCCTTCAGGCTAAC	501
Db	433	GTGCTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTTCCTTCAGGCTAAC	492
Qy	502	AGAGACCTCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTATTT	561
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Qy	562	CAGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA	621
Db	553	CAGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA	612
Qy	622	CGAAGTGTGCTCATTTGAGAAAGTCTTTCAGAAAGTCTTTCAGAAAGTCTTTCAGAA	681
Db	613	CGAAGTGTGCTCATTTGAGAAAGTCTTTCAGAAAGTCTTTCAGAAAGTCTTTCAGAA	672
Qy	682	ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGACAACTACTCTTTCGCTGTT	741
Db	673	ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGACAACTACTCTTTCGCTGTT	732
Qy	742	GTGAAATCTATTGGAAGTATACCTGCTACCTTCAGAGACCCCTCTATTATGCTATGAAG	801
Db	733	GTGAAATCTATTGGAAGTATACCTGCTACCTTCAGAGACCCCTCTATTATGCTATGAAG	792
Qy	802	GGAGCTGGACAGATGATCATACCTCTATCAGAGTACATGTTTCCAGAGTGAGATGAT	861
Db	793	GGAGCTGGACAGATGATCATACCTCTATCAGAGTACATGTTTCCAGAGTGAGATGAT	852
Qy	862	CTGTTTAAACATCAGGAAGGAGTTTGAAGAAATTTTGCACCTCTCTTTATTCATGATT	921
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Qy	922	AAGGAGATACATCTGGGACTATAGAAGCTCTTCTGCTGCTCTCGGAGAGATGAC	981
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RESULT 13
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LOCUS BC001429 1538 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, annexin A5, clone MGC:2261 IMAGE:3140878, mRNA,
complete cds.
ACCESSION BC001429
VERSION BC001429.1 GI:12655148
KEYWORDS MGC.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 1538)
TITLE Strausberg, R.
JOURNAL Direct Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tlongson, E.E., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: TRAL plate: 4 Row: 0 Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 219480.
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Qy 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGCGATTGATGAGCGGCGTGAAT 81
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RESULT 14
HSVAC
LOCUS
DEFINITION
ACCESSION
VERSION
X12454.1 GI:37636
KEYWORDS
phospholipid-binding protein; vascular anticoagulant.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1560)
AUTHORS
Maurer-Fogy,I., Reutlingsperger,C.P., Pieters,J., Bodo,G.,
Stratowa,C. and Hauptmann,R.
TITLE
Cloning and expression of cDNA for human vascular anticoagulant, a
Ca2+-dependent phospholipid-binding protein
JOURNAL
Eur. J. Biochem. 174 (4), 585-592 (1988)
MEDLINE
88271329
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2455636
2 (bases 1 to 1560)
REFERENCE
AUTHORS
Hauptmann,R.
TITLE
Direct Submission
JOURNAL
Submitted (15-AUG-1988) Hauptmann R., Ernst Boehringer Institut
fuer Arzneimittelforschung, Dr. Boehringer-Gasse 5/11, A-1121 Wien,
Austria
COMMENT
Data kindly reviewed (11-Nov-1988) by Hauptmann R.
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Best Local Similarity 99.8%; Pred. No. 1,1e-241;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 22 ATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
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DEFINITION cDNA encoding human antioaguln.
ACCESSION E01816
VERSION E01816.1 GI:2170068
KEYWORDS JP 1989020095-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1566)
Salino, S., Iwasaki, A., and Suda, M.
POLYPEPTIDE HAVING ANTI-BLOOD COAGULATING ACTION
JOURNAL Patent: JP 1989020095-A 1 24-JAN-1989;
KONA CO
COMMENT
OS Homo sapiens (man)
PN JP 1989020095-A/1
PD 24-JAN-1989
PP 23-JUL-1987 JP 1987184428
PR 20-FEB-1987 JP 87P 37227
PI SAINO SUKEYUKI, IWASAKI AKIO, SUDA MAKOTO
PC C12P21/02,C07K13/00,C12N15/00//A61K37/02,(C12P21/02,C12R1:19);
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FT CDS 136..1098
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Best Local Similarity 99.8%; Pred. No. 1.le-241;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 22 ATGCACAGGTTCTCAGAGGACGTGACTGCTTCCCTGGATTTGATGAGCGGGCTGAT 81
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Title: US-09-970-969-3

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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14: gb_vl.*

15: em_ba.*

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20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

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29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rtd.*

36: em_htg_mam.*

37: em_htg_vrt.*

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39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	958	97.7	1536	9	BC004993 Homo sapi
6	958	97.7	1539	9	BC012804 Homo sapi
7	958	97.7	1539	9	BC012822 Homo sapi
8	958	97.7	1582	9	HUMRAP4
9	956.8	97.5	963	6	A01769 Human place
10	956.8	97.5	1432	6	A01769 DNA sequenc
11	956.8	97.5	1444	9	I07345 Sequence 21
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19	956.8	97.5	1574	9	I33410 Sequence 2
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ACCESSION AR262470
VERSION AR262470.1 GI:28073914
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Tait,J.F. and Brown,D.S.
TITLE Annexin derivative with endogenous chelation sites
JOURNAL Patent: US 6323313-A 3 27-NOV-2001;
FEATURES Location/Qualifiers

AR262470 981 bp DNA linear PAT 29-JAN-2003

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Qy	241	ACTGGAAAATTTGAAAATTAATTTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCT	300	
Db	241			
Qy	301	TATGAACCTGAAACATGCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAAT	360	
Db	301			
Qy	361	ATTGCTTCAAGGACACCTGAAAGACTGAGAGCCATCAAAACAGTTTATGAAGAATAT	420	
Db	361			
Qy	421	GGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTACCAGCGGATGTTG	480	
Db	421			
Qy	481	GTGGTTCTCTTCAGGCTTAACAGAGACCCCTGATGCTGGATGATGAAGCTCAAGTTGGA	540	
Db	481			
Qy	541	CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG	600	
Db	541			
Qy	601	TTTATCACCATCTTTGGAACACGAGTGTGTCTCATTTTGAAAAGGTGTTTGACAAGTAC	660	
Db	601			
Qy	661	ATGACTATATCAGGATTTCAAATTTGAGAAACCATTTGACCCGAGACTTCTGGCAATTTA	720	
Db	661			
Qy	721	GAGCACTACTCTCTGTTGTGAAATCTATTTCGAAAGTATACCTGCTACCTTCGACAG	780	
Db	721			
Qy	781	ACCTCTATTATGCTATCAAGGAGCTGGGACAGATGATCATACCTCATCAGATCATG	840	
Db	781			
Qy	841	GTPTCCAGGAGTGAGATGATCTCTTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTTGC	900	
Db	841			
Qy	901	ACCTCTCTTATTCATGATTAAGGGAGATACATCTCGGGACTATAAGAAAAGCTCTCTG	960	
Db	901			

RESULT 2	AR262469	981 bp	DNA	linear	PAT 29-JAN-2003
LOCUS	AR262469	Sequence 1 from patent US 6323313.			
DEFINITION	AR262469				
ACCESSION	AR262469				
VERSION	AR262469.1	GI:28073913			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 981)				
AUTHORS	Tait,J.F. and Brown,D.S.				
TITLE	Annexin derivative with endogenous chelation sites				
JOURNAL	Patent: US 6323313-A 1 27-NOV-2001;				
FEATURES	Location/Qualifiers				
source	1..981				
BASE COUNT	286 a 187 c 251 g 257 t				
ORIGIN	Unknown.				
Query Match	99.7%;	Score 977.8;	DB 6;	Length 981;	
Best Local Similarity	99.8%;	Pred. No. 2.4e-247;			
Matches	979;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ATGGCAGGTGGCTGTGGCCATATGGCCACAGGTCTTCAGAGGCACCTGTGACTGACTTCCCT	60		
Db	1	ATGGCATGTGGCGGTGGCCATATGGCCACAGGTCTTCAGAGGCACCTGTGACTGACTTCCCT	60		
Qy	61	GGATTTTCATGAGCGGGCTGATGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACA	120		
Db	61	GGATTTTCATGAGCGGGCTGATGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACA	120		
Qy	121	GATGAGGAGACATCTGACTCTGTTCACATCCCGAAGTAATGCTCAGCGCCAGGAATC	180		
Db	121	GATGAGGAGACATCTGACTCTGTTCACATCCCGAAGTAATGCTCAGCGCCAGGAATC	180		
Qy	181	TCGTCAGCTTTTAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTA	240		
Db	181	TCGTCAGCTTTTAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTA	240		
Qy	241	ACTGGAAAAATTTGAAAAATTAATTTGTGGCTCTCATGAAACCCCTCTCGGCTTTTATGATGCT	300		
Db	241	ACTGGAAAAATTTGAAAAATTAATTTGTGGCTCTCATGAAACCCCTCTCGGCTTTTATGATGCT	300		
Qy	301	TATGAAGTGAACATGCTTGAAGGGAGCTGGAAACAAATGAAAAGTACTGCACAGAAATT	360		
Db	301	TATGAAGTGAACATGCTTGAAGGGAGCTGGAAACAAATGAAAAGTACTGCACAGAAATT	360		
Qy	361	ATTGCTTCAAGGACACCTGAAAGACTCAGAGCCATCAACAAAGTTTATGAAGAAGATAT	420		
Db	361	ATTGCTTCAAGGACACCTGAAAGACTCAGAGCCATCAACAAAGTTTATGAAGAAGATAT	420		
Qy	421	GGCTCAAGCCCTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACACAGCGATGTTG	480		
Db	421	GGCTCAAGCCCTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACACAGCGATGTTG	480		
Qy	481	GTGGTTCTCCTTCAGGCTAACAGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAA	540		
Db	481	GTGGTTCTCCTTCAGGCTAACAGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAA	540		
Qy	541	CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG	600		
Db	541	CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG	600		
Qy	601	TTTATCACCATCTTTTGGAACACGAAAGTGTCTCTCATTTTGAAGAAGTGTGTTGACAAGTAC	660		
Db	601	TTTATCACCATCTTTTGGAACACGAAAGTGTCTCTCATTTGAGAAGTGTGTTGACAAGTAC	660		


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QY 661 ATGACTATATCAGGATTTCAAAATGAGGAACCAATGACCGGAGACTTCTGGCAATTTA 720
Db 661 ATGACTATATCAGGATTTCAAAATGAGGAACCAATGACCGGAGACTTCTGGCAATTTA 720
QY 721 GAGCAACTACTCCTTGGCTGTGTGAATCTATTGGAAGTATACCTTGCAGAG 780
Db 721 GAGCAACTACTCCTTGGCTGTGTGAATCTATTGGAAGTATACCTTGCAGAG 780
QY 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
Db 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
QY 841 GTTCCAGGAGTGAGATGATCTGTTTAACTATCAGGAAGGAGTTAGGAAGAAATTTGCC 900
Db 841 GTTCCAGGAGTGAGATGATCTGTTTAACTATCAGGAAGGAGTTAGGAAGAAATTTGCC 900
QY 901 ACCTCTCTTTATCCATGATTAAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTG 960
Db 901 ACCTCTCTTTATCCATGATTAAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGGAGAGATGAC 981
Db 961 CTGCTCTCCGGAGAGATGAC 981

RESULT 3
LOCUS AR262471 981 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 5 from patent US 6323313.
ACCESSION AR262471
VERSION AR262471.1 GI:28073915
KEYWORDS Location/Qualifiers
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Tail,J.F. and Brown,D.S.
TITLE Annexin derivative with endogenous chelation sites
JOURNAL Patent: US 6323313-A 5 27-NOV-2001;
FEATURES Location/Qualifiers
BASE COUNT 286 a 187 c 250 g 258 t
ORIGIN

Query Match 99.5%; Score 976.2; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 6.3e-247;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCAGTGGCTGGGCGCATATGCGACAGGTTCTCAGAGGCACTGTGACTGACTTCCCT 60
Db 1 ATGGCAGTGGCTGGGCGCATATGCGACAGGTTCTCAGAGGCACTGTGACTGACTTCCCT 60
QY 61 GGATTTGATGACGGGCTGATGCGAAGTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
Db 61 GGATTTGATGACGGGCTGATGCGAAGTCTTCGGAAGGCTATGAAGGCTTGGGCACA 120
QY 121 GATGAGGAGAGCATCTGACTCTGTGACATCCGCAAGTAAATGCTCAGCGCCAGGAATC 180
Db 121 GATGAGGAGAGCATCTGACTCTGTGACATCCGCAAGTAAATGCTCAGCGCCAGGAATC 180
QY 181 TCTGCACTTTTAAAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTA 240
Db 181 TCTGCACTTTTAAAGACTCTGTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTA 240
QY 241 ACTGGAATAATTTGAAAATTAATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCT 300
Db 241 ACTGGAATAATTTGAAAATTAATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCT 300
QY 301 TATGAATGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAAT 360
Db 301 TATGAATGAAACATGCTTGAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAAT 360

QY 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAAACAGTTTATGAGAAGAATAT 420
Db 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAAACAGTTTATGAGAAGAATAT 420
QY 421 GGCTCAAGCCTGGAAGATGACGTGGTGGGGACACTTCAGGGTACTACCAAGCGGATGTTG 480
Db 421 GGCTCAAGCCTGGAAGATGACGTGGTGGGGACACTTCAGGGTACTACCAAGCGGATGTTG 480
QY 481 GTGGTTCTCCTTCAGGCTAAACAGACACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAA 540
Db 481 GTGGTTCTCCTTCAGGCTAAACAGACACCTGATGCTGGAATTTGATGAAGCTCAAGTTGAA 540
QY 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAG 600
Db 541 CAAGATGCTCAGGCTTTATTTTCAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAG 600
QY 601 TTTATCACCATCTTTTGGAAACAGAGTGTGTCTCATTTGAGAAAGGTGTTTCAAGATGAC 660
Db 601 TTTATCACCATCTTTTGGAAACAGAGTGTGTCTCATTTGAGAAAGGTGTTTCAAGATGAC 660
QY 661 ATGACTATATCAGGATTTCAAAATGAGGAACCAATGACCGGAGACTTCTGGCAATTTA 720
Db 661 ATGACTATATCAGGATTTCAAAATGAGGAACCAATGACCGGAGACTTCTGGCAATTTA 720
QY 721 GAGCAACTACTCCTTGGCTGTGTGAATCTATTGGAAGTATACCTTGCAGAG 780
Db 721 GAGCAACTACTCCTTGGCTGTGTGAATCTATTGGAAGTATACCTTGCAGAG 780
QY 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
Db 781 ACCCTCTATTATGCTATGAGGAGCTGGGACAGATGATACCTCATCAGAGTCATG 840
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Db 841 GTTCCAGGAGTGAGATGATCTGTTTAACTATCAGGAAGGAGTTAGGAAGAAATTTGCC 900
QY 901 ACCTCTCTTTATCCATGATTAAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTG 960
Db 901 ACCTCTCTTTATCCATGATTAAGGAGATACATCTGGGACTATAAGAAAGCTCTTCTG 960
QY 961 CTGCTCTCCGGAGAGATGAC 981
Db 961 CTGCTCTCCGGAGAGATGAC 981

RESULT 4
LOCUS M.musculus VAC-alpha cdna.
DEFINITION A07367
ACCESSION A07367
VERSION A07367.1 GI:412270
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1466)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
JOURNAL Patent: DE 3810331-A 3 05-OCT-1989;
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RSNAQRQELSAFAKTLFGRDLDDLLKSLTGKPEKLIIVALKMPKPSRLYDAYELKHLKG
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 BASE COUNT 423 a 291 c 327 g 425 t
 ORIGIN

Query Match 97.7%; Score 958; DB 6; Length 1466;
 Best Local Similarity 99.5%; Pred. No. 4.1e-242;
 Matches 961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	16	GGCCATATGACAGAGTTCTCAGAGGCACCTGTGACTGACATCCCTGCTGATTTGATGACGGG	75
Db	29	GTCCCTATGGCAGAGTTCTCAGAGGCACCTGTGACTGACATCCCTGCTGATTTGATGACGGG	88
Qy	76	GCTGATCAGAACTCTTCGGAAGCTTATGAAAGCTTGGGACAGATGAGGAGGACATC	135
Db	89	GCTGATCAGAACTCTTCGGAAGCTTATGAAAGCTTGGGACAGATGAGGAGGACATC	148
Qy	136	CTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAG	195
Db	149	CTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGACGCTTTTAAG	208
Qy	196	ACTCTGTTTGGCAGGATCTCTGGATGACCTGAATCAGAACTAACTGGAATTTTGA	255
Db	209	ACTCTGTTTGGCAGGATCTCTGGATGACCTGAATCAGAACTAACTGGAATTTTGA	268
Qy	256	AAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACAT	315
Db	269	AAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACAT	328
Qy	316	GCCTTGAAGGAGCTGGAACAAATGAAGTACTGACAGAAATATTTGCTTCAAGGACA	375
Db	329	GCCTTGAAGGAGCTGGAACAAATGAAGTACTGACAGAAATATTTGCTTCAAGGACA	388
Qy	376	CCTGAACACTGAGAGCCATCAACAAGTTTATGAAGAAGTATGCTCAAGCCTCGAA	435
Db	389	CCTGAACACTGAGAGCCATCAACAAGTTTATGAAGAAGTATGCTCAAGCCTCGAA	448
Qy	436	GATGACGTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTCTCCTTCAG	495
Db	449	GATGACGTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTCTCCTTCAG	508
Qy	496	GCTAACAGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCT	555
Db	509	GCTAACAGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCT	568
Qy	556	TTATTTTCAGGCTGGAGAACTTAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTT	615
Db	569	TTATTTTCAGGCTGGAGAACTTAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTT	628
Qy	616	GGACACGAAGTGTCTCATTTGAGAAAGGTTTGACAAGTACATGATATATCAGGA	675
Db	629	GGACACGAAGTGTCTCATTTGAGAAAGGTTTGACAAGTACATGATATATCAGGA	688
Qy	676	TTCAAAATTCAGGAACCATTCACCGGACACTTCGGCAATTTAGAGCAACTACTCTTT	735
Db	689	TTCAAAATTCAGGAACCATTCACCGGACACTTCGGCAATTTAGAGCAACTACTCTTT	748
Qy	736	GCTGTTGTGAAATCTATTGAAAGTATACCTCGCTTACCTTGCAGAGACCCCTCTATTATGCT	795
Db	749	GCTGTTGTGAAATCTATTGAAAGTATACCTCGCTTACCTTGCAGAGACCCCTCTATTATGCT	808
Qy	796	ATGAAGGAGCTGGGACAGATGATACACCTCATCAGAGTCAATGTTCCAGGAGTGAG	855
Db	809	ATGAAGGAGCTGGGACAGATGATACACCTCATCAGAGTCAATGTTCCAGGAGTGAG	868
Qy	856	ATTGATCTGTTTAACTACAGAGGAGTTTATGGAAGAAATTTTGGCACCTCTCTTTATTC	915
Db	869	ATTGATCTGTTTAACTACAGAGGAGTTTATGGAAGAAATTTTGGCACCTCTCTTTATTC	928
Qy	916	ATGATTAAAGGAGATACATCTGGGACATATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAA	975
Db	929	ATGATTAAAGGAGATACATCTGGGACATATAAGAAAGCTCTTCTGCTGCTCTGGAGAA	988

Qy 976 GATGAC 981
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 Db 989 GATGAC 994

RESULT 5
 BC004993
 LOCUS
 DEFINITION
 BC004993
 complete cds.
 VERSION
 BC004993.1 GI:13436442
 KEYWORDS
 MGC.
 SOURCE
 Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS

1 (bases 1 to 1536)
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, N.K.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002).

JOURNAL
 MEDLINE
 PUBMED
 12477932

REFERENCE
 2 (bases 1 to 1536)
 Strausberg, R.
 Direct Submission
 Submitted (21-NAR-2001), National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DP7
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smallos, Michael Smith, Lorraine Spence, Jeff Scott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 Location/Qualifiers

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CDS	
Query Match	97.7%; Score 958; DB 9; Length 1536;
Best Local Similarity	99.5%; Pred. No. 4.le-242;
Matches 961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY 16	GGCCATATGGCAGAGTCTTCAGAGCAGCTGTGACTGACTTCCTCGGATTGATGAGCG 75
DB 118	GTGCGTATGGCAGAGTCTTCAGAGCAGCTGTGACTGACTTCCTCGGATTGATGAGCG 177
QY 76	GCTGATGACAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 135
DB 178	GCTGATGACAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 237
QY 136	CTGACTCTTTGACATCCCGAGTAAATGCTGAGCGCCAGCAATCTCGAGCTTTTAA 195
DB 238	CTGACTCTTTGACATCCCGAGTAAATGCTGAGCGCCAGCAATCTCGAGCTTTTAA 297
QY 196	ACTCTCTTTGGCAGGATCTCTCGATGACCTGAATCAGAACTCACTGAAATTTGAA 255
DB 298	ACTCTCTTTGGCAGGATCTCTCGATGACCTGAATCAGAACTCACTGAAATTTGAA 357
QY 256	AAATTAATTTGGCTCTGATGAACCCCTCTCGCTTTATGCTTTATGAACCTGAACAT 315
DB 358	AAATTAATTTGGCTCTGATGAACCCCTCTCGCTTTATGCTTTATGAACCTGAACAT 417
QY 316	GCTTGAAGGAGCTGGACAAATGAAGAAGTACTGACAGAAATTTGCTTCAAGACA 375
DB 418	GCTTGAAGGAGCTGGACAAATGAAGAAGTACTGACAGAAATTTGCTTCAAGACA 477
QY 376	CTTGAAGAACTGAGACCATCAACAAGTTTATGAAGAAGTATGGCTCAAGCTGGAA 435
DB 478	CTTGAAGAACTGAGACCATCAACAAGTTTATGAAGAAGTATGGCTCAAGCTGGAA 537
QY 436	GATGAGCTGGTGGGGACACTTCAGGCTACTACCAGCGGATTTGGTGGTTCCTCTCAG 495
DB 538	GATGAGCTGGTGGGGACACTTCAGGCTACTACCAGCGGATTTGGTGGTTCCTCTCAG 597
QY 496	GCTAAGAGACCTGATGCTGGAATTTGATGAGCTCAAGTGAACAAAGTATGCTCAGCT 555
DB 598	GCTAAGAGACCTGATGCTGGAATTTGATGAGCTCAAGTGAACAAAGTATGCTCAGCT 657
QY 556	TTATTTTCAGCTGGAGAACTTAATTCGGGACAGATGAGAAAGTTTATCACCATCTTT 615
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DB 718	GGACACGAAAGTGTCTCTCATTTGAGAAAGTGTGTTGACAAAGTACATGACTATATCAGGA 777
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DB 778	TTTCAAAATTGAGAAACCAATTGACCGGAGAGCTTCTGGCAANTTTAGAGCAACTACTCTT 837
QY 736	GCTGTGTGCAAAATCTATTGCAAGTATACCTGCTACCTTTCGAGAGACCTCTATTATGCT 795
DB 838	GCTGTGTGCAAAATCTATTGCAAGTATACCTGCTACCTTTCGAGAGACCTCTATTATGCT 897
QY 796	ATGAAGGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGGAGTGAG 855
DB 898	ATGAAGGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGGAGTGAG 957
QY 856	ATTGATCTCTTTAAACATCAGGAAGGAGTTTAGGAAGAATTTTGGCACTCTCTTTATTC 915
DB 958	ATTGATCTCTTTAAACATCAGGAAGGAGTTTAGGAAGAATTTTGGCACTCTCTTTATTC 1017
QY 916	ATGATTAAAGGGAGATACATCTGGGAGCTATAAGAAAGCTCTTCTGCTGCTCTCTTATTC 975
DB 1018	ATGATTAAAGGGAGATACATCTGGGAGCTATAAGAAAGCTCTTCTGCTGCTCTTATTC 1077
QY 976	GATGAC 981
DB 1078	GATGAC 1083
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LOCUS	
DEFINITION	Homo sapiens annexin A5, mRNA (cdna clone MGC:2795 IMAGE:2961097), complete cds.
ACCESSION	BC012804
VERSION	BC012804.1 GI:15215411
KEYWORDS	MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1539) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,A.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Loquellano,N.A., Peters,G.J., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalobon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Schnerk,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1539) Strausberg,R.
AUTHORS	Direct Submission
TITLE	Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
JOURNAL	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT

Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadansystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 2 Row: b Column: 4.
Location/Qualifiers

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BASE COUNT 432 a 320 c 355 g 432 t
ORIGIN
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Query Match 97.7%; Score 958; DB 9; Length 1539;

Best Local Similarity 99.5%; Pred. NO. 4.1e-242;

Matches 961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 181 GCTATGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 240
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DB 361 AAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATCAACAT 420
QY 316 GCCTTGAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACA 375
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RESULT 7

BC012822

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 1539)

Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, M., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

QY 862 CTGTTTAAACATCAGGAAGAGTTTAGGAAGAAATTTGGCCACCTCTCTTTATTCATGATT 921
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QY 922 AAGGGAGATACATCTGGGAGCTATAGAAGAGCTTCTGCTGCTCCGGAGAGATGAC 981
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RESULT 11
HUMATC 1444 bp mRNA linear PRI 27-APR-1993
LOCUS Human placental anticoagulant protein (PAP) mRNA, complete cds.
M18366
DEFINITION
ACCESSION M18366.1 GI:179131
VERSION
KEYWORDS anticoagulant.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1444)
AUTHORS Funakoshi, T., Hendrickson, L.E., McMullen, B.A. and Fujikawa, K.
TITLE Primary structure of human placental anticoagulant protein
JOURNAL Biochemistry 26 (25), 8087-8092 (1987)
MEDLINE 88163463
PUBMED 2964863
COMMENT Original source text: Human placenta, cdna to mRNA, clones
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Query Match 97.5%; Score 956.8; DB 9; Length 1444;
Best Local Similarity 99.8%; Pred. No. 8.4e-242;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 142 CTGTTTGACATCCCGAGTAATGCTCAGCCCGAGGAATCTCTGCAGCTTTTAAGACTCG 201
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RESULT 12
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LOCUS Sequence 3 from Patent WO 8805659.
DEFINITION I08832
ACCESSION I08832
VERSION I08832.1 GI:588459
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1454)
AUTHORS Fujikawa, K., Irani, M.H. and Carter, B.L.A.
TITLE HUMAN PROTEINS HAVING ANTICOAGULANT AND ANTI-INFLAMMATORY ACTIVITY
JOURNAL Patent: WO 8805659-A 3 11-AUG-1988;
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BASE COUNT 434 a 279 c 325 g 416 t
ORIGIN

Query Match 97.5%; Score 956.8; DB 6; Length 1454;
Best Local Similarity 99.8%; Pred. No. 8.4e-242;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
 LOCUS BC001429
 DEFINITION Homo sapiens, annexin A5, clone MGC:2261 IMAGE:3140878, mRNA, linear PRI 12-JUL-2001 complete cds.
 ACCESSION BC001429
 VERSION BC001429.1 GI:12655148
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1538)
 Strausberg, R.
 Direct Submission
 Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 4 Row: 0 Column: 24
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA qt: 219480.

FEATURES

Location/Qualifiers
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CDS

BASE COUNT 456 a 304 c 342 g 436 t
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 140 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTTGGGCACAGATGAGGAGCATCCTGACT 199
 142 CTGTTGACATCCCGAAGTAACTGCTCAGCGCCAGGAAATCTCTGCGAGCTTTTAAGACTCTG 201

Query Match 97.5%; Score 956.8; DB 9; Length 1538;
 Best Local Similarity 99.8%; Pred. No. 8.4e-242;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 200 CTGTTGACATCCCGAAGTATGCTCAGCGCCAGGAAATCTCTCGAGCTTTTAAGACTCTG 259
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QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTGG 321
Db 320 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTGG 379
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RESULT 14
HSVAC
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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X12454
X12454.1 GI:37636
phospholipid-binding protein; vascular anticoagulant.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1560)
Maurer-Fogy,I., Reutelingersperger,C.P., Pieters,J., Bodo,G.,
Stratowa,C. and Hauptmann,R.
Cloning and expression of cDNA for human vascular anticoagulant, a
Ca2+-dependent phospholipid-binding protein
Eur. J. Biochem. 174 (4), 585-592 (1988)
86271329

2455636
2 (bases 1 to 1560)
Hauptmann,R.
Direct Submission
Submitted (15-AUG-1988) Hauptmann R., Ernst Boehringer Institut
fuer Arzneimittelforschung, Dr. Boehringer-Gasse 5/11, A-1121 Wien,
Austria
Data kindly reviewed (11-Nov-1988) by Hauptmann R.
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RESULT 15
LOCUS E01816 1566 bp RNA linear PAT 29-SEP-1997
DEFINITION CDNA encoding human antioagulnnt.
ACCESSION E01816
VERSION E01816.1 GI:2170068
KEYWORDS JP 1989020095-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Saino, S., Iwasaki, A. and Suda, M.
JOURNAL POLYPEPTIDE HAVING ANTI-BLOOD COAGULATING ACTION
Patent: JP 1989020095-A 1 24-JAN-1989;
KOWA CO
COMMENT OS Homo sapiens (man)
PN JP 1989020095-A/1
PD 24-JAN-1989
PF 23-JUL-1987 JP 1987184428
PR 20-FEB-1987 JP 87P 37227
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PC C12P21/02,C07K13/00,C12N15/00//A61K37/02,(C12P21/02,C12R1:19);
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Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 5.1.6
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Run on: August 28, 2003, 15:43:40 ; Search time 2602.33 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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2	977.8	99.7	981	6	AR262470	AR262470 Sequence
3	976.2	99.5	981	6	AR262471	AR262471 Sequence
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6	958.2	97.7	1539	9	BC012804	BC012804 Homo sapi
7	958.2	97.7	1539	9	BC012822	BC012822 Homo sapi
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ALIGNMENTS

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LOCUS AR262469 981 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 1 from patent US 6323313.
ACCESSION AR262469
VERSION AR262469.1 GI:28073913
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Tait,J.F. and Brown,D.S.
TITLE Annexin derivative with endogenous chelation sites
JOURNAL Patent: US 6323313-A 1 27-NOV-2001;
FEATURES Location/Qualifiers

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DEFINITION Sequence 5 from patent US 6323313.
ACCESSION AR262471
VERSION AR262471.1 GI:28073915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
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  Tait,J.F. and Brown,D.S.
  Annexin derivative with endogenous chelation sites
  JOURNAL Patent: US 6323313-A 5 27-NOV-2001;
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    Location/Qualifiers
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Query Match 99.5%; Score 976.2; DB 6; Length 981;
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RESULT 4
A07367
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DEFINITION A07367
ACCESSION A07367
VERSION A07367.1 GI:412270
KEYWORDS
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ORGANISM Mus musculus
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BASE COUNT 423 a 291 c 327 g 425 t
ORIGIN

Query Match		97.7%	Score 958.2;	DB 6;	Length 1466;
Best Local Similarity		99.2%;	Pred. No. 6.8e-242;		
Matches 963;		Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
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QY	551	AGGCTTTATTTAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAGTTTATCACC	610		
DB	564	AGGCTTTATTTAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAGTTTATCACC	623		
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DB	624	TCCTTTGGAACAGAGTGTCTCATTTGAGAAAGTGTGTTGACAAAGTACATGACTAT	683		
QY	671	CAGGATTTCAAAATGAGGAAACCTTTGACCGGAGACTTCTGCAATTTAGAGCACTAC	730		
DB	684	CAGGATTTCAAAATGAGGAAACCTTTGACCGGAGACTTCTGCAATTTAGAGCACTAC	743		
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DB	804	ATGCTATGAAGGAGCTGGGACAGATGATACCTTCATCAGAGTATGTTTCCAGGA	863		
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DB 984 GAGAAGATGAC 994

RESULT 5
BC004993
LOCUS

DEFINITION
Homo sapiens annexin A5, mRNA (cDNA clone MGC:4402 IMAGE:2906015), complete cds.

ACCESSION
BC004993
VERSION
BC004993.1 GI:13436442
SOURCE
MGC.

ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 1536)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donaldson, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalobon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. 2002. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
MEDLINE
22388257
PubMed
12477932

2 (bases 1 to 1536)
Strausberg, R.

Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@remail.nih.gov

Tissue Procurement: ATCC/DCTD/BTP

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kutache, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schain, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 9 Row: 1 Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4809273.
Location/Qualifiers

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
Email: cgapbs-remail.nth.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 2 Row: b Column: 4.
Location/Qualifiers

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BASE COUNT
ORIGIN

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Query Match 97.7% Score 958.2; DB 9; Length 1539;
Best Local Similarity 99.2% Pred. No. 6.8e-242;
Matches 963; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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LOCUS BC012822
DEFINITION Homo sapiens annexin A5, mRNA (cDNA clone MGC:2961097), complete cds.
ACCESSION BC012822
VERSION BC012822.1 GI:15215458
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1539)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, J., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Rulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1539)

Strausberg, R.

Direct Submission

Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-remail.nih.gov

Tissue Procurement: AFCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 10 Row: k Column: 21.

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Location/Qualifiers

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432 a 320 c 355 g 432 t

BASE COUNT

ORIGIN

Query Match 97.7%; Score 958.2; DB 9; Length 1539;

Best Local Similarity 99.2%; Pred. No. 6.8e-242;

Matches 963; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 11 GCGGTGGCCATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATG 70

Db 116 GATGATGCGTATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATG 175

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Db 1076 GAGAAGATGAC 1086

RESULT 8

HUMPAP4

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

HUMPAP4
Human placenta anticoagulant protein PP4 mRNA linear PRI 11-AUG-1995
M19384.1 J03264
M19384.1 GI:189614
anticoagulant protein; thromboplastin inhibitor.

1 (bases 1 to 1582)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1582)

Grundmann, U., Abel, K.J., Bohn, H., Lobermann, H., Lottspeich, F. and

Kupper, H.

TITLE Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3708-3712 (1988)
MEDLINE 88234495
PUBMED 2967495

COMMENT Original source text: Homo sapiens (clone: PP4-[14,20,26,48]).
 Placenta cDNA to mRNA.
 Draft entry and computer-readable sequence for [1] kindly provided by U.Grundman, 19-APR-1988.

FEATURES

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 151..1113
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 RPDAGIDEAOEODAOALFOAGELKWTGDEKFTTFGTRSVSHLRVFKYMTISG
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 214
variation
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BASE COUNT 433 a 336 c 364 g 449 t
ORIGIN 82 bp upstream of SmaI site.

Query Match 97.7%; Score 958.2; DB 9; Length 1582;
Best Local Similarity 99.2%; Pred. No. 6.8e-242;
Matches 963; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 11 GCGGTGGCCATATGCCAGGTTCTCAGAGGACATGTGACTGACTTCCTCGATGATTTGATG 70
 DB 140 GAGTAGTCGTATGCCAGAGTTCTCAGAGGACATGTGACTGACTTCCTCGATGATTTGATG 199

QY 71 AGCGGGCTGATGCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGCCACAGATGAGGAGA 130
 DB 200 AGCGGGCTGATGCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGCCACAGATGAGGAGA 259

QY 131 GCATCTGACTCTGTGACATCCGCAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTT 190
 DB 260 GCATCTGACTCTGTGACATCCGCAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTT 319

QY 191 TTAAGACTCTGTTGGCAGGATCTTCTGGATGACTGAAATCAGAACTAACTGGAAAT 250
 DB 320 TTAAGACTCTGTTGGCAGGATCTTCTGGATGACTGAAATCAGAACTAACTGGAAAT 379

QY 251 TTGAAAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGA 310
 DB 380 TTGAAAATTAATTTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGA 439

QY 311 AACATGCTCTGAGGAGCTCGAACAAATGAAGTAGTACTGACAGAAATTTATGCTTCAA 370
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QY 371 GGACACCTTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCC 430
 DB 500 GGACACCTTGAAGAACTGAGAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCC 559

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 DB 800 CAGGATTTCAAATTCAGGAAACCATTTGACCGGAGACATCTCTGCCAATTTAGAGCAATAC 859
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 DB 860 TCTTTGCTGTTGTGAAATCTATTTCGAAGTATACCTGCCTACCTTCGAGAGACCCCTCTATT 919
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 QY 851 GTGAGATGATGCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTCCACCTCTCTTT 910
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 QY 911 ATTCCATGATTAAGGAGATACATCTGGGAGTATGAAGAAGCTCTCTGCTGCTCTCG 970
 DB 1040 ATTCCATGATTAAGGAGATACATCTGGGAGTATGAAGAAGCTCTCTGCTGCTCTCG 1099

QY 971 GAGAAAGATGAC 981
 DB 1100 GAGAAAGATGAC 1110

RESULT 9
LOCUS A01769
DEFINITION DNA sequence (gas) for vascular anticoagulating protein.
ACCESSION A01769
VERSION A01769.1 GI:410787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 963)
AUTHORS
TITLE VASCULAR ANTICOAGULANT PROTEINS, DNAs WHICH CODE FOR THEM,
JOURNAL MANUFACTURE AND APPLICATION THEREOF
FEATURES Patent: WO 8807576-A 1 06-OCT-1988;
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CDS
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BASE COUNT 285 a 181 c 243 g 254 t
ORIGIN
 Query Match 97.5%; Score 956.8; DB 6; Length 963;
 Best Local Similarity 99.8%; Pred. No. 1.6e-241;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	862	CTGTTTAAACATCAGGAAGAGTATTAGGAAGAAATTTTGCCACCTCTCTCTTTATTCCATGATT	921
Db	841	CTGTTTAAACATCAGGAAGAGTATTAGGAAGAAATTTTGCCACCTCTCTTTATTCCATGATT	900
Qy	922	AAGGGAGATACATCTGGGGACTATAGAAAGCTCTTCTGCTGCTCTCCGAGAGATGAC	981
Db	901	AAGGGAGATACATCTGGGGACTATAGAAAGCTCTTCTGCTGCTCTGAGAGATGAC	960
RESULT 11			
HUMATC			
LOCUS	HUMATC 1444 bp mRNA linear PRI 27-APR-1993		
DEFINITION	Human placental anticoagulant protein (PAP) mRNA, complete cds.		
ACCESSION	M18366		
VERSION	M18366.1 GI:179131		
KEYWORDS	anticoagulant.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1444)		
AUTHORS	Funakoshi, T., Hendrickson, L.E., McMullen, B.A. and Fujikawa, K.		
TITLE	Primary structure of human placental anticoagulant protein		
JOURNAL	Biochemistry 26 (25), 8087-8092 (1987)		
MEDLINE	88163463		
PUBMED	2364863		
COMMENT	Original source text: Human placenta; cDNA to mRNA, clones lambda-HPAP[1.0,1.1,1.6].		
FEATURES	Location/Qualifiers		
source	1..1444		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
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CDS	13..975		
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	FQEETIDRETSNLSOLLAVVKSINSIPAYLAETLIYAMKAGTGADHTDLIRKVMVS		
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ORIGIN	177 bp upstream of PstI site.		
Query Match	97.5%; Score 956.8; DB 9; Length 1444;		
Best Local Similarity	99.8%; Pred. No. 1.6e-241;		
Matches	958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	22	ATGGCAGAGTCTCAGAGGCATGTGACTTCCCTGGATTGATGACGGGCTGAT	81
Db	13	ATGGCAGAGTCTCAGAGGCATGTGACTTCCCTGGATTGATGACGGGCTGAT	72
Qy	82	GCAGAACTCTCCGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCTGACT	141
Db	73	GCAGAACTCTCCGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCCTGACT	132
Qy	142	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTCAGGCTTTTAGACACTG	201
Db	133	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTCAGGCTTTTAGACACTG	192
Qy	202	TTTGGCAGGATCTCTCGGATGACCTCAAACTCAGAACTAAGTGAATTTGAAATAA	261
Db	193	TTTGGCAGGATCTCTCGGATGACCTCAAACTCAGAACTAAGTGAATTTGAAATAA	252
Qy	262	ATTGTGGCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACATGAACATGCCTG	321

Db	13	ATGGCAGAGTTCTCAGAGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT	72
Qy	82	GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT	141
Db	73	GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT	132
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Db	133	CTGTTGACATCCGGAAGTAAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTCTG	192
Qy	202	TTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAACTGGAATTTGAAAATTA	261
Db	193	TTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAACTGGAATTTGAAAATTA	252
Qy	262	ATTGTGCTCTGATGAACCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTG	321
Db	253	ATTGTGCTCTGATGAACCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTG	312
Qy	322	AAGGAGCTGGAACAAATGAAAGTACTGACGAAATTAATGCTTCAAGCACCTGAA	381
Db	313	AAGGAGCTGGAACAAATGAAAGTACTGACGAAATTAATGCTTCAAGCACCTGAA	372
Qy	382	GAACTGAGAGCCATCAACAACTTTATGAAGAATATGCTCAAGCCTGGAGATGAC	441
Db	373	GAACTGAGAGCCATCAACAACTTTATGAAGAATATGCTCAAGCCTGGAGATGAC	432
Qy	442	GTGCTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTCTCTCCCTCAGGCTAAC	501
Db	433	GTGCTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTCTCTCCCTCAGGCTAAC	492
Qy	502	AGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT	561
Db	493	AGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT	552
Qy	562	CAGCTGGGAACTTAATCGGGGACAGATGAAGAAAGTTATCACCATCTTTGGAAAC	621
Db	553	CAGCTGGGAACTTAATCGGGGACAGATGAAGAAAGTTATCACCATCTTTGGAAAC	612
Qy	622	CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA	681
Db	613	CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA	672
Qy	682	ATTGAGAAACCATTCACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGTGTT	741
Db	673	ATTGAGAAACCATTCACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGTGTT	732
Qy	742	GTGAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG	801
Db	733	GTGAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG	792
Qy	802	GGAGCTGGGACAGATGATACCTCATCAGATGATGCTTCCAGGAGCTGAGATGAT	861
Db	793	GGAGCTGGGACAGATGATACCTCATCAGATGATGCTTCCAGGAGCTGAGATGAT	852
Qy	862	CTGTTTAACTCAGGAAGGAGTTTAGGAAGAAATTTTCCACCTCTCTTTTCCATGATT	921
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Qy	922	AAGGAGATACATCTGGGAGCTATTAAGAAAGCTTCTGCTGCTCCCGGAGAGATGAC	981
Db	913	AAGGAGATACATCTGGGAGCTATTAAGAAAGCTTCTGCTGCTCCCGGAGAGATGAC	972

RESULT 13

BC001429

LOCUS

DEFINITION

complete cds.

ACCESSION

BC001429

VERSION

BC001429.1

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

1538 bp mRNA. linear PRI 12-JUL-2001

Homo sapiens, annexin A5, clone MGC:2261 IMAGE:3140878, mRNA,

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1538)
TITLE	Strausberg, R.
JOURNAL	Direct Submission
REMARK	Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgaps-email.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Sequencing Center (NISC), Gaithersburg, Maryland. Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Shevchenko, V., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: O Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 219480. Location/Qualifiers 1..1538 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="LocusID:308" /db_xref="taxon:9606" /clone="MGC:2261 IMAGE:3140878" /tissue_type="Ovary, adenocarcinoma" /clone_lib="NIH_MGC_g" /lab_host="DH10B-R" /note="Vector: pOTB7" 80..1042 /codon_start=1 /product="annexin A5" /protein_id="AAH01429.1" /db_xref="GI:12655149" /translation="MAQVLRGTVTFDFPDERADAETLRKAMKLGTSDESLTLLTS RSNRQBEISAAPKTLGRDLDDLSKLEKLEKLVLMKPSRLYDAVELHAKLG AGNEKVLVEIIASRTPEELRAIKQVYEEYGSLEDDYDVGTSYQYRMVLLQAN RDPDAGIDEAQVODQAQFQAGELKMGWDEKFTITGFRSVSHLRKVDKTYTISG FQLEIDRETLGNLEQLLAVYKSTIRSPAYLAETLYAMKGAQDDHLLIRVMVSR SEIDLFNIRKFRNFATSLYSIMKIGTSGDYKKALLLGGED"
CDS	BASE COUNT 456 a 304 c 342 g 436 t ORIGIN Query Match 97.5%; Score 956.8; DB 9; Length 1538; Best local Similarity 99.8%; Pred. No. 1.6e-241; Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

22

ATGGCAGAGTTCTCAGAGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT

81

Db

80

ATGGCAGAGTTCTCAGAGCACTGTGACTGCTCCCTGGATTTGATGAGCGGCTGAT

139

Qy

82

GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT

141

Db

140

GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT

199

Qy

142

CTGTTGACATCCGGAAGTAAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTCTG

201

Db 200 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 259
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Db 260 TTGTCAGGATCTTCTTGATGACCTGAAATCAGAACTAACTGGAAATTTGAAATAATTA 319
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QY 322 AAGGAGCTGGGAACAAATGAAAGTAACTGACAGAAATTTATGCTTCAAGGACACTGAA 381
Db 380 AAGGAGCTGGGAACAAATGAAAGTAACTGACAGAAATTTATGCTTCAAGGACACTGAA 439
QY 382 GAAGTGGAGCCATCAACAACTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 441
Db 440 GAAGTGGAGCCATCAACAACTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 499
QY 442 GTGGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
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Db 560 AGAGCCCTGATGCTGGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 619
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 621
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QY 622 CCAAGTGTCTCATTTGAGAAAGTGTGTTGACAGTACATGACTATATCAGGATTTCAA 681
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Db 740 ATTGAGAAACCATGACCGGAGACTCTGCAATTTAGACAACACTACTCTCTGCTGTT 799
QY 742 GTGAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCTCTATTATGCTATGAAG 801
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QY 922 AAGGAGATACATCTGGGGACTATAGAAGCTCTTCTGCTGCTCTCCGGAGAAAGATGAC 981
Db 980 AAGGAGATACATCTGGGGACTATAGAAGCTCTTCTGCTGCTCTGCTGCTGCTGGAAGATGAC 1039

RESULT 14
HSVAC
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human mRNA for vascular anticoagulant..
X12454
X12454.1 GI:37636
phospholipid-binding protein; vascular anticoagulant.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1560)
Maurer-Foxy, I., Reutellingsperger, C.P., Pieters, J., Bodo, G.,
Stratowa, C. and Hauptmann, R.
Cloning and expression of cDNA for human vascular anticoagulant, a
Ca²⁺-dependent phospholipid-binding protein
Eur. J. Biochem. 174 (4), 585-592 (1988)
88271329

PUBMED 2455636
REFERENCE 2 (bases 1 to 1560)
AUTHORS Hauptmann, R.
TITLE Direct Submision
JOURNAL Submitted (15-AUG-1988) Hauptmann R., Ernst Boehringer Institut
fuer Arzneimittelforschung, Dr. Boehringer-Gasse 5/11, A-1121 Wien,
Austria
COMMENT Data kindly reviewed (11-Nov-1988) by Hauptmann R.
FEATURES
Location/Qualifiers
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129..1091
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879..1079
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BASE COUNT 429 a 330 c 357 g 444 t
ORIGIN
Query Match 97.5%; Score 956.8; DB 9; Length 1560;
Best Local Similarity 99.8%; Pred. No. 1.6e-241;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATCAGCGGCTGAT 81
Db 129 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATCAGCGGCTGAT 188
QY 82 GCAGAAACCTCTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141
Db 189 GCAGAAACCTCTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 248
QY 142 CTGTTGACATCCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201
Db 249 CTGTTGACATCCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 308
QY 202 TTGTCAGGATCTTCTTGATGACCTGAAATCAGAACTAACTGGAAATTTGAAATAATTA 261
Db 309 TTGTCAGGATCTTCTTGATGACCTGAAATCAGAACTAACTGGAAATTTGAAATAATTA 368
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Db 369 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAAATGAAATGAAATG 428
QY 322 AAGGAGCTGGGAACAAATGAAAGTAACTGACAGAAATTTATGCTTCAAGGACACTGAA 381
Db 429 AAGGAGCTGGGAACAAATGAAAGTAACTGACAGAAATTTATGCTTCAAGGACACTGAA 488
QY 382 GAAGTGGAGCCATCAACAACTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 441


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QY 442 GTGGTGGGGGACACTTCAGGGTACTACACGCGGATGTGGTGGTCTCTCTTCAGGCTAAC 501
Db 549 GTGGTGGGGGACACTTCAGGGTACTACACGCGGATGTGGTGGTCTCTCTTCAGGCTAAC 608
QY 502 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 561
Db 609 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 668
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 621
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Db 969 CTGTTTAAACATCAGGAAGAGTTTAGGAAGAAATTTTGGCCACCCTCTCTTTATCCATGAT 1028
QY 922 AAGGGAGATACATCTGGGAGTATAGAAAGCTCTTCTGCTCTCCCGGAGAGATGAC 981
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RESULT 15
E01816
LOCUS E01816 1566 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human anticoagulant.
ACCESSION E01816
VERSION E01816.1 GI:2170068
KEYWORDS JP 1989020095-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Saino, S., Iwasaki, A. and Suda, M.
POLYPEPTIDE HAVING ANTI-BLOOD COAGULATING ACTION
Patent: JP 1989020095-A 1 24-JAN-1989;
KOWA CO
OS Homo sapiens (man)
PN JP 1989020095-A/1
PD 24-JAN-1989
PF 23-JUL-1987 JP 1987184428
PR 20-FEB-1987 JP 87P 37227
PI SAINO SUKEYUKI, IWASAKI AKIO, SUDA MAKOTO
PC C12P21/02.C07K13/00.C12N15/00//A61K37/02, (C12P21/02, C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=placenta;
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FT CDS 136..1098
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Best Local Similarity 99.88; Pred. No. 1.6e-241;
Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Search completed: August 28, 2003, 18:14:01
 Job time : 2606.33 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:48:20 ; Search time 1675.67 Seconds
(without alignments)
14228.779 Million cell updates/sec

Title: US-09-970-969-1

Perfect score: 981

Sequence: 1 atggcatgtggcgtggcca.....tgctcccgagagaagatgac 981

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vri.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	958.2	97.7	1602	11 BC032093	BC032093 Homo sapi
2	874.4	89.1	1076	12 BM464122	BM464122 AGENCOURT
3	868.6	88.5	1071	13 BX441583	BX441583 BX441583
4	858.4	87.5	1201	13 BX379189	BX379189 BX379189

ALIGNMENTS

RESULT 1	BC032093	1602 bp	linear	HTC 06-JUN-2002
LOCUS	Homo sapiens, clone IMAGE:3924873, mRNA.			
DEFINITION	BC032093			
ACCESSION	BC032093.1	GI:21327830		
VERSION	BC032093.1			
KEYWORDS	HTC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 1602)			
TITLE	Strausberg, R.			
JOURNAL	Direct Submission			
	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DRP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC			

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 848.2 86.5 1062 13 BX396240
 839.6 85.6 1201 13 BX379218
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 835.8 85.2 1076 13 BX358605
 832.2 84.8 1007 13 BX402751
 831.6 84.8 1201 9 AL547761
 828.6 84.5 1201 9 AL517516
 822 83.8 1201 9 AL541412
 820.4 83.6 1022 9 AL583578
 806.8 82.2 969 13 BU168479
 791.2 80.7 1201 13 BX365074
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 766.2 78.1 1201 13 BX424940
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 718 73.2 892 9 AU117640
 717.6 73.1 1201 13 BX377166
 717 73.1 878 12 BM016480

web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK plate: 26 Row: f Column: 11
 This clone has the following problem: no 5' EST match.

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RESULT 2

BM464122

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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 Average insert size 2 kb. Library constructed by Life
 Technologies."

BASE COUNT 296 a 229 c 273 g 274 t 4 others

ORIGIN

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CS0DF019K11 5-PRIME, mRNA sequence.
ACCESSION BX441583
VERSION BX441583.1 GI:30775951
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1071)
JOURNAL Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
COMMENT Full-length cDNA libraries and normalization
Unpublished
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF019AF06QPl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DF019AF06QPl.
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vector. Library was not normalized."
BASE COUNT 291 a 229 c 274 g 272 t 5 others
ORIGIN
Query Match 88.5%; Score 868.6; DB 13; Length 1071;
Best local Similarity 98.6%; Pred. No. 8e-222;
Matches 874; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
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Dy 418 TTGAAAAATTAATGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAATGA 477
Qy 311 AACATGCTTGAAGGGAGCTGGAACTAAATGAAAGTACTGACAGAAATATTCTCTCAA 370
Dy 478 AACATGCTTGAAGGGAGCTGGAACTAAATGAAAGTACTGACAGAAATATTCTCTCAA 537
Qy 371 GGACACCTGAAGAACTGAGAGCCTCAACAAAGTTTATGAAGAAATATGGCTCAAGCC 430
Dy 538 GGACACCTGAAGAACTGAGAGCCTCAACAAAGTTTATGAAGAAATATGGCTCAAGCC 597
Qy 431 TGAAGATGACGTGGTGGGGACACTTTCAGGGTACTACACGCGGATGTGGTGGTTCTCC 490
Dy 598 TGAAGATGACGTGGTGGGGACACTTTCAGGGTACTACACGCGGATGTGGTGGTTCTCC 657
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QY 491 TTCAGGCTAACAGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAAGATGCTC 550
 Db 658 TTCAGGCTAACAGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAAGATGCTC 717
 QY 551 AGGCTTTATTCAGGCTGGAGACCTTAATGAGGAGACAGATGAAGAAAGTTTATCACA 610
 Db 718 AGGCTTTATTCAGGCTGGAGACCTTAATGAGGAGACAGATGAAGAAAGTTTATCACA 777
 QY 611 TCTTTGGAACAGAAAGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATAT 670
 Db 778 TCTTTGGAACAGAAAGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATAT 837
 QY 671 CAGGATTTCAATTCAGGAAACCATTCAGCCGAGACCTTCGCGCAATTTAGAGCAACTAC 730
 Db 838 CAGGATTTCAATTCAGGAAACCATTCAGCCGAGACCTTCGCGCAATTTAGAGCAACTAC 897
 QY 731 TCCTTGCTGTGTAAGTATTCAGAACTATTCAGAACTATACCTGCCTACCTTCAGAGACCCCTTAT 790
 Db 898 TCCTTGCTGTGTAAGTATTCAGAACTATTCAGAACTATACCTGCCTACCTTCAGAGACCCCTTAT 957
 QY 791 ATGCTATGAAGGAGCTGGGACAGATGATCATACCTCATACAGAGTATGTTTCCAGGA 850
 Db 958 ATGCTATGAAGGAGCTGGGACAGATGATCATACCTCATACAGAGTATGTTTCCAGGA 1017
 QY 851 GTGAGATTGATCTGTTTAACTATCAGGAGGAGTTTGGAAAGATTT 896
 Db 1018 GTGAGATTGATCTGTTTAACTATCAGGAGGAGTTTGGAAAGATTT 1063

RESULT 4

LOCUS

DEFINITION BX379189 1201 bp mRNA linear EST 08-MAY-2003
 clone CS0D1030YL18 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match 87.5%; Score 858.4; DB 13; Length 1201;
 Best Local Similarity 94.9%; Pred. No. 4.7e-219;
 Matches 892; Conservative 15; Mismatches 27; Indels 6; Gaps 2;
 QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATCAGCGGCTGAT 81
 Db 203 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATCAGCGGCTGAT 262
 QY 82 GCAGAAATCTTTCGGAAGGCTATGAAAGGCTTTGGGCACAGATGAGGAGAGCATCTGACT 141
 Db 263 GCAGAAATCTTTCGGAAGGCTATGAAAGGCTTTGGGCACAGATGAGGAGAGCATCTGACT 322
 QY 142 CTGTTGACATCCCGAAGTAATCTCAGCGCCAGGAAATCTCTGCAAGCTTTTAAAGACTCG 201
 Db 323 CTGTTGACATCCCGAAGTAATCTCAGCGCCAGGAAATCTCTGCAAGCTTTTAAAGACTCG 382
 QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTCAAAAATTA 261
 Db 383 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTCAAAAATTA 442
 QY 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTTATGATGCTTATGAATGAACATGCCCTTG 321
 Db 443 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTTATGATGCTTATGAATGAACATGCCCTTG 502
 QY 322 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 Db 503 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 562
 QY 382 GAACCTGAGAGCCATCAACAACTTTATGAAGAAATATGCTCAAGCTGGAAGATGAC 441
 Db 563 GAACCTGAGAGCCATCAACAACTTTATGAAGAAATATGCTCAAGCTGGAAGATGAC 622
 QY 442 GTGGTGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 501
 Db 623 GTGGTGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 682
 QY 502 AGAGACCCCTGATGCTGGAAATTTGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTATTT 561
 Db 683 AGAGACCCCTGATGCTGGAAATTTGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTATTT 742
 QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 621
 Db 743 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 802
 QY 622 CGAAGTGTCTCTCATTTTGAAGAAAGTGTGACAAAGTACATGACATATATCAGGATTTCAA 681
 Db 803 CGAAGTGTCTCTCATTTTGAAGAAAGTGTGACAAAGTACATGACATATATCAGGATTTCAA 862
 QY 682 ATTGAGGAACACCATTTGACCGGAGACTTCTGCAATTTAGAGCAACTACTCCTTCTGTT 741
 Db 863 ATTGAGGAACACCATTTGACCGGAGACTTCTGCAATTTAGAGCAACTACTCCTTCTGTT 922
 QY 742 GTGAATCTTATTCGAAGTATACCTGCTACCTTCAGAGACCCCTCTATTATGCTATGAAG 801
 Db 923 GTGAATCTTATTCGAAGTATACCTGCTACCTTCAGAGACCCCTCTATTATGCTATGAAG 982
 QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGGAGTGAAGTATGAT 861
 Db 983 GGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGGAGTGAAGTATGAT 1042
 QY 862 CTGTTTAACTATCAGGAAGGAGTTTAGGAAGAAATTTTGGCACTCTCTCTTATTCATGAT 921
 Db 1043 CTGTTTAACTATCAGGAAGGAGTTTAGGAAGAAATTTTGGCACTCTCTCTTATTCATGAT 1099
 QY 922 AAGGAGATACATCTGGGAGCTATGAAGAAAGCTCTCTGCG 961
 Db 1100 AAGGAGAAATA---YTKGGGCAATAAAACCTCTCTCKCK 1136

RESULT 5

LOCUS

DEFINITION BX417429 Homo sapiens PLACENTA 1201 bp mRNA linear EST 13-MAY-2003
 clone CS0DE009116

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5-PRIME, mRNA sequence.
BX417429
VERSION BX417429.1 GI:30654405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1201)
JOURNAL Full-length cDNA libraries and normalization
COMMENT Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE009BE080P1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DE009BE080P1.
FEATURES
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DE009BE080P1"
            /tissue_type="PLACENTA"
            /note="Vector: pCMVSPORT-6; 1st strand cDNA was primed
            with a NotI-oligo(dT) primer. Five prime end enriched,
            double-strand cDNA was digested with Not I and cloned into
            the Not I and EcoRV sites of the pCMVSPORT 6 vector.
            Library was not normalized."
BASE COUNT 310 a 260 c 297 g 295 t 39 others
ORIGIN
    Query Match 87.2%; Score 855.2; DB 13; Length 1201;
    Best Local Similarity 95.0%; Pred. No. 3.4e-218;
    Matches 893; Conservative 10; Mismatches 30; Indels 7; Gaps 2;
QY 22 ATGCACAGCTTCTCAGGACCTGTGACCTGCTCCCTGGATTTGATGAGCGGCTGAT 81
DB 206 ATGCACAGCTTCTCAGGACCTGTGACCTGCTCCCTGGATTTGATGAGCGGCTGAT 265
QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 266 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 325
QY 142 CTGTTGACATCCGGAAGTATGCTCAGCGCCAGGAATCTCGAGCTTTTAAAGCTCTG 201
DB 326 CTGTTGACATCCGGAAGTATGCTCAGCGCCAGGAATCTCGAGCTTTTAAAGCTCTG 385
QY 202 TTTGGCAGGAGTCTTCTGGATGACCTGAAATCAGAACTAACTGGAATTTGAAAATTA 261
DB 386 TTTGGCAGGAGTCTTCTGGATGACCTGAAATCAGAACTAACTGGAATTTGAAAATTA 445
QY 262 ATTGTGGCTCTGATGAACCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTTG 321
DB 446 ATTGTGGCTCTGATGAACCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTTG 505
QY 322 AAGGAGCTGGAACAATGAAAGTACTCAGCAAGATTTATCTTCAAGGACCTGAA 381
DB 506 AAGGAGCTGGAACAATGAAAGTACTCAGCAAGATTTATCTTCAAGGACCTGAA 565
QY 382 GAATCAGAGCCATCAACCAAGTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGAC 441
DB 566 GAATCAGAGCCATCAACCAAGTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGAC 625
QY 442 GTGGTGGGGACACTTCAGGCTACTACACCGGATGTTGCTTCTCCTTCAGGCTAAC 501

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626 GTGGTGGGGACACCTTCAGGGTACTACACGGGATGTTGGTCTCTCCTTCAGGGCTAAC 685
QY 502 AGAGACCCCTGATGCTGGAATTGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 561
DB 686 AGAGACCCCTGATGCTGGAATTGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 745
QY 562 CAGGCTGGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCAGCATCTTTGGAAACA 621
DB 746 CAGGCTGGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCAGCATCTTTGGAAACA 805
QY 622 CGAAGTGTGCTCATTTTGAGAAAGGTTTGAACAAGTACATGACTATATCAGGATTTCAA 681
DB 806 CGAAGTGTGCTCATTTTGAGAAAGGTTTGAACAAGTACATGACTATATCAGGATTTCAA 865
QY 682 ATTGAGGAAACCAATTCACCGGAGACTCTGGCAATTTAGAGCAACTACTCTTGGCTGTT 741
DB 866 ATTGAGGAAACCAATTCACCGGAGACTCTGGCAATTTAGAGCAACTACTCTTGGCTGTT 925
QY 742 GTCAATCTATTTCGAGTATACCTGCTACCTTGCAGAGACCTCTATATATGCTATGAAG 801
DB 926 GTCAATCTATTTCGAGTATACCTGCTACCTTGCAGAGACCTCTATATATGCTATGAAG 985
QY 802 GGAGCTGGGACAGATGATCATCCCTCATCAGATGATGTTTCCAGAGTGAAGATGAT 861
DB 986 GGAGCTGGGACAGATGATCATCCCTCATCAGATGATGTTTCCAGAGTGAAGATGAT 1045
QY 862 CTGTTTAAACATCAGGAGGAGTTTAGGAAGAATTTGCCACCTCTCTTTATTCATGATT 921
DB 1046 CTGTTTAAACATCAGGAGGAGTTTAGGAAGAATTTGCCACCTCTCTTTATTCATGATT 1101
QY 922 AAGGGAGATACATCTGGGACTATAGAAGAGCTCTTCTGC 961
DB 1102 RGGGAWA---MCTGGGACWATAAAACCTCTCTCTSY 1138

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RESULT 6
LOCUS BX398791
DEFINITION BX398791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI064YH19 5-PRIME, mRNA sequence.
ACCESSION BX398791
VERSION BX398791
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI064CD10QPl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DI064CD10QPl.
FEATURES
    source
        1..996
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI064YH19"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)

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primer. Five prime end enriched; double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 282 a 192 c 248 g 256 t 18 others
ORIGIN

Query Match 86.8%; Score 851.6; DB 13; Length 996;

Best Local Similarity 97.6%; Pred. No. 2.8e-217;
Matches 856; Conservative 15; Mismatches 5; Indels 1; Gaps 1;

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QY 22 ATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 81
DB 121 ATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 180
QY 82 GCAGAACTCTTCGGAAGCTATGAAAGCTTGGGCACAGATGAGGAGAGCATCTGACT 141
DB 181 GCAGAACTCTTCGGAAGCTATGAAAGCTTGGGCACAGATGAGGAGAGCATCTGACT 240
QY 142 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGGAAATCTCTGACGTTTTAAGACTCTG 201
DB 241 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGGAAATCTCTGACGTTTTAAGACTCTG 300
QY 202 TTGGCAGAGATCTTCTGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 261
DB 301 TTGGCAGAGATCTTCTGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 360
QY 262 ATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCTTG 321
DB 361 ATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCTTG 420
QY 322 AAGGAGCTTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB 421 AAGGAGCTTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 480
QY 382 GAACCTGAGAGCCATCAACAAAGTTTATGAGAGATATGGCTCAAGCCCTGGAAGATGAC 441
DB 481 GAACCTGAGAGCCATCAACAAAGTTTATGAGAGATATGGCTCAAGCCCTGGAAGATGAC 540
QY 442 GTGGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCTCAGGCTAAC 501
DB 541 GTGGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCTCAGGCTAAC 600
QY 502 AGAGACCTTGATGCTGGAATGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 561
DB 601 AGAGACCTTGATGCTGGAATGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 660
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 621
DB 661 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 720
QY 622 CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAGTACATGACTATATCAGGATTTCAA 681
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QY 682 ATTGAGAAACCATTTGACCGGAGACTTCTGGAATTTAGACAACTACTCTCTGCTGTT 741
DB 780 ATTGAGAAACCATTTGACCGGAGACTTCTGGAATTTAGACAACTACTCTCTGCTGTT 839
QY 742 GTGAAATCTATTGGAAGTATACCTGCCTACCTTGCAGAGACCTCTATTATGCTATGAG 801
DB 840 GTGAAATCTATTGGAAGTATACCTGCCTACCTTGCAGAGACCTCTATTATGCTATGAG 899
QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGATCATGGTTCCAGGAGTGAATTTGAT 861
DB 900 GGAGCTGGGACAGATGATCATACCTCATCAGAGATCATGGTTCCAGGAGTGAATTTGAT 959
QY 862 CTGTTTAAACATCAGGAAGAGTTTAGGAAGAATTTTG 898
DB 960 YTKTTTAAATMAGGRARGGGTTTGGGARAATTTT 996
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RESULT 7
BX396240

LOCUS BX396240 1062 bp mRNA linear EST 13-MAY-2003
DEFINITION BX396240 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1014YI09 5-PRIME, mRNA sequence.
ACCESSION BX396240
VERSION BX396240.1 GI:30624830
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1014AE05QP1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1014AE05QP1.
FEATURES
Location/Qualifiers
1..1062
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1014YI09"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 285 a 234 c 272 g 270 t 1 others
ORIGIN

Query Match 86.5%; Score 848.2; DB 13; Length 1062;
Best Local Similarity 99.4%; Pred. No. 2.4e-216;
Matches 850; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 22 ATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 81
DB 208 ATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 267
QY 82 GCAGAACTCTTCGGAAGCTATGAAAGCTTGGGCACAGATGAGGAGAGCATCTGACT 141
DB 268 GCAGAACTCTTCGGAAGCTATGAAAGCTTGGGCACAGATGAGGAGAGCATCTGACT 327
QY 142 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGGAAATCTCTGACGTTTTAAGACTCTG 201
DB 328 CTGTTGACATCCGGAAGTAAATGCTCAGCCGAGGAAATCTCTGACGTTTTAAGACTCTG 387
QY 202 TTGGCAGGAGTCTTCTGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 261
DB 388 TTGGCAGGAGTCTTCTGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 447
QY 262 ATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAACATGCTTG 321
DB 448 ATTTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACTGAACATGCTTG 507
QY 322 AAGGAGCTTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB 508 AAGGAGCTTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 567
QY 382 GAACCTGAGAGCCATCAACAAAGTTTATGAGAGAAATATGGCTCAAGCCTGGAAGATGAC 441
DB 568 GAACCTGAGAGCCATCAACAAAGTTTATGAGAGAAATATGGCTCAAGCCTGGAAGATGAC 627
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AL542496      1201 bp      mRNA      linear      EST 12-MAY-2003
LOCUS      AL542496 Homo sapiens PLACENTA Homo sapiens cdna clone CS0DE012Y114
DEFINITION      5-PRIME, mRNA sequence.
ACCESSION      AL542496
VERSION      AL542496.2 GI:30547699
SOURCE      EST.
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cdna libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12874598.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE012BE07QPl6cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DE012BE07QPl.
FEATURES
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            /organism="Homo sapiens"
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            /clone="CS0DE012Y114"
            /tissue_type="PLACENTA"
            /clone_lib="Homo sapiens PLACENTA"
            /note="Vector: pCMVSPORT_6; 1st strand cdna was primed
            with a NotI-oligo(dT) primer. Five prime end enriched,
            double-strand cdna was digested with Not I and cloned into
            the Not I and EcoRV sites of the pCMVSPORT 6 vector.
            Library was not normalized."
            BASE COUNT      310 a      243 c      293 g      307 t      48 others
            ORIGIN
                Query Match      85.5%; Score 838.4; DB 9; Length 1201;
                Best Local Similarity 98.2%; Pred. No. 1,1e-213;
                Matches 875; Conservative 3; Mismatches 10; Indels 3; Gaps 3;

QY      22  ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTGATGAGCGGCTGAT 81
Db      167  ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTGATGAGCGGCTGAT 226
QY      82  GCAGAACTCTTCGGAAGCTATGAAGCTTGGGCACAGATGAGGAGCATCTGACT 141
Db      227  GCAGAACTCTTCGGAAGCTATGAAGCTTGGGCACAGATGAGGAGCATCTGACT 286
QY      142  CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 201
Db      287  CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 346
QY      202  TTGGCAGGATCTCTCTGGATGACCTGAATCAGAACTAACCTGGAAAAATTTGAAAAATTA 261
Db      347  TTGGCAGGATCTCTCTGGATGACCTGAATCAGAACTAACCTGGAAAAATTTGAAAAATTA 406
QY      262  ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTG 321
Db      407  ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTG 466
QY      322  AAGGAGCTGGAAACAAATGAAAAAGTACTGCAGAAATTTATTGCTTCAAGGACACCTGAA 381
Db      467  AAGGAGCTGGAAACAAATGAAAAAGTACTGCAGAAATTTATTGCTTCAAGGACACCTGAA 526
QY      382  GAACTGAGAGCCATCAACAAGCTTTATGAGGAAGAAATATGGCTCAAGCCTGGAAGATGAC 441

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527  GAACCTGAGAGCCATCAACAAGTTTATGAAGAAGAAATATGGCTCAAGCCCTGGAAGATGAC 596
QY      442  GTGGTGGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTCTTCTCCTCCTCAGGGTAAC 501
Db      587  GTGGTGGGGGACACTTCAGGGTACTACCAAGCGGATGTTGGTCTTCTCCTCCTCAGGGTAAC 646
QY      502  AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561.
Db      647  AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 706
QY      562  CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAATTTATCACCATCTTTTGAACA 621
Db      707  CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAATTTATCACCATCTTTTGAACA 766
QY      622  CGAAGTGTCTCTCA-TTTGAGAAAGGTGTTTGAACAAGTACATGACTATATCAGGATTTCA 680
Db      767  CGAAGTGTCTCTCA-TTTGAGAAAGGTGTTTGAACAAGTACATGACTATATCAGGATTTCA 826
QY      681  AATTGAGGAAACC-ATTGACCCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGTCTG 739
Db      827  AATTGAGGAAACAATTGACCCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGTCTG 886
QY      740  TTGTGAAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGA 799
Db      887  TTGTGAAATCTATTGGAAGTATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGA 946
QY      800  AGGAGCTGGGACAGATGATCATACCTCATCAGAGTCACTGTTCCAGGAGTGAATTTG 859
Db      947  AGGAGCTGGGACAGATGATCATACCTCATCAGAGTCACTGTTCCAGGAGTGAATTTG 1006
QY      860  ATCTGTTTAAACATCAGGAAGGAGTTTAGGAAGAAATTTTCCACCTCTCTTT 910
Db      1007  ATCTGTTT-ACATCAGGAAGGAGTTTAGGAAGAAATTTTCCACCTCTCTTTAT 1056

RESULT 10
LOCUS      BX358605
DEFINITION      1076 bp      mRNA      linear      EST 05-MAY-2003
clone CS0DI041YI02 5-PRIME, mRNA sequence.
ACCESSION      BX358605
VERSION      BX358605.1 GI:30382268
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cdna libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI041BE01QPl6cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DI041BE01QPl.
FEATURES
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 5 vector. Library was normalized. a 233 c 274 g 278 t 4 others

BASE COUNT	287 a	233 c	274 g	278 t	4 others
ORIGIN					
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Best Local Similarity	97.4%;	Pred. No. 5.1e-213;			
Matches	866;	Conservative 4;	Mismatches 16;	Indels 3;	Gaps 2;
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Db	191	ATGGCAGAGTTCTCAGAGGCACTGTGACATGACTTCCCTGGATTGATGAGCGGGCTGAT	250		
Qy	82	GCAGAAACTCTTCGGAAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT	141		
Db	251	GCAGAAACTCTTCGGAAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT	310		
Qy	142	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGACTTTTAAGACTCTG	201		
Db	311	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGACTTTTAAGACTCTG	370		
Qy	202	TTTGGCAGGATCTTCTGGATGACTCGAAATCAGAATCTAACTGGAATAATTTGAAAAATTA	261		
Db	371	TTTGGCAGGATCTTCTGGATGACTCGAAATCAGAATCTAACTGGAATAATTTGAAAAATTA	430		
Qy	262	ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGAACATGCCTTG	321		
Db	431	ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGAACATGCCTTG	490		
Qy	322	AAGGGAGCTGGACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA	381		
Db	491	AAGGGAGCTGGACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA	550		
Qy	382	GAATGAGAGCCATCAACAAAGTTTATGAAGAAGATATGCTCAAGCCCTGGAAGATGAC	441		
Db	551	GAATGAGAGCCATCAACAAAGTTTATGAAGAAGATATGCTCAAGCCCTGGAAGATGAC	610		
Qy	442	GTGGTGGGGACACTTCAGGCTACTACCAGGGATGTTGGTGGTTCCTTCAGGCTAAC	501		
Db	611	GTGGTGGGGACACTTCAGGCTACTACCAGGGATGTTGGTGGTTCCTTCAGGCTAAC	670		
Qy	502	AGAGACCTTGATGCTGGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	561		
Db	671	AGAGACCTTGATGCTGGAAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	730		
Qy	562	CAGGCTCGAAGACTTAAATGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA	621		
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Qy	622	CGAAGTGTGTCTATTTGAGAAAGGCTGTTTGACAAGTACATGACTATATCAGGATTTCAA	681		
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Qy	682	ATTGAGAAACCAATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTCGCTGT	741		
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Qy	742	GTGAAATCTATTCAAGTATACCTTGCCTACCTTCGACAGACCCCTCTATTATGCTATGAAG	801		
Db	910	GTGAAATCTATTCAAGTATACCTTGCCTACCTTCGACAGACCCCTCTATTATGCTATGAAG	969		
Qy	802	GGAGCTGGGACAGATGATACACCTCATCAGAGTCATGGTTCGAGAGTGGATGATGAT	861		
Db	970	GGAGCTGGGACAGATGATACACCTCATCAGAGTATGGTTCGAGAGTGGATGATGAT	1029		
Qy	862	CTGTTTTAACATCAGGAAGGAGTTTAGGAAGAAATTTTGCACCTCTCTTTT	910		
Db	1030	CTGTTTAA--CATCAGGAGGAGTTTAGGAGGATTTTCCCACTCTCTTTT	1076		

RESULT 11
BX402751

LOCUS	BX402751	1007 bp	mRNA	linear	EST 13-MAY-2003
DEFINITION	BX402751	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1084YA05 5-PRIME, mRNA sequence.			
ACCESSION	BX402751				
KEYWORDS	BX402751.1	GI:30607254			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.				
AUTHORS	Full-length CDNA libraries and normalization				
TITLE	Unpublished				
JOURNAL	Contact: Genoscope				
COMMENT	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2353.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSIAI021zG030pi&cluster=2353.r . Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSIAI021zG030QPI. Location/Qualifiers 1..1007				
FEATURES					
SOURCE					

BASE COUNT	277 a	216 c	257 g	236 t	1 others
ORIGIN					
Query Match	84.8%	Score 832.2;	DB 13;	Length 1007;	
Best Local Similarity	99.6%	Pred. No. 4.6e-212;			
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Qy	22	ATGCAACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGAGCGGGCTGAT	81		
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Qy	82	GCAGAAACTCTTCGGAAGGCTATCAAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT	141		
Db	231	GCAGAAACTCTTCGGAAGGCTATCAAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT	290		
Qy	142	CTGTGTGACATCCCAAGCTAATGCTCAGCGCCAGGAAATCTCTGCAGACTTTTAAAGACTCTG	201		
Db	291	CTGTGTGACATCCCAAGCTAATGCTCAGCGCCAGGAAATCTCTGCAGACTTTTAAAGACTCTG	350		
Qy	202	TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA	261		
Db	351	TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA	410		
Qy	262	ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTTG	321		
Db	411	ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCGCTTG	470		
Qy	322	AAGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAAATTTTGCTTCAAGGACACCTGAA	381		
Db	471	AAGGAGCTGGAAACAAATGAAAAAGTACTGACAGAAAATTTTGCTTCAAGGACACCTGAA	530		
Qy	382	GAACCTGAGGCCATCAACCAAGTTTATGAAGAAGAAATATGGCTCAAGCCCTGGGAAGATGAC	441		
Db	531	GAACCTGAGGCCATCAACCAAGTTTATGAAGAAGAAATATGGCTCAAGCCCTGGGAAGATGAC	590		

QY 442 GTGCTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
 Db 591 GTGCTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 650
 QY 502 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 Db 651 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 710
 QY 562 CAGGCTGGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATACCATCTCTTGGAAACA 621
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 QY 682 ATTGAGAAACCATTCACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGGCTGTT 741
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 Db 891 GTGAATCTATTGCAAGTATACCTGCTACCTTGCAGAGACCTCTTATGATGCTATGAAG 950
 QY 802 GGAGCTGGGACAGATGATATACCTTCATCAGAGTCAATGTTTCCAGGAGTGAATTT 958
 Db 951 GGAGCTGGGACAGATGATATACCTTCATCAGAGTCAATGTTTCCAGGAGTGAATTT 1007

RESULT 12 AL547761

LOCUS AL547761 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1017YJ11 5-PRIME, mRNA sequence.

ACCESSION AL547761

VERSION 1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (bases 1 to 1201)

JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

COMMENT Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2353.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1017CE06QPlcluster=2353.r. Contact :

Feng Liang Email: fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0D1017CE06QPl.

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 311 a 252 c 305 g 306 t 27 others

ORIGIN

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 Matches 911; Conservative 11; Mismatches 26; Indels 11; Gaps 6;
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 Db 268 GCAGAAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCTCTGACT 327
 QY 142 CTGTTGACATCCCGAAGTAAATGCTCAGCGCCAGCAAAATCTCTCAGCTTTTAAAGACTCTG 201
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 QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACTCGAAATTTTGAATAATTA 261
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 Db 508 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 567
 QY 382 GAAGTGGAGCCATCAACAAAGTTTATGAGAGAAATATGGCTCAAGCCTGGAGATGAC 441
 Db 568 GAAGTGGAGCCATCAACAAAGTTTATGAGAGAAATATGGCTCAAGCCTGGAGATGAC 627
 QY 442 GTGCTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
 Db 628 GTGCTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 687
 QY 502 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
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 QY 922 AAGGGAGATACATCTCGGACTATAGAAGCTCTCTGCTGCTCTCCGGAGAGATGA 980
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 AL517516
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 DEFINITION

AL517516

1201 bp mRNA linear EST 12-MAY-2003

DEFINITION

[illegible]

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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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ORIGIN

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Best Local Similarity 94.3%; Pred. No. 2.7e-209;
Matches 886; Conservative 18; Mismatches 29; Indels 7; Gaps 5;

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DB 196 ATGGCAGAGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 255
QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGAGCATCTGACT 141
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DB 376 TTGGGAGGAGTCTCTCGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAATTA 435
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DB 556 GAAGTGAAGCCATCAACAAAGTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGAC 615
QY 442 GTGGTGGGACACTTCAGGGTACTACCGCGGATGTGGTGGTCTTCTCTTCAGGCTAAC 501
DB 616 GTGGTGGGACACTTCAGGGTACTACCGCGGATGTGGTGGTCTTCTCTTCAGGCTAAC 675
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DB 1036 GATCTGTAAACATCAGGAGGAGTTTATGGAAGAAATTTTCCACACCTCTCTTTATCCATG 1091
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DB 1092 ATTAGGGGATATCTGGGAGBWWARAAACCTTTSYKC 1131

RESULT 15
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DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL583578
VERSION AL583578.2 GI:30606551
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1022)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12952676.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE004CB11QPI&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE004CB11QPI.

FEATURES
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/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 282 a 219 c 261 g 255 t
ORIGIN

Query Match 83.6%; Score 820.4; DB 9; Length 1022;
Best Local Similarity 99.1%; Pred. No. 6.7e-209;
Matches 840; Conservative 5; Mismatches 1; Indels 2; Gaps 2;

QY 22 ATGGCAGAGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
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DB 236 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGAGCATCTGACT 295
QY 142 CTCTTGACATCCCGAAGTAACTGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 201
DB 296 CTCTTGACATCCCGAAGTAACTGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 355
QY 202 TTGGGAGGAGTCTCTCGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAATTA 261
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Qy	622	CGAAGTGTGCTCATTTTGACAAAAGTGTTTGACAAGTACATGACTATATCAGGATTTCAA	681
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:27:21 ; Search time 37.6667 Seconds
(without alignments)
1377.971 Million cell updates/sec

Title: US-09-970-969-2

Perfect score: 1639

Sequence: 1 MACGGGHMAQVLRGFTVDFP.....KGTSGDYKKALLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639	100.0	327	22 AAB50863	Modified human ann
2	1630	99.5	327	22 AAB50865	Modified human ann
3	1618	98.7	327	22 AAB50864	Modified human ann
4	1590	97.0	320	9 AAP80511	Placental coagul
5	1590	97.0	320	10 AAP91953	Vascular anti-coag
6	1590	97.0	320	12 AAR13082	PAP-I. Homo sapie
7	1590	97.0	320	20 AAY13923	S65T GFP variant/h
8	1590	97.0	320	21 AAY84788	Amino acid sequenc
9	1590	97.0	320	23 AAB31220	Human annexin V, c

10	1587	96.8	320	10 AAP90053	anticoagulant PP4
11	1587	96.8	600	21 AAY92930	Annexin V/urokinas
12	1586	96.8	320	9 AAP82317	PAP-I isolated fro
13	1585	96.7	319	13 AAR26276	CPB-I. Homo sapie
14	1585	96.7	319	14 AAR41021	Calphobindin I (CP
15	1585	96.7	319	23 ABG32550	Human CPB-I protei
16	1584	96.6	320	9 AAP80242	Sequence vascular
17	1584	96.6	320	9 AAP80714	Sequence vascular
18	1584	96.6	320	12 AAR11910	Vascular anticoagu
19	1580	96.4	319	13 AAR26180	CPB-I. Homo sapie
20	1577	96.2	320	10 AAP91363	Human lipocortin-V
21	1553	94.8	319	13 AAR25718	CPB-I. Homo sapie
22	1479.5	90.3	319	23 AAY13924	S65T GFP variant/h
23	1479.5	90.3	319	23 AAB57067	Mouse ischaemic co
24	1455.5	88.8	318	20 AAY13925	S65T GFP variant/h
25	1448.5	88.4	319	16 AAR75695	Rat annexin-V. Ra
26	1442.5	88.0	319	24 AAB56248	Human annexin V pr
27	1442.5	88.0	669	24 AAB56249	Modified annexin p
28	1012	61.9	208	21 AAB58393	Lung cancer associ
29	932	56.9	672	11 AAR03725	Human placenta-der
30	932	56.9	675	24 AAB54621	Human NOVX polypep
31	931	56.8	786	11 AAR03726	Human placenta-der
32	923	56.3	321	20 AAY13926	S65T GFP variant/h
33	923	56.3	321	23 AAB56279	Human ovarian canc
34	923	56.3	324	21 AAB34617	Human cancer assoc
35	922	56.3	321	10 AAP91913	Anticoagulative PP
36	906.5	55.3	320	21 AAY84790	Amino acid sequenc
37	872	53.2	736	22 AAB19948	Novel human diagn
38	865	52.8	503	14 AAR34127	Annexin XI type I
39	857	52.3	505	14 AAR34128	Annexin XI type I
40	855	52.2	505	20 AAY07117	Lung cancer associ
41	844	51.5	299	23 AAB69394	Human polypeptide
42	831.5	50.7	327	9 AAP80715	Sequence vascular
43	831.5	50.7	327	10 AAP91954	Vascular anti-coag
44	831.5	50.7	327	14 AAR35754	VAC-beta. Synthet
45	831.5	50.7	327	22 AAR78665	Human protein SEQ

ALIGNMENTS

RESULT 1
AAB50863
ID AAB50863 standard; Protein: 327 AA.
XX
AC AAB50863;
XX
XX
XX
XX 16-MAR-2001 (first entry)
XX
DE Modified human annexin, SEQ ID NO: 2.
XX
KW Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplacental rejection.
XX
XX Homo sapiens.
OS
PN WO200073332-A1.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US14324.
XX
PR 01-JUN-1999; 99US-0324096.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Tait JF, Brown DS;
XX
DR WPI; 2001-080465/09.
XX
N-PSDB; AAC91368.
PT Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid

extension which comprises a glycine and a cysteine residue -
 Claim 12; Page 30-31; 39pp; English.
 The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bioactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.

XX Sequence 327 AA;
 Query Match 100.0%; Score 1639; DB 22; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACGGHMAQVLRGTVPDPPGDERADATLRAKMGKLGTDDESIILTLTSRNSAQRQEI 60
 DB 1 MACGGHMAQVLRGTVPDPPGDERADATLRAKMGKLGTDDESIILTLTSRNSAQRQEI 60
 QY 61 SAAFTLFRDLDLKLSELTGKFEKLIYALMKPSRLYDAYELKHALKAGAGTNEKVLTEI 120
 DB 61 SAAFTLFRDLDLKLSELTGKFEKLIYALMKPSRLYDAYELKHALKAGAGTNEKVLTEI 120
 QY 121 IASRTPPEELRAIKQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVE 180
 DB 121 IASRTPPEELRAIKQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVE 180
 QY 181 ODAQALFOAGELKWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFIETIDRETSGNL 240
 DB 181 ODAQALFOAGELKWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFIETIDRETSGNL 240
 QY 241 EQLLAVKSIKSIIPAYLAETLYYAMKGAGTDDHTLIRVWVSERSEIDLNFIRKEFKNFA 300
 DB 241 EQLLAVKSIKSIIPAYLAETLYYAMKGAGTDDHTLIRVWVSERSEIDLNFIRKEFKNFA 300
 QY 301 TSLYSMIKGTSGDYKALLLSGDD 327
 DB 301 TSLYSMIKGTSGDYKALLLSGDD 327

RESULT 2
 AAB50865
 ID AAB50865 standard; Protein; 327 AA.
 AC AAB50865;
 XX AAB50865;
 DT 16-MAR-2001 (first entry)
 DE Modified human annexin, SEQ ID NO: 6.
 KW Human; annexin; chelation site; nuclear imaging; apoptosis;
 KW transplant rejection.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200073332-A1.
 XX WO200073332-A1.
 PD 07-DEC-2000.
 XX 07-DEC-2000.
 PF 25-MAY-2000; 2000WO-US14324.
 XX 01-JUN-1999; 99US-0324096.
 PA (UNIV) UNIV WASHINGTON.
 XX Tait JF, Brown DS;

XX WPI; 2001-080465/09.
 DR N-PSDB; AAC91370.
 XX Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue -
 Claim 18; Page 37-38; 39pp; English.
 The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bioactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.

XX Sequence 327 AA;
 Query Match 99.5%; Score 1630; DB 22; Length 327;
 Best Local Similarity 99.7%; Pred. No. 7.7e-142;
 Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MACGGHMAQVLRGTVPDPPGDERADATLRAKMGKLGTDDESIILTLTSRNSAQRQEI 60
 DB 1 MACGGHMAQVLRGTVPDPPGDERADATLRAKMGKLGTDDESIILTLTSRNSAQRQEI 60
 QY 61 SAAFTLFRDLDLKLSELTGKFEKLIYALMKPSRLYDAYELKHALKAGAGTNEKVLTEI 120
 DB 61 SAAFTLFRDLDLKLSELTGKFEKLIYALMKPSRLYDAYELKHALKAGAGTNEKVLTEI 120
 QY 121 IASRTPPEELRAIKQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVE 180
 DB 121 IASRTPPEELRAIKQVVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVE 180
 QY 181 ODAQALFOAGELKWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFIETIDRETSGNL 240
 DB 181 ODAQALFOAGELKWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFIETIDRETSGNL 240
 QY 241 EQLLAVKSIKSIIPAYLAETLYYAMKGAGTDDHTLIRVWVSERSEIDLNFIRKEFKNFA 300
 DB 241 EQLLAVKSIKSIIPAYLAETLYYAMKGAGTDDHTLIRVWVSERSEIDLNFIRKEFKNFA 300
 QY 301 TSLYSMIKGTSGDYKALLLSGDD 327
 DB 301 TSLYSMIKGTSGDYKALLLSGDD 327

RESULT 3
 AAB50864
 ID AAB50864 standard; Protein; 327 AA.
 AC AAB50864;
 XX AAB50864;
 DT 16-MAR-2001 (first entry)
 DE Modified human annexin, SEQ ID NO: 4.
 KW Human; annexin; chelation site; nuclear imaging; apoptosis;
 KW transplant rejection.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200073332-A1.
 XX WO200073332-A1.
 PD 07-DEC-2000.
 XX 07-DEC-2000.
 PF 25-MAY-2000; 2000WO-US14324.

XX 01-JUN-1999; 9905-0324096.
 XX (UNIW) UNIV WASHINGTON.
 XX PI Tait JF, Brown DS;
 XX WIPI; 2001-080465/09.
 XX DR N-PSDB; AAC91369.
 XX Novel modified annexin useful for imaging vascular thrombi and
 PT apoptosis, has N-terminal chelation site comprising amino acid
 PT extension which comprises a glycine and a cysteine residue -
 XX
 PS Claim 15; Page 33-35; 39pp; English.
 CC The present sequence is a modified annexin having an N-terminal
 CC chelation site, which comprises an amino acid extension including a
 CC glycine and a cysteine residue. The modified annexin is useful for
 CC imaging vascular thrombi or apoptosis which is associated with response
 CC to a chemotherapeutic agent or with rejection as a result of
 CC transplantation. The modified annexin can effectively chelate a
 CC radionuclide and retain annexin bioactivity. It can be readily prepared
 CC in high radiochemical yield and with high radiochemical purity. In
 CC contrast to conventional conjugation chemistries that provide a
 CC distribution of conjugation products, the modified annexin has a single
 CC chelation site remote from the site of biological activity.
 XX
 SQ Sequence 327 AA;
 Query Match 98.7%; Score 1618; DB 22; Length 327;
 Best Local Similarity 99.4%; Pred. No. 9.8e-141;
 Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MACGGHMAOVLRGTVDPEFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEI 60
 DB 1 MACGGHMAOVLRGTVDPEFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEI 60
 QY 61 SAAFKTLFGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
 DB 61 SAAFKTLFGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
 QY 121 IASRTPEELRAIKOVYEEYEGSSLEDDVVGDTSGYYORMLVLLQANRDPDAGIDEAQVE 180
 DB 121 IASRTPEELRAIKOVYEEYEGSSLEDDVVGDTSGYYORMLVLLQANRDPDAGIDEAQVE 180
 QY 181 ODAQALFQAGELKWTGDEEKFIFIGTRSVSHLRKVPDKYMTISGQIETIDRETSGNL 240
 DB 181 ODAQALFQAGELKWTGDEEKFIFIGTRSVSHLRKVPDKYMTISGQIETIDRETSGNL 240
 QY 241 EQLLAVVKSIRSPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFA 300
 DB 241 EQLLAVVKSIRSPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFA 300
 QY 301 TSLYSMIKGTSGDYKALLLSGDD 327
 DB 301 TSLYSMIKGTSGDYKALLLSGDD 327
 RESULT 4
 AAP80511 standard; protein; 320 AA.
 XX AAP80511;
 AC
 XX 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 12-NOV-1990 (first entry)
 XX Placental coagulation inhibitor.
 DE Placental coagulation inhibitor; disseminated vascular coagulation;
 XX thrombosis.
 KW

XX Homo sapiens.
 XX OS
 XX PN EP279459-A.
 XX PN JP03219875-A.
 XX PD
 XX PD 24-AUG-1988.
 XX PF 19-FEB-1988; 88EP-0102468.
 XX PR 20-FEB-1987; 87JP-0037227.
 XX PR 23-JUL-1987; 87JP-0184428.
 XX PA (KOWA) KOWA CO LTD.
 XX PI Saino Y, Iwasaki A, Suda M;
 XX WIPI; 1988-236733/34.
 XX WIPI; 1991-329110/45.
 XX N-PSDB; AAN81113.
 XX Recombinant placental coagulation inhibitor - useful for the prevention
 PT and treatment of thromboses or disseminated intra-vascular coagulation.
 XX Disclosure; Page 7; 7pp; English.
 CC This polypeptide exhibits strong anticoagulant activities and is useful
 CC for the treatment and prevention of e.g. thrombosis or disseminated
 CC intravascular coagulation in the brain, heart and peripheral blood
 CC vessels, such as cerebral and myocardial infarction. It has no
 CC antigenicity against man and can be produced in large amounts using
 CC recombinant methods.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 320 AA;
 Query Match 97.0%; Score 1590; DB 9; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3.6e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVDPEFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEI SAAFKTL 67
 DB 1 MAQVLRGTVDPEFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEI SAAFKTL 60
 QY 68 FGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTP 127
 DB 61 FGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTP 120
 QY 128 ELRAIKOVYEEYEGSSLEDDVVGDTSGYYORMLVLLQANRDPDAGIDEAQVE DQAALF 187
 DB 121 ELRAIKOVYEEYEGSSLEDDVVGDTSGYYORMLVLLQANRDPDAGIDEAQVE DQAALF 180
 QY 188 QAGELKWTGDEEKFIFIGTRSVSHLRKVPDKYMTISGQIETIDRETSGNL EQLLAV 247
 DB 181 QAGELKWTGDEEKFIFIGTRSVSHLRKVPDKYMTISGQIETIDRETSGNL EQLLAV 240
 QY 248 VKSIRSPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 307
 DB 241 VKSIRSPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
 QY 308 KGDTSGDYKALLLSGDD 327
 DB 301 KGDTSGDYKALLLSGDD 320
 RESULT 5
 AAP91953 standard; protein; 320 AA.
 XX AAP91953;
 AC

XX 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 30-JUL-1989 (first entry)
 XX Vascular anti-coagulating protein-alpha.
 DE Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
 XX Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
 KW Chimeric - Homo sapiens.
 OS Chimeric - Mus musculus.
 XX Key Location/Qualifiers
 FH CDS 1..320
 FT /product=VAC-alpha protein
 XX DE3810331-A.
 XX 05-OCT-1989.
 XX 26-MAR-1988; 88DE-3810331.
 XX 26-MAR-1988; 88DE-3810331.
 XX (BOEH) BOEHRINGER INGELHEIM.
 XX Gunther A;
 XX WPI: 1989-293724/41.
 XX N-PSDB; AAN91353.
 XX Monoclonal antibodies to vascular anti-coagulating proteins - and
 PT hybridomas producing such antibodies.
 XX Disclosure; fig 1; lipp; German.
 XX This vascular anti-coagulating protein (VAC)-alpha is used in the
 CC preparation of monoclonal antibodies (MABs). The VAC-alpha is injected
 CC into a host animal, in conjugation with eg keyhole limpet haemocyanin,
 CC and the B-cells from immunised hosts are then fused with myeloma cells.
 CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-
 CC alpha. Abs can be used as immunoassay reagents to detect VAC proteins,
 CC as affinity ligands for protein purification, and as medicaments for binding
 CC and/or neutralising VAC proteins in vivo. See also AAN91354 and
 CC EP-181465.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 320 AA;
 SQ
 Query Match 97.0%; Score 1590; DB 10; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3.6e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLGTVDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTL 67
 DB 1 MAQVLGTVDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTL 60
 QY 68 FGRLDLLKSELTKGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRLDLLKSELTKGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 128 ELRAIKQVYEEYSGSLEDVVDGTSYQYRMLVLLQANRPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVYEEYSGSLEDVVDGTSYQYRMLVLLQANRPDAGIDEAQVEQDAQALF 180
 QY 198 QAGELKWTGDEKFTIFGTRSVSHLRKVFDMYMTISGFOIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKWTGDEKFTIFGTRSVSHLRKVFDMYMTISGFOIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINRKEPKNFATSLYSMI 307
 DB 241 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINRKEPKNFATSLYSMI 300

QY 308 KGDTSGDYKKALLLSGEDD 327
 DB 301 KGDTSGDYKKALLLSGEDD 320
 RESULT 6
 AAR13082
 ID AAR13082 standard; Protein; 320 AA.
 XX AAR13082;
 XX 25-MAR-2003 (updated)
 DT 30-SEP-1991 (first entry)
 DE PAP-I.
 XX Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;
 KW gla-domain; VKDP.
 XX Homo sapiens.
 OS WO9109953-A.
 PN 11-JUL-1991.
 XX 13-DEC-1990; 90WO-US07335.
 XX 29-DEC-1989; 89US-0459082.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Foster DC;
 XX WPI: 1991-222905/30.
 XX N-PSDB; AAQ12679.
 XX Recombinant prodn. of hybrid phospholipid-binding proteins -
 PT comprising lipocortin phospholipid-binding domain and
 PT vitamin K-dependent protein
 XX Disclosure; Fig 7; 57pp; English.
 XX This sequence, or a fragment of it, is used in the construction of
 CC hybrid phospholipid-binding proteins (PBP) comprising at least one
 CC lipocortin phospholipid binding domain (PBD), e.g. of PAP-I, joined
 CC to a gla-domainless vitamin K-dependent protein, e.g. protein C or
 CC activated protein C. See AAQ12680-81 for such examples.
 CC See also AAQ12678-81.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 320 AA;
 SQ
 Query Match 97.0%; Score 1590; DB 12; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3.6e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLGTVDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTL 67
 DB 1 MAQVLGTVDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTL 60
 QY 68 FGRLDLLKSELTKGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRLDLLKSELTKGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 128 ELRAIKQVYEEYSGSLEDVVDGTSYQYRMLVLLQANRPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVYEEYSGSLEDVVDGTSYQYRMLVLLQANRPDAGIDEAQVEQDAQALF 180
 QY 188 QAGELKWTGDEKFTIFGTRSVSHLRKVFDMYMTISGFOIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKWTGDEKFTIFGTRSVSHLRKVFDMYMTISGFOIETIDRETSGNLEQLLAV 240

QY 248 VKSIRSPAYLAETLYYAMKAGCTDDHTLIRVWVSRSEIDLFIKRNKFNATSLYSMI 307
 DB 241 VKSIRSPAYLAETLYYAMKAGCTDDHTLIRVWVSRSEIDLFIKRNKFNATSLYSMI 300

QY 308 KGDTSGDYKKALLLGGEDD 327
 DB 301 KGDTSGDYKKALLLGGEDD 320

RESULT 7
 AAY13923
 ID AAY13923 standard; protein; 320 AA.
 XX
 AC AAY13923;
 XX
 DT 13-JUL-1999 (first entry)
 XX
 DE S65T GFP variant/hannexin V protein.
 XX
 KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KW fluorescent intensity; anionic phospholipid binding affinity;
 KW asymmetric distribution; anionic phospholipid binding affinity;
 KW apoptotic cell detection.
 XX
 OS Aequorea victoria.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W09919470-A2.
 XX
 PD 22-APR-1999.
 XX
 XX 09-OCT-1998; 98WO-US21444.
 XX
 XX 09-OCT-1997; 97US-0948276.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 PI Ernst JD;
 XX
 PI WPI; 1999-277634/23.
 XX
 DR Bifunctional fusion protein useful for the detection of apoptotic
 PT cells
 PT
 PS Claim 2; Page 14-15; 23pp; English.
 XX
 CC This sequence represents an example of a protein of the invention.
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labelled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes.
 XX
 SQ Sequence 320 AA;

Query Match 97.08; Score 1590; DB 20; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3.6e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 MAQVLRTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQROEISAAPKTL 67
 DB 1 MAQVLRTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQROEISAAPKTL 60

QY 68 FGRDLDDLKSEYTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRDLDDLKSELTKGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

QY 128 ELRAIKOVYEEYEGSSLEDDVVGDTSCYYORMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKOVYEEYEGSSLEDDVVGDTSCYYORMLVVLLQANRDPDAGIDEAQVEQDAQALF 180

QY 188 QAGELKMGTDDEKFTITFTGRSVSHLRKVFQKMTISGFOETEETIDRETSGNLEQLLAV 247
 DB 181 QAGELKMGTDDEKFTITFTGRSVSHLRKVFQKMTISGFOETEETIDRETSGNLEQLLAV 240

QY 248 VKSIRSPAYLAETLYYAMKAGCTDDHTLIRVWVSRSEIDLFIKRNKFNATSLYSMI 307
 DB 241 VKSIRSPAYLAETLYYAMKAGCTDDHTLIRVWVSRSEIDLFIKRNKFNATSLYSMI 300

QY 308 KGDTSGDYKKALLLGGEDD 327
 DB 301 KGDTSGDYKKALLLGGEDD 320

RESULT 8
 AAY84788
 ID AAY84788 standard; peptide; 320 AA.
 XX
 AC AAY84788;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Amino acid sequence of annexin V.
 XX
 KW Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory;
 KW coating; thrombogenic biomaterial; labelling compound; negative charge.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Domain 16..91
 FT /note= "domain 1"
 XX
 PN FR2784106-A1.
 XX
 PD 07-APR-2000.
 XX
 PF 02-OCT-1998; 98FR-0012366.
 XX
 PR 02-OCT-1998; 98FR-0012366.
 XX
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 XX (UYPA-) UNIV CURIE PARIS VI P & M.
 XX
 XX Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerois R;
 XX WPI; 2000-320664/28.
 DR
 XX Chemical structure having affinity for phospholipid comprises chemical
 XX platform comprising six residues supporting set of chemical functions
 XX that are capable of binding to phospholipid -
 XX
 PS Claim 13; Fig 6b; 63pp; French.
 XX
 CC The present sequence represents an annexin polypeptide. The domain of
 CC annexin, which may be modified, is used to construct the chemical
 CC compounds of the invention. The specification describes chemical
 CC compounds which have an affinity for a phospholipid. The chemical
 CC compounds comprise at least one chemical platform comprising six
 CC residues supporting a set of chemical functions that are capable of
 CC binding to the phospholipid and at least partly define the affinity
 CC of the structure for the phospholipid. The compounds act as
 CC phospholipid sequestrers. The compounds are useful for preparing
 CC antithrombotic, antitumor and antiinflammatory medicaments, for
 CC making coatings for thrombogenic biomaterials, and for preparing
 CC labelling compounds useful for analysing and detecting negative

CC charges on cell surfaces and microvesicles in blood.

XX Sequence 320 AA; Query Match 97.0%; Score 1590; DB 21; Length 320; Best Local Similarity 99.7%; Pred. No. 3.6e-138; Mismatches 0; Indels 0; Gaps 0; Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 MAQVLRGVTDPGPFDERADAEETLRKAMKGLGTDDEESILTLTSRNAQROEISAAFKTL 67

DB 1 MAQVLRGVTDPGPFDERADAEETLRKAMKGLGTDDEESILTLTSRNAQROEISAAFKTL 60

QY 68 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127

DB 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

QY 128 ELRAIKQVVEEYSGSLEDVVGDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 187

DB 121 ELRAIKQVVEEYSGSLEDVVGDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 180

QY 188 QAGELKWCETDEKFTITFGRSVSHLRKVFVKYMTISGFQIETIDRETSGNLEQLLAV 247

DB 181 QAGELKWCETDEKFTITFGRSVSHLRKVFVKYMTISGFQIETIDRETSGNLEQLLAV 240

QY 248 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKNFATSLYSMI 307

DB 241 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKNFATSLYSMI 300

QY 308 KGDTSQDYKKALLLLSGEDD 327

DB 301 KGDTSQDYKKALLLLCGEDD 320

RESULT 10

AAP90053

ID AAP90053 standard; protein; 320 AA.

XX

AC AAP90053;

XX

DT 25-MAR-2003 (updated)

DT 01-NOV-1989 (first entry)

XX

DE anticoagulant PP4 protein.

XX

KW Anticoagulant; PP4 protein; thromboplastin.

XX

OS Homo sapiens (human).

XX

PN EP318703-A.

XX

PD 07-JUN-1989.

XX

PF 29-OCT-1988; 88EP-0118039.

XX

PR 03-NOV-1987; 87DE-3737239.

XX

CC

CC pseudo-delta receptors for activated C-kinase (RACK), deltaV1-5 or their derivatives or fragments. Protein kinase C (PKC) is a key enzyme in signal transduction involved in a variety of cellular functions including cell growth, regulation of gene expression and ion channel activity. The localisation of different PKC isozymes to different areas of the cell in turn appears due to binding of the activated isozymes to the specific anchoring molecules (RACKs). Peptides that mimic either the PKC-binding site on RACKs or the RACK-binding site on PKC are isozyme specific translocation inhibitors of PKC. The disclosed peptides are useful in activating or inhibiting translocation or function of deltaPKC. The deltaPKC agonists or antagonists are useful in reducing, enhancing or protecting against damage to cells or tissues due to ischaemic or hypoxic event caused by stroke. Acute administration of the peptides, conjugated to a carrier peptide or a Tat-derived peptide, protected hearts against ischaemic damage as shown by decreased release of creatine kinase. The data indicate that in an intact heart, inhibition of deltaPKC conferred greater than 50% protection against ischaemic damage. The sequence presented is human annexin V, which contains a delta RACK binding site.

XX Sequence 320 AA;

Query Match 97.0%; Score 1590; DB 23; Length 320; Best Local Similarity 99.7%; Pred. No. 3.6e-138; Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 MAQVLRGVTDPGPFDERADAEETLRKAMKGLGTDDEESILTLTSRNAQROEISAAFKTL 67

DB 1 MAQVLRGVTDPGPFDERADAEETLRKAMKGLGTDDEESILTLTSRNAQROEISAAFKTL 60

QY 68 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127

DB 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

QY 128 ELRAIKQVVEEYSGSLEDVVGDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 187

DB 121 ELRAIKQVVEEYSGSLEDVVGDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 180

QY 188 QAGELKWCETDEKFTITFGRSVSHLRKVFVKYMTISGFQIETIDRETSGNLEQLLAV 247

DB 181 QAGELKWCETDEKFTITFGRSVSHLRKVFVKYMTISGFQIETIDRETSGNLEQLLAV 240

QY 248 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKNFATSLYSMI 307

DB 241 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSREIDLFNIRKEFRKNFATSLYSMI 300

QY 308 KGDTSQDYKKALLLLSGEDD 327

DB 301 KGDTSQDYKKALLLLCGEDD 320.

RESULT 9

ABG31220

ID ABG31220 standard; Protein; 320 AA.

XX

AC ABG31220;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human annexin V, containing a delta RACK binding site.

XX

KW Human; annexin V; delta RACK; delta protein kinase C; deltaPKC; V1 domain; vasotrophic; cerebroprotective; deltaV1-1; deltaV1-2; RACK; pseudo-delta RACK; pseudo-delta receptor for activated C-kinase; deltaV1-5; PKC; protein kinase C; signal transduction; cell growth; gene expression; ion channel activity; translocation; hypoxia; stroke; ischaemic damage; creatine kinase.

XX

OS Homo sapiens.

XX

PN WO200257413-A2.

XX

PD 25-JUL-2002.

XX

PF 09-NOV-2001; 2001WO-US47556.

XX

PR 18-JAN-2001; 2001US-262060P.

XX

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX

PI Mochly-Rosen D;

XX

DR WPI; 2002-599715/64.

XX

PT New delta protein kinase C peptide for reducing or enhancing damage to cells or tissues exposed to ischemic or hypoxic event caused by stroke, or for protecting tissue from damage due to ischemia -

XX

PS Claim 45; Page 64-65; 65pp; English.

XX

CC The invention discloses peptides comprising deltaV1-1, deltaV1-2,

PA (BEHW) BEHRINGERWERKE AG.
 XX
 PI Grundmann U, Abel KJ, Kupper H;
 XX
 DR WPI; 1989-166767/23.
 XX
 PT New DNA sequence encoding anticoagulant PP4 protein
 PT - and new recombinant protein, vectors, antibodies, etc.,
 PT useful therapeutically and diagnostically.
 XX
 PS Claim 1; page 11 and Table 1; 12pp; German.
 XX
 CC Amino acid sequence of anticoagulant PP4 protein. This
 CC inhibits blood coagulation at the thromboplastin stage.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 320 AA;
 Query Match 96.8%; Score 1587; DB 10; Length 320;
 Best Local Similarity 99.4%; Pred. No. 6.9e-138;
 Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDDEESILTLTSRQAQOEISAFAFKTL 67
 DB 1 MAQVLRGTVTDPPGDERADAOTLRKAMKGLGTDDEESILTLTSRQAQOEISAFAFKTL 60
 QY 68 FGRDLDDLLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
 DB 61 FGRDLDDLLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
 QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYTYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYTYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 188 QAGELKWGTDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGQIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKWGTDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGQIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 307
 DB 241 VKSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 300
 QY 308 KGDTSGDYKKALLLGGEDD 327
 DB 301 KGDTSGDYKKALLLGGEDD 320
 RESULT 11
 AAY92930
 ID AAY92930 standard; Protein; 600 AA.
 AC AAY92930;
 XX
 XX 25-OCT-2000 (first entry)
 DT
 DE Annexin V/urokinase fusion protein.
 XX
 KW Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;
 KW urokinase; insect cell; fibrinolysis.
 OS Unidentified.
 XX
 XX CN1247195-A.
 XX
 XX 15-MAR-2000.
 PD
 XX
 XX 12-MAR-1999; 99CN-0113524.
 PF
 XX
 PR 12-MAR-1999; 99CN-0113524.
 XX
 XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
 PA

XX
 PI Wu X, Sun J, Yang G;
 XX
 DR WPI; 2000-413098/36.
 DR N-PSDB; AAA11241.
 XX
 PT New thrombolytic fusion protein for targeting thrombus - comprises
 PT fusion of Annexin V and urokinase
 XX
 PS Claim 2; Page 2-4; 20pp; Chinese.
 XX
 CC Annexin V, which has high affinity for active thrombocytes, is used
 CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion
 CC protein. The protein (this sequence) is the result of expression of a
 CC fusion gene comprising the Annexin V gene and a low-molecular urokinase
 CC gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed
 CC in insect cell strain Tn-5B1-4, has high affinity for active thrombocytes
 CC and has the fibrinolytic activity of urokinase.
 XX
 SQ Sequence 600 AA;
 Query Match 96.8%; Score 1587; DB 21; Length 600;
 Best Local Similarity 99.4%; Pred. No. 1.7e-137;
 Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDDEESILTLTSRQAQOEISAFAFKTL 67
 DB 281 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDDEESILTLTSRQAQOEISAFAFKTL 340
 QY 68 FGRDLDDLLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
 DB 341 FGRDLDDLLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 400
 QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYTYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187
 DB 401 ELRAIKQVYEEYEGSSLEDDVVGDTSGYTYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 460
 QY 188 QAGELKWGTDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGQIETIDRETSGNLEQLLAV 247
 DB 461 QAGELKWGTDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGQIETIDRETSGNLEQLLAV 520
 QY 248 VKSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 307
 DB 521 VKSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 580
 QY 308 KGDTSGDYKKALLLGGEDD 327
 DB 581 KGDTSGDYKKALLLGGEDD 600
 RESULT 12
 AAP82317
 ID AAP82317 standard; protein; 320 AA.
 XX
 AC AAP82317;
 XX
 XX 25-MAR-2003 (updated)
 DT 13-NOV-1990 (first entry)
 DE
 DE PAP-I isolated from biological fluid, used as anticoagulant.
 XX
 KW PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;
 KW phospholipase A2; disseminated intravascular coagulation;
 KW deep vein thrombosis.
 XX
 OS Homo sapiens.
 XX
 XX WO805659-A.
 PN
 XX
 PD 11-AUG-1988.
 XX
 XX 05-FEB-1988; 88WO-US00340.
 PF
 XX

PR 06-FEB-1987; 87US-0011782.
 PR 05-JUN-1987; 87US-0059355.
 XX (ZYM) ZYMOGENETICS INC.
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Fujikawa K, Iranl MH, Carter BLA;
 XX WPI; 1988-235049/33.
 DR N-PSDB; AAN82107.
 XX
 PT Human proteins having anticoagulant and antiinflammatory activity -
 PT isolated from biological fluid by anion-exchange chromatographoc media.
 XX
 PS Disclosure: Page ?; ?pp; English.
 XX
 CC The protein does not contain a leader peptide sequence,
 CC indicating that PAP-I is probably not constitutively secreted.
 CC The Met residue is removed at in a post-translational event and the
 CC newly formed NH2-terminal Ala residue is blocked by acetylation.
 CC It binds to phospholipid and inhibits phospholipase A2.
 CC The protein can substitute heparin or other anticoagulants in
 CC the treatment of disseminated intravascular coagulation, deep vein
 CC thrombosis, or other disorders. It also has antiinflammatory
 CC properties.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 320 AA;
 Query Match 96.8%; Score 1586; DB 9; Length 320;
 Best Local Similarity 99.4%; Pred. No. 8.5e-138;
 Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 MAOVLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 67
 DB 1 MAOVLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 60
 QY 68 FGRLDLDLKSLETKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
 DB 61 FGRLDLDLKSLETKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
 QY 128 ELRAIKQVVEEYGSSEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVVEEYGSSEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
 QY 188 QAGELKMGTDDEKFTIFGTRSVSHLRKVFQKYMITSFGFQIEETIDRETSGNLEQLLAV 247
 DB 181 QAGELKMGTDDEKFTIFGTRSVSHLRKVFQKYMITSFGFQIEETIDRETSGNLEQLLAV 240
 QY 248 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVMSRSSEIDLFNIRKFRKFNATSLYSMI 307
 DB 241 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVMSRSSEIDLFNIRKFRKFNATSLYSMI 300
 QY 308 KGTSGDYKKALLLLSGEDD 327
 DB 301 KGTSGDYKKALLLLCGEDD 320
 RESULT 13
 AAR26276
 ID AAR26276 standard; protein; 319 AA.
 XX
 AC AAR26276;
 XX
 DT 10-MAR-2003 (updated)
 DT 04-FEB-1993 (first entry)
 XX
 DE CPB-I.
 XX
 KW CPB-I; stabilisation; frozen; molten; processed; activity.
 XX
 OS Homo sapiens.
 XX

PN JP04198195-A.
 XX 17-JUL-1992.
 PD
 XX 28-NOV-1990; 90JP-0328286.
 PF
 XX 28-NOV-1990; 90JP-0328286.
 PR
 XX (KAGA) KAGAKU OYOBI KESSEI RYOH.
 PA (KOWA) KOWA CO LTD.
 XX
 DR WPI; 1992-288937/35.
 XX
 PT Stabilisation of CPB-I for drug compan. - by adding basic
 PT aminoacid selected from lysine, arginine and/or ornithine
 XX
 PS Disclosure: Page 2; 4pp; Japanese.
 XX
 CC The sequence given is the amino acid sequence of CPB-I. CPB-I was
 CC used within a method which involved adding basic amino acids to it
 CC which resulted in its stabilisation. This lead to the production of
 CC CPB-I which keeps its activity when it is frozen, molten or has been
 CC processed by several procedures.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 319 AA;
 Query Match 96.7%; Score 1585; DB 13; Length 319;
 Best Local Similarity 99.7%; Pred. No. 1e-137;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 AQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 68
 DB 1 AQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 60
 QY 69 GRDLDDLDKSELTKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEE 128
 DB 61 GRDLDDLDKSELTKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEE 120
 QY 129 LRAIKQVVEEYGSSEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKQVVEEYGSSEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 180
 QY 189 AGELKMGTDDEKFTIFGTRSVSHLRKVFQKYMITSFGFQIEETIDRETSGNLEQLLAV 248
 DB 181 AGELKMGTDDEKFTIFGTRSVSHLRKVFQKYMITSFGFQIEETIDRETSGNLEQLLAV 240
 QY 249 KSIRSIAPYLAETLYYAMKAGTDDHTLIRVMSRSSEIDLFNIRKFRKFNATSLYSMIK 308
 DB 241 KSIRSIAPYLAETLYYAMKAGTDDHTLIRVMSRSSEIDLFNIRKFRKFNATSLYSMIK 300
 QY 309 GDTSGDYKKALLLLSGEDD 327
 DB 301 GDTSGDYKKALLLLCGEDD 319
 RESULT 14
 AAR41021
 ID AAR41021 standard; protein; 319 AA.
 XX
 AC AAR41021;
 XX
 DT 29-MAR-1994 (first entry)
 DT
 DE Calphobindin I (CPB-I).
 XX
 KW Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
 XX
 OS Homo sapiens.
 XX
 PN JP05213769-A.
 XX
 PD 24-AUG-1993.

XX 04-FEB-1992; 92JP-0019032.
 XX
 XX 04-FEB-1992; 92JP-0019032.
 XX
 XX (KOWA) KOWA CO LTD.
 XX (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO.
 XX WPI; 1993-299558/38.
 XX
 XX Protein kinase C inhibitor effective against malignant tumours -
 PT contg. (opt. recombinant) calphobindin I
 XX
 XX Claim 1; Page 2-3; 6pp; Japanese.
 XX
 XX Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)
 CC inhibits protein kinase C (PKC) and is useful in the treatment of
 CC malignant tumours caused by abnormal activation of PKC. CPB-I is
 CC extracted from human or animal organs and may be applied
 CC intravenously, orally, intramuscularly, percutaneously or rectally.
 XX
 XX Sequence 319 AA;
 SQ

Query Match 96.7%; Score 1585; DB 14; Length 319;
 Best Local Similarity 99.7%; Pred. No. 1e-137;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNAQROEISAAFKTLF 68
 DB 1 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNAQROEISAAFKTLF 60
 QY 69 GRLLDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
 DB 61 GRLLDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 120
 QY 129 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
 QY 189 AGELKNGTDEEKFITFGTRSVSHLRKVFDKYMTISGFOEETIDRETSGNLEQLLAVV 248
 DB 181 AGELKNGTDEEKFITFGTRSVSHLRKVFDKYMTISGFOEETIDRETSGNLEQLLAVV 240
 QY 249 KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKKEFRKNFATSLYSMIK 308
 DB 241 KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKKEFRKNFATSLYSMIK 300
 QY 309 GDTSGDYKKALLLLSGEDD 327
 DB 301 GDTSGDYKKALLLLCGEDD 319

RESULT 15

ABG32550
 ID ABG32550 standard; protein; 319 AA.

XX AC ABG32550;

XX DT 29-NOV-2002 (first entry)

XX DE Human CPB-1 protein.

XX KW Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
 XX KW calcium/phospholipid binding protein; polyhydric alcohol.

XX OS Homo sapiens.

XX FN WO200267977-A1.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-JP01563.

XX

PR 26-FEB-2001; 2001JP-0050297.
 XX
 XX (KOWA) KOWA CO LTD.
 PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX
 XX Naruse H, Sano M, Shinoda Y, Inagi T;
 XX WPI; 2002-674988/72.
 XX
 XX Eye drops for treating e.g. corneal diseases, contain CPB-I and
 PT polyhydric alcohol with specific carbonyl value, without unpleasant
 PT irritation upon dropping but with satisfactory long-term storability -
 XX
 XX Disclosure; Page 13-14; 16pp; Japanese.
 PS
 XX The invention relates to eye drops contain CPB-I (anexin V) and a
 CC polyhydric alcohol having a carbonyl value of not more than
 CC Smicro Mol./g. The eye drops are for treating e.g. corneal diseases.
 CC Such eye drops are without unpleasant irritation upon dropping but with
 CC satisfactory long-term storage stability. The present sequence is
 CC the human CPB-I (calcium/phospholipid binding) protein.
 XX
 XX Sequence 319 AA;
 SQ

Query Match 96.7%; Score 1585; DB 23; Length 319;
 Best Local Similarity 99.7%; Pred. No. 1e-137;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNAQROEISAAFKTLF 68
 DB 1 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNAQROEISAAFKTLF 60
 QY 69 GRLLDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
 DB 61 GRLLDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 120
 QY 129 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
 QY 189 AGELKNGTDEEKFITFGTRSVSHLRKVFDKYMTISGFOEETIDRETSGNLEQLLAVV 248
 DB 181 AGELKNGTDEEKFITFGTRSVSHLRKVFDKYMTISGFOEETIDRETSGNLEQLLAVV 240
 QY 249 KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKKEFRKNFATSLYSMIK 308
 DB 241 KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLNFIRKKEFRKNFATSLYSMIK 300
 QY 309 GDTSGDYKKALLLLSGEDD 327
 DB 301 GDTSGDYKKALLLLCGEDD 319

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(without alignments)
1037.674 Million cell updates/sec

Title: US-09-970-969-2

Perfect score: 1639

Sequence: 1 MACGGHMAQVLRGTVDFF.....KGTSGDYKKALLLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639	100.0	327	4	US-09-324-096A-2
2	1630	99.5	327	4	US-09-324-096A-6
3	1618	98.7	327	4	US-09-324-096A-4
4	1590	97.0	320	1	US-08-125-746-3
5	1590	97.0	320	4	US-08-948-276-1
6	1590	97.0	320	6	5225537-4
7	1585	96.7	319	1	US-08-125-746-1
8	1479.5	90.3	319	4	US-08-948-276-2
9	1455.5	88.8	318	4	US-08-948-276-3
10	1448.5	88.4	319	2	US-08-149-975A-2
11	923	56.3	321	4	US-08-948-276-4
12	914	55.8	319	3	US-08-526-136-14
13	865	52.8	503	3	US-08-526-136-2
14	865	52.8	505	3	US-08-526-136-4
15	802.5	49.0	323	4	US-08-948-276-5
16	779	47.5	466	3	US-08-526-136-13
17	643	39.2	346	4	US-08-948-276-6
18	377.5	23.0	315	4	US-09-325-932A-62
19	245.5	15.0	239	4	US-09-325-932A-65
20	232	14.2	184	4	US-09-325-932A-66
21	130	7.9	849	4	US-09-157-257-4
22	120	7.3	111	4	US-09-325-932A-63
23	109	6.7	73	4	US-09-325-932A-64
24	106.5	6.5	701	3	US-08-923-511-2
25	106.5	6.5	701	4	US-09-416-874A-2
26	105.5	6.4	533	3	US-09-603-185-2
27	105.5	6.4	539	4	US-09-157-257-6

28	103.5	6.3	501	4	US-09-157-257-8	Sequence 8, Appli
29	101.5	6.2	421	4	US-09-252-991A-26478	Sequence 26478, A
30	100.5	6.1	504	4	US-09-234-245-4	Sequence 4, Appli
31	99.5	6.1	504	4	US-09-234-245-2	Sequence 2, Appli
32	99.5	6.1	1051	3	US-08-965-762-14	Sequence 14, Appli
33	99.5	6.1	1051	4	US-09-911-927-14	Sequence 14, Appli
34	99.5	6.1	1051	4	US-09-911-888-14	Sequence 14, Appli
35	99.5	6.1	1051	4	US-09-911-888-14	Sequence 14, Appli
36	99	6.0	498	4	US-08-858-207A-310	Sequence 310, App
37	98.5	6.0	1056	4	US-09-595-684B-29	Sequence 29, Appli
38	98	6.0	2270	4	US-09-581-909-3	Sequence 3, Appli
39	95.5	5.8	900	2	US-08-630-822A-62	Sequence 62, Appli
40	95.5	5.8	900	2	US-09-005-069-62	Sequence 62, Appli
41	95.5	5.8	900	4	US-09-171-156A-21	Sequence 21, Appli
42	95.5	5.8	900	4	US-09-004-730A-21	Sequence 21, Appli
43	95.5	5.8	900	4	US-08-981-799A-21	Sequence 21, Appli
44	95.5	5.8	1057	3	US-09-541-782-10	Sequence 10, Appli
45	95.5	5.8	1057	4	US-09-723-820-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-324-096A-2
; Sequence 2, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-2

Query Match	100.0%	Score 1639;	DB 4;	Length 327;
Best Local Similarity	100.0%	Pred. No. 1.8e-150;		
Matches	327;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Qy	1	MACGGHMAQVLRGTVDFFPGFDERADAETLRKAMKGLGTDEESILTLTTSR	NAQROEI	60
Db	1	MACGGHMAQVLRGTVDFFPGFDERADAETLRKAMKGLGTDEESILTLTTSR	NAQROEI	60
Qy	61	SAAFKTLFGRDLDDKSELTKFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI	120	
Db	61	SAAFKTLFGRDLDDKSELTKFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI	120	
Qy	121	IASRTPRELRAIKQVYEEYSGSLFDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVE	180	
Db	121	IASRTPRELRAIKQVYEEYSGSLFDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVE	180	
Qy	181	QDAQALFOAGELKMGTDDEEKFTITFGTRSVSHLRKVPDKYMTISGFTTEETIDRTS	GNL	240
Db	181	QDAQALFOAGELKMGTDDEEKFTITFGTRSVSHLRKVPDKYMTISGFTTEETIDRTS	GNL	240
Qy	241	EQLLAVVKSIRSPAYLAETLYYAMKAGTDDHTLIRVWVSRSFIDLNRKPKFNFA	300	
Db	241	EQLLAVVKSIRSPAYLAETLYYAMKAGTDDHTLIRVWVSRSFIDLNRKPKFNFA	300	
Qy	301	TSLSYSMIKGDTSGDYKKALLLLSGEDD	327	
Db	301	TSLSYSMIKGDTSGDYKKALLLLSGEDD	327	

RESULT 2

US-09-324-096A-6

; Sequence 6, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-6

Query Match 99.5%; Score 1630; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.3e-149;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MAGCGGHAQVLRTGVTDFPGDERADAE	TLRKAMKGLGTDEESILTLTSRSNAQOEI	60
DB	1	MAGCGGHAQVLRTGVTDFPGDERADAE	TLRKAMKGLGTDEESILTLTSRSNAQOEI	60
QY	61	SAAFKTLFGDRLLDLKSELTKGFEKLI	VALMKPSRLYDAYELKHALKAGTNEKVLTEI	120
DB	61	SAAFKTLFGDRLLDLKSELTKGFEKLI	VALMKPSRLYDAYELKHALKAGTNEKVLTEI	120
QY	121	IASRTPPEELRAIKQVYEEYEGSLED	VVGDTSGYYQRMVLVLLQANRPDAGIDEAQVE	180
DB	121	IASRTPPEELRAIKQVYEEYEGSLED	VVGDTSGYYQRMVLVLLQANRPDAGIDEAQVE	180
QY	181	QDAQALFOAGELKMGTDDEKFTIFG	TRSVSHLRKVFDDKVTMTISGFOIETIDRETSGNL	240
DB	181	QDAQALFOAGELKMGTDDEKFTIFG	TRSVSHLRKVFDDKVTMTISGFOIETIDRETSGNL	240
QY	241	EQLLLAVVKSIRSIPAYLAETLIYAM	KGAGTDDHTLIRVMSRSEIDLNFNIRKEPRKFA	300
DB	241	EQLLLAVVKSIRSIPAYLAETLIYAM	KGAGTDDHTLIRVMSRSEIDLNFNIRKEPRKFA	300
QY	301	TSLSYMIKGTSGDYKKALLLSGDD	327	
DB	301	TSLSYMIKGTSGDYKKALLLSGDD	327	

RESULT 3

US-09-324-096A-4
; Sequence 4, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-4

Query Match 98.7%; Score 1618; DB 4; Length 327;
Best Local Similarity 99.4%; Pred. No. 1.9e-148;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MAGCGGHAQVLRTGVTDFPGDERADAE	TLRKAMKGLGTDEESILTLTSRSNAQOEI	60
DB	1	MAGCGGHAQVLRTGVTDFPGDERADAE	TLRKAMKGLGTDEESILTLTSRSNAQOEI	60

QY	61	SAAFKTLFGDRLLDLKSELTKGFEKLI	VALMKPSRLYDAYELKHALKAGTNEKVLTEI	120
DB	61	SAAFKTLFGDRLLDLKSELTKGFEKLI	VALMKPSRLYDAYELKHALKAGTNEKVLTEI	120
QY	121	IASRTPPEELRAIKQVYEEYEGSLED	VVGDTSGYYQRMVLVLLQANRPDAGIDEAQVE	180
DB	121	IASRTPPEELRAIKQVYEEYEGSLED	VVGDTSGYYQRMVLVLLQANRPDAGIDEAQVE	180
QY	181	QDAQALFOAGELKMGTDDEKFTIFG	TRSVSHLRKVFDDKVTMTISGFOIETIDRETSGNL	240
DB	181	QDAQALFOAGELKMGTDDEKFTIFG	TRSVSHLRKVFDDKVTMTISGFOIETIDRETSGNL	240
QY	241	EQLLLAVVKSIRSIPAYLAETLIYAM	KGAGTDDHTLIRVMSRSEIDLNFNIRKEPRKFA	300
DB	241	EQLLLAVVKSIRSIPAYLAETLIYAM	KGAGTDDHTLIRVMSRSEIDLNFNIRKEPRKFA	300
QY	301	TSLSYMIKGTSGDYKKALLLSGDD	327	
DB	301	TSLSYMIKGTSGDYKKALLLSGDD	327	

RESULT 4

US-08-125-746-3
; Sequence 3, Application US/08125746
; Patent No. 5591633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IWASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 037227/1987
; FILING DATE: 20-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184426/1987
; FILING DATE: 23-JUL-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5591633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-125-746-3

Query Match 97.0%; Score 1590; DB 1; Length 320;
 Best Local Similarity 99.7%; Pred. No. 9.5e-146;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MAQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSRNSAQRQEIISAAPKTL 67
 Db 1 MAQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSRNSAQRQEIISAAPKTL 60

Qy 68 FGRDLLDLKSELGKPEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
 Db 61 FGRDLLDLKSELGKPEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120

Qy 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187
 Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180

Qy 188 QAGELKWTDEEKEFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 247
 Db 181 QAGELKWTDEEKEFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 240

Qy 248 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMYSRSEIDLFIKPKFKNFATSLYSMI 307
 Db 241 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMYSRSEIDLFIKPKFKNFATSLYSMI 300

Qy 308 KGDTSGDYKKALLLLSGEDD 327
 Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 5
 US-08-948-276-1
 ; Sequence 1, Application US/08948276
 ; Patent No. 6511829
 ; GENERAL INFORMATION:
 ; APPLICANT: Ernst, Joel D.
 ; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
 ; FILE REFERENCE: UCSF97-113
 ; CURRENT APPLICATION NUMBER: US/08/948.276
 ; CURRENT FILING DATE: 1997-10-09
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: human
 US-08-948-276-1

Query Match 97.0%; Score 1590; DB 4; Length 320;
 Best Local Similarity 99.7%; Pred. No. 9.5e-146;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MAQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSRNSAQRQEIISAAPKTL 67
 Db 1 MAQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSRNSAQRQEIISAAPKTL 60

Qy 68 FGRDLLDLKSELGKPEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
 Db 61 FGRDLLDLKSELGKPEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120

Qy 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187
 Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180

Qy 188 QAGELKWTDEEKEFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 247
 Db 181 QAGELKWTDEEKEFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 240

Qy 248 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMYSRSEIDLFIKPKFKNFATSLYSMI 307
 Db 241 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMYSRSEIDLFIKPKFKNFATSLYSMI 300

Qy 308 KGDTSGDYKKALLLLSGEDD 327
 Db 301 KGDTSGDYKKALLLLCGEDD 320

Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 6
 5225537-4
 ; Patent No. 5225537
 ; APPLICANT: FOSTER, DONALD
 ; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
 ; PHOSPHOLIPID-BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 14
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/459,082
 ; FILING DATE: 29-DEC-1989
 ; SEQ ID NO: 4
 ; LENGTH: 320
 5225537-4

Query Match 97.0%; Score 1590; DB 6; Length 320;
 Best Local Similarity 99.7%; Pred. No. 9.5e-146;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MAQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSRNSAQRQEIISAAPKTL 67
 Db 1 MAQVLRGVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSRNSAQRQEIISAAPKTL 60

Qy 68 FGRDLLDLKSELGKPEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
 Db 61 FGRDLLDLKSELGKPEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120

Qy 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187
 Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180

Qy 188 QAGELKWTDEEKEFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 247
 Db 181 QAGELKWTDEEKEFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 240

Qy 248 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMYSRSEIDLFIKPKFKNFATSLYSMI 307
 Db 241 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMYSRSEIDLFIKPKFKNFATSLYSMI 300

Qy 308 KGDTSGDYKKALLLLSGEDD 327
 Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 7
 US-08-125-746-1
 ; Sequence 1, Application US/08125746
 ; Patent No. 5591633
 ; GENERAL INFORMATION:
 ; APPLICANT: SAINO, YUSHI
 ; APPLICANT: IWASAKI, AKIO
 ; APPLICANT: SODA, MAKOTO
 ; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MALER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/125,746
 ; FILING DATE: 24-SEP-1993
 ; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/807,623
;; FILING DATE: 13-DEC-1991
;; PRIOR APPLICATION DATA: JP 037227/1987
;; APPLICATION NUMBER: JP 037227/1987
;; FILING DATE: 20-FEB-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 184428/1987
;; FILING DATE: 23-JUL-1987
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Orlon, No. 5591633man F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 319 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-125-746-1

Query Match 96.7%; Score 1585; DB 1; Length 319;
Best Local Similarity 99.7%; Pred. No. 2.9e-145;
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 AQLRGTVDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAFKTLF 69
DB 1 AQLRGTVDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAFKTLF 60
QY 69 GRLLDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
DB 61 GRLLDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120
QY 129 LRAIKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQ 188
DB 121 LRAIKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQ 180
QY 189 AGELKMGTDDEEKFTITFGTRSVSHLRKVFDDKYMTISGFOIETIDRETSGNLEQLLAVV 248
DB 181 AGELKMGTDDEEKFTITFGTRSVSHLRKVFDDKYMTISGFOIETIDRETSGNLEQLLAVV 240
QY 249 KSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFI NRKPKNFATSLYSMIK 308
DB 241 KSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFI NRKPKNFATSLYSMIK 300
QY 309 GDTSGDYKALLLLSGEDD 327
DB 301 GDTSGDYKALLLLCGEDD 319

RESULT 8
US-08-948-276-2
; Sequence 2, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PRT
; ORGANISM: mouse
US-08-948-276-2

Query Match 90.3%; Score 1479.5; DB 4; Length 319;

Best Local Similarity 93.7%; Pred. No. 4.6e-135;
Matches 296; Conservative 9; Mismatches 10; Indels 1; Gaps 1;
QY 13 RGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAFKTLFGRDL 72
DB 4 RGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAFKTLFGRDL 63
QY 73 LDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 132
DB 64 VDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELSAI 123
QY 133 KOVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQAGEL 192
DB 124 KOVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQAGEL 183
QY 193 KMGTDDEEKFTITFGTRSVSHLRKVFDDKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252
DB 184 KMGTDDEEKFTITFGTRSVSHLRKVFDDKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 243
QY 253 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFI NRKPKNFATSLYSMIKGDTS 312
DB 244 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFI NRKPKNFATSLYSMIKGDTS 303
QY 313 GDYKALLLL-SGEDD 327
DB 304 GDYKALLLLCGEDD 319

RESULT 9
US-08-948-276-3
; Sequence 3, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 318
; TYPE: PRT
; ORGANISM: rat
US-08-948-276-3

Query Match 88.8%; Score 1455.5; DB 4; Length 318;
Best Local Similarity 91.8%; Pred. No. 9.6e-133;
Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
QY 12 LRGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAFKTLFGRD 71
DB 2 LRGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAFKTLFGRD 61
QY 72 LDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 131
DB 62 LYNDKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 121
QY 132 IKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQAGE 191
DB 122 IKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQAGE 181
QY 192 LKMGTDDEEKFTITFGTRSVSHLRKVFDDKYMTISGFOIETIDRETSGNLEQLLAVVKS 251
DB 182 LKMGTDDEEKFTITFGTRSVSHLRKVFDDKYMTISGFOIETIDRETSGNLEQLLAVVKS 241
QY 252 RSIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFI NRKPKNFATSLYSMIKGD 311
DB 242 RSIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFI NRKPKNFATSLYSMIKGD 301
QY 312 SGDYKALLLL-SGEDD 327
DB 302 SGDYKALLLLCGEDD 318

RESULT 10

US-08-149-975A-2
; Sequence 2, Application US/08149975A
; Patent No. 5849600
; GENERAL INFORMATION:
; APPLICANT: Nixon, Ralph
; APPLICANT: Honda, Toshiyuki
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149.975A
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-149-975A-2

Query Match 88.4%; Score 1448.5; DB 2; Length 319;
Best Local Similarity 91.5%; Pred. No. 4.6e-132;
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 12 LRGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGRD 71
Db 3 LRGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGRD 62
QY 72 LDDLKSELTKFEKLIYALKMPSRLYDAYELKHALKAGCTNEKVLTEIIASRTPEELRA 131
Db 63 LVNDKMKSETKFEKLIYALKMPSRLYDAYELKHALKAGCTNEKVLTEIIASRTPEELRA 122
QY 132 IQVYEEYSGSLEDVVGDTSYVQRMVLLQANRPDPAGIDEAOVEODAALFQAGE 191
Db 123 IQVYEEYSGSLEDVVGDTSYVQRMVLLQANRPDPAGIDEAOVEODAALFQAGE 182
QY 192 LKMGDEKFTITFGTRSVSHLRKVFQKYMISGFOIEETIDRETSGNLEQLLAVVRSI 251
Db 183 LKMGDEKFTITFGTRSVSHLRKVFQKYMISGFOIEETIDRETSGNLEQLLAVVRSI 242
QY 252.RSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEPKNFATSLYSMIKGD 311
Db 243 RSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEPKNFATSLYSMIKGD 302
QY 312 SGDKYKALLLL-SGDD 327
Db 303 SGDKYKALLLLCGGDD 319

RESULT 11

US-08-948-276-4
; Sequence 4, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: human
US-08-948-276-4

Query Match 56.3%; Score 923; DB 4; Length 321;
Best Local Similarity 58.3%; Pred. No. 3.2e-81;
Matches 183; Conservative 53; Mismatches 78; Indels 0; Gaps 0;
QY 14 GTVTDFPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGDLL 73
Db 8 GTVKAASGCFNAMEDAQTLRKAMKGLGTDEDAISVLAIRNTAQRQEIATYKSTIGRDLI 67
QY 74 DDLKSELTKFEKLIYALKMPSRLYDAYELKHALKAGCTNEKVLTEIIASRTPEELRAIK 133
Db 68 DDLKSELSGNFQIVGMNPTVLYDQVELFRAMKAGTDEGCLTEILASRTPEIRIRIS 127
QY 134 QVYREYSGSLEDVVGDTSYVQRMVLLQANRPDPAGIDEAOVEODAALFQAGE 193
Db 128 QYQYQYGRSLEDVIRSDTSPMFQVLYSLSGGDEGNYLDDALVRODQADLYAGEKK 187
QY 194 WGTDEEKFTITFGTRSVSHLRKVFQKYMISGFOIEETIDRETSGNLEQLLAVVKSINS 253
Db 188 WGTDEVKFELTVLCSSRNHLLHVFDEYKRSIQKDEQSTKSETSGSFEDALLAIVKCMRN 247
QY 254 IPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEPKNFATSLYSMIKGDTS 313
Db 248 KSAFPAEKLYKSMKGLGDDNPTLIRVWVSRAEIDMLDIRAHFKRLYKSLYSFIKGDTS 307
QY 314 DYKKAALLLSGDD 327
Db 308 DYKRVLLVLCGDD 321

RESULT 12

US-08-526-136-14
; Sequence 14, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; US-08-526-136-14

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Query Match 55.8%; Score 914; DB 3; Length 319;
Best Local Similarity 56.0%; Pred. No. 2.3e-80;
Matches 182; Conservative 51; Mismatches 81; Indels 0; Gaps 0;

QY 14 GTVTDFPGDERADAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRLD 73
DB 6 GTVKAASGNAEDAOTLRKAMKGLGTDEDAIINVLAYSTAQRIYAKTTIGRDLM 65
QY 74 DDLKSELTKFEKLIYAKMPSRLYDAYELKHALKGAGNEKVLTEIIASRTPEELRAI 133
DB 66 DDLKSELGNFEQVILGMMTPTVLYDQELRKAMKAGTDEGLIEILASRTPEELRIN 125
QY 134 QYVEEYEGSSLEDDVVGDTSGYQYRMVLVLOANRPDAGIDEAQVEQDAALFOAGELK 193
DB 126 QYVQLQYGRSLDDIIRSDTSFMFORVLVLSAGGRDESNYLDDALMRQADQIYAGEKK 185
QY 194 WGTDEKFTITIGTSVSHLRKRVFKYMTISGQIEETIDRETSGNLEQLLAVVKSIRS 253
DB 186 WGTDEKFTLVLCSSRNHLHVFDEYKRIAQDIEQSIKSETSGSFEDALLAIVKCMRN 245
QY 254 IPAYLAETLYAMKAGTDDHLLIRVWVSREIDLENIRKEPKNFATSLYSMIKGTSG 313
DB 246 KSAYFAERLYKSMKGLGTDOTTLIRVWVSRAEIDMLDIRANFKRLYKSLYSPIKGTSG 305
QY 314 DYKALLLLSGDD 327
DB 306 DYKVLILLGGDD 319

```

```

RESULT 13
US-08-526-136-2
; Sequence 2, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555x
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503
; TYPE: amino acid
; TOPOLOGY: N/A
; US-08-526-136-2

Query Match 52.8%; Score 865; DB 3; Length 503;
Best Local Similarity 54.9%; Pred. No. 2.5e-75;
Matches 173; Conservative 58; Mismatches 84; Indels 0; Gaps 0;

QY 13 RGVTFPPGDERADAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRLD 72
DB 189 RGVTFPPGDERADAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRLD 248
QY 73 LDKSELTKFEKLIYAKMPSRLYDAYELKHALKGAGNEKVLTEIIASRTPEELRAI 132
DB 249 IKDLKSELGNFEQVILGMMTPTVLYDQELRKAMKAGTDEGLIEILASRTPEELRIN 308
QY 133 QYVEEYEGSSLEDDVVGDTSGYQYRMVLVLOANRPDAGIDEAQVEQDAALFOAGEL 192
DB 309 NRVYEFKFTLVLCSSRNHLHVFDEYKRIAQDIEQSIKSETSGSFEDALLAIVKCMRN 368
QY 193 KAGTDEKFTITIGTSVSHLRKRVFKYMTISGQIEETIDRETSGNLEQLLAVVKSIR 252
DB 369 RGVTFPPGDERADAETLRKAMKGLGTDEESILTLTSRQAQRQISAAFKTLFGRLD 428
QY 253 SIPAYLAETLYAMKAGTDDHLLIRVWVSREIDLENIRKEPKNFATSLYSMIKGTSG 312
DB 429 NTPAFAERLYKSMKGLGTDOTTLIRVWVSRAEIDMLDIRANFKRLYKSLYSPIKGTSG 488
QY 313 GYKALLLLSGDD 327
DB 489 GYKVLILLGGDD 503

```

```

RESULT 14
US-08-526-136-4
; Sequence 4, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555x
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-4

Query Match 52.8%; Score 865; DB 3; Length 505;
Best Local Similarity 54.9%; Pred. No. 2.5e-75;
Matches 173; Conservative 58; Mismatches 84; Indels 0; Gaps 0;
QY 13 RGVTPDPGDERADAEITLTKAMKGLTDEESILTLTSSNAQORQISAFKTLFGROL 72
Db 191 RGTITDASGDFDLRDAEVLRLKAMKGFCTDEQAIDCLGSRNKRQOQILLSFKTAYGKDL 250
QY 73 LDCLKSLTKGFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
Db 251 IKDLKSLSNFETILALMKTPVLFDAEIKAKRGAGTDEACLEILASRSNEHIREL 310
QY 133 KQYEEYSGSLEDVVGDTSYGYQRMVLLQANRPDAGIDEAOVEODQAALFQAGEL 192
Db 311 NRVYKTEFKTLEEAIRSDTSGHFORLLISLQGNRDESTNVDMLVQDVQELYAAGEN 370
QY 193 KWTDEKFTITGTRSVSHLRKVKFYMTISGFIQIETDRETSGNLEQLLAVKSIK 252
Db 371 RLCTDESKFNAILCSRAHLVAVFNEYQRTGRIEKSICREMSGDLQGLAVVVKCLK 430
QY 253 SIPAYLAETLYYAMKAGTDDHTLIRVWVSERSEIDLNFIRKEPKNFATSLYSMIKGDTS 312
Db 431 NTPAFFAERLNKAMRGAGTKDRTLIRVWVSERSEIDLDIRAEYKRLYKSLYHDTIGDTS 490
QY 313 GDYKALLLSGEDD 327
Db 491 GDYKILLKICGGND 505

RESULT 15
US-08-948-276-5
Sequence 5, Application us/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 323
TYPE: PRT
ORGANISM: human
US-08-948-276-5

Query Match 49.0%; Score 802.5; DB 4; Length 323;
Best Local Similarity 49.4%; Pred. No. 1.5e-69;
Matches 159; Conservative 61; Mismatches 97; Indels 5; Gaps 1;
QY 6 GHMAQVLRGTVTDPFGDERADAEITLTKAMKGLTDEESILTLTSSNAQORQISAFK 65
Db 7 GH-----RGTVRDYDPDFSPSVDAAIQAKIRGIGTDEKMLTSLTSSNAQORQLIVKEYQ 61
QY 66 TLFGRDLDDLKSELTKGFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRT 125
Db 62 AAYGKELKDDLKGDLSGHFEHLVALVTPPAVFDKOLKSKMKGAGTNEALIEILTTRT 121
QY 126 PEELRAIKQYEEYSGSLEDVVGDTSYGYQRMVLLQANRPDAGIDEAOVEODQAAL 185
Db 122 SRQMKDISQAYTVYVYKSLGDDISSETSGDFRKALLTLADGRDRDESLKVDHLAKQDAQI 181
QY 186 LFOAGELKMGCTDEKFTITGTRSVSHLRKVKFYMTISGFIQIETDRETSGNLEQLL 245
Db 182 LYKAGENRWGTDEDKFTIILCLRSFPQKLTFEYRNISQKDIVDSIKGELSGHFEDLL 241
QY 246 AVYKSIKSIIPAYLAETLYYAMKAGTDDHTLIRVWVSERSEIDLNFIRKEPKNFATSLYS 305
Db 242 AIVNCYENTPAFLAERLHRAKLGIGTDEFTLNRIMVSRSEIDLDIRTEFKKHGYGSLYS 301
QY 306 MIKGDTSYKKAALLSGEDD 327
Db 302 AIKSDTSGDYEITLLKICGGDD 323

Search completed: August 22, 2003, 21:37:04
Job time : 20.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2003, 21:30:17 ; Search time 15 seconds
(without alignments)
2096.477 Million cell updates/sec

Title: US-09-970-969-2

Perfect score: 1639

Sequence: 1 MACGGHMAQVLRGTVDFFP.....KGDTSQDYKALLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1590	97.0	320	1 AQHUP	annexin V [validat
2	1536.5	93.7	320	1 S27214	annexin V - bovine
3	1455.5	88.8	319	1 LUR5	annexin V - rat
4	1279	78.0	321	1 LUCH5	annexin V - chicke
5	932	56.9	673	1 AQH068	annexin VI [valida
6	932	56.9	673	1 S01786	annexin VI - mouse
7	923	56.3	321	1 A42077	annexin IV - human
8	921	56.2	318	1 LUPGA	annexin IV - pig
9	921	56.2	318	1 S52844	annexin VI - rat
10	914	55.8	319	1 LUB04	annexin IV - bovin
11	896.5	54.7	671	2 JC2029	annexin - chicken
12	865	52.8	503	1 LUB011	annexin XI form A
13	865	52.8	503	1 S23447	annexin XI form B
14	863	52.7	503	1 LURB11	annexin XI - rabbi
15	855	52.2	505	2 A53152	annexin XI - human
16	831.5	50.7	327	1 LUB08	annexin VIII - huma
17	802.5	49.0	323	1 LUB03	annexin III - huma
18	779	47.5	488	1 LUB07	annexin VII, long
19	775	47.3	324	1 LUR73	annexin III - rat
20	773	47.2	463	2 S29170	annexin VII - mous
21	718	43.8	316	1 LUB12	annexin XII - Hydr
22	711	43.4	512	2 S70644	annexin VII - Afri
23	709	43.3	676	2 S41022	hypothetical prote
24	698.5	42.6	339	1 LUB036	annexin II - human
25	694.5	42.4	339	1 LUB036	annexin II - bovin
26	693.5	42.3	339	2 S33700	annexin II - rat
27	691.5	42.2	339	1 LUB036	annexin II - mouse
28	682.5	41.6	341	2 S55277	annexin II - rat
29	682	41.6	296	1 LUFF9	annexin IX - fruit

ALIGNMENTS

RESULT 1

AQHUP

annexin V [validated] - human
N;Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; place
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence.revision 30-Jun-1992 #text.change 08-Dec-2000
C;Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S06646;
R;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Brownin
J. Biol. Chem. 263, 10799-10811, 1988
A;Title: Five distinct calcium and phospholipid binding proteins share homology with
A;Reference number: A92659; MUID:88273202; PMID:2968983
A;Accession: D29250
A;Molecule type: mRNA
A;Residues: 1-320 <PEP>
R;Grundmann, U.; Abel, K.J.; Bohn, H.; Loebermann, H.; Lottspeich, F.; Kuepper, H.
Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988
A;Title: Characterization of cDNA encoding human placental anticoagulant protein (PPA
A;Reference number: A30206; MUID:88234495; PMID:2967495
A;Accession: A30206
A;Molecule type: mRNA
A;Residues: 1-320 <GRU>
A;Cross-references: GB:M19384; NID:g189614; PIDN:AA59545.1; PID:g189615
R;Kaplan, R.; Jaye, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.
J. Biol. Chem. 263, 8037-8043, 1988
A;Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phosphol
A;Reference number: A28076; MUID:88228020; PMID:2967291
A;Accession: A28076
A;Molecule type: mRNA
A;Residues: 1-320 <KAP>
A;Cross-references: GB:J03745; NID:g182111; PIDN:AA52386.1; PID:g182112
R;Maurer-Fogy, I.; Reutlingsperger, C.P.M.; Pieters, J.; Bodo, G.; Stratowa, C.; Hau
Eur. J. Biochem. 174, 585-592, 1988
A;Title: Cloning and expression of cDNA for human vascular anticoagulant, a Ca-depend
A;Reference number: S01016; MUID:88271329; PMID:2455636
A;Accession: S01016
A;Molecule type: mRNA
A;Residues: 1-320 <MAU>
A;Cross-references: EMBL:X12454; NID:g37636; PIDN:CAA30985.1; PID:g37637
A;Note: part of this sequence was confirmed by protein sequencing
R;Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
Biochemistry 26, 8087-8092, 1987
A;Title: Primary structure of human placental anticoagulant protein.
A;Reference number: A29417; MUID:88163463; PMID:2964863
A;Contents: amino-terminal acetylation
A;Accession: A29417
A;Molecule type: mRNA
A;Residues: 1-320 <FUN>
A;Cross-references: EMBL:M18366; NID:g179131; PIDN:AAA35570.1; PID:g179132
R;Iwasaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saino, Y.; Arai, K.; Mizoguchi, T.; S.
J. Biochem. 102, 1261-1273, 1987
A;Title: Structure and expression of cDNA for an inhibitor of blood coagulation isoia

annexin XIII, inte
annexin II type 2
annexin X - fruit
annexin II type 1
annexin XIIfa - do
annexin XIIfb - do
annexin XIIfc - do
annexin II - chick
annexin I - guinea
annexin I - human
annexin I - bovine
annexin I - rat
annexin I type 2 -
annexin I - mouse
protein ZC155.1 [1
annexin I type 1 -
annexin I - Rodent

30 679 41.4 316 1 LUHUIS
31 678.5 41.4 340 1 JQ1298
32 678 41.4 321 1 LUFF10
33 675.5 41.2 340 1 JQ1297
34 671 40.9 316 2 A57076
35 671 40.9 357 2 B57076
36 666.5 40.7 339 1 LUCH2
37 648 39.5 346 1 LUGP1
38 643 39.2 346 1 LUHU
39 643 39.2 346 1 S28228
40 632 38.6 346 1 LUR71
41 630 38.4 343 1 A44118
42 624 38.1 346 1 LUMS1
43 582 35.5 322 2 B88452
44 578.5 35.3 341 1 LUPV1
45 542 33.1 346 2 LUPJ1

A:Reference number: A41514; MUID:88139278; PMID:2963810
 A:Accession: A41514
 A:Molecule type: mRNA
 A:Residues: 1-320 <TWA>
 A:Cross-references: GB:D00172; NID:9219480; PIDN:BAA00122.1; PID:9219481
 A:Note: part of this sequence was confirmed by protein sequencing
 R:Schlaepfer, D.D.; Mehlan, T.; Burgess, W.H.; Haigler, H.T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987
 A:Title: Structural and functional characterization of endonexin II, a calcium- and phospholipid-binding protein
 A:Reference number: A28038; MUID:87317598; PMID:2957692
 A:Accession: A28038
 A:Molecule type: protein
 A:Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
 R:Ahn, N.G.; Teller, D.C.; Blenkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
 J. Biol. Chem. 263, 18657-18663, 1998
 A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2 inhibitors.
 A:Reference number: A92696; MUID:89066652; PMID:2974032
 A:Accession: C31953
 A:Molecule type: protein
 A:Residues: 85-93 <AHN>
 R:Rothhut, B.; Comera, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; Coudane, J.
 Biochem. J. 263, 929-935, 1989
 A:Title: A 32 kDa lipocortin from human mononuclear cells appears to be identical with the lipocortin from sheep vesicular stomatitis virus.
 A:Reference number: S06646; MUID:90088443; PMID:2532007
 A:Accession: S06646
 A:Molecule type: protein
 A:Residues: 7-25; 27-42; 51-74, 'X', 76-151; 181-198; 202-207; 209-226; 228-238; 246-271; 277-282; 284-297
 R:Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.
 FEBS Lett. 275, 15-21, 1990
 A:Title: The calcium binding sites in human annexin V by crystal structure analysis at 2.0 Å resolution.
 A:Reference number: A37250; MUID:91085549; PMID:2148156
 A:Contents: annotation; X-ray crystallography, 2.0 Å resolution
 A:Note: three calcium ions are strongly bound at sites in the first, second, and fourth loops.
 R:Funkoshi, T.; Helmark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
 Biochemistry 26, 5572-5578, 1987
 A:Title: Human placental anticoagulant protein: isolation and characterization.
 A:Reference number: A29670; MUID:88050845; PMID:2960376
 A:Accession: A29670
 A:Molecule type: protein
 A:Residues: 29-73; 274-297; 300-320 <PU2>
 R:Fernandez, M.P.; Morgan, R.O.; Fernandez, M.R.; Carcedo, M.T.
 Gene 149, 253-260, 1994
 A:Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C content.
 A:Reference number: I37172; MUID:95047484; PMID:7958998
 A:Accession: I37172
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-320 <RES>
 A:Cross-references: EMBL:U01691; NID:9430964; PIDN:AAB40047.1; PID:9430966
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipids.
 C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation.
 C:Genetics:
 A:Gene: GDB:ANX5
 A:Cross-references: GDB:120555; OMIM:131230
 A:Map position: 4q26-4q28
 A:Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
 A:Superfamily: annexin I; annexin repeat homology
 C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin
 F:2-320/Product: annexin V #status experimental <MAY>
 F:18-89/Domain: annexin repeat homology <AX1>
 F:29-45/Region: endonexin fold #status predicted
 F:90-161/Domain: annexin repeat homology <AX2>
 F:101-117/Region: endonexin fold #status predicted
 F:173-245/Domain: annexin repeat homology <AX3>
 F:185-201/Region: endonexin fold #status predicted
 F:249-320/Domain: annexin repeat homology <AX4>
 F:260-276/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (ala) (in mature form) #status experimental
 F:23/Binding site: phosphate (Thr) (covalent) #status predicted
 F:28,30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experimental

F:33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental
 F:73,78/Binding site: calcium, low affinity (Leu, Glu) #status experimental
 F:100,102,104,144/Binding site: calcium, high affinity (Leu, Gly, Glu, Asp) #status experimental
 F:259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Glu, Asp) #status experimental

Query Match 97.0%; Score:1590; DB 1; Length 320;
 Best Local Similarity 99.7%; Pred. No. 8.6e-95;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	8	MAQVLRTVDPFGDERADAE	TLRKAMKGLCTDEESIL	TLTSRSNAQRQISAAFKTL	67
DB	1	MAQVLRTVDPFGDERADAE	TLRKAMKGLCTDEESIL	TLTSRSNAQRQISAAFKTL	60
QY	68	FGRLDLLDLKSELTKGFKEL	IVALKMPSRLYDAYELKHAL	KGAGTNEKVLTIITASRYPE	127
DB	61	FGRLDLLDLKSELTKGFKEL	IVALKMPSRLYDAYELKHAL	KGAGTNEKVLTIITASRYPE	120
QY	128	ELRAIKQVVEEYEGSSLED	VYVGGTSGYYQRMVLLV	LQANRPDAGIDBAQVEQDAQLF	187
DB	121	ELRAIKQVVEEYEGSSLED	VYVGGTSGYYQRMVLLV	LQANRPDAGIDBAQVEQDAQLF	180
QY	188	QAGELKMGTDDEKFTIFG	TRSVSHLRKVFQVMTISG	FQIETIDRETSGNLEQLLAV	247
DB	181	QAGELKMGTDDEKFTIFG	TRSVSHLRKVFQVMTISG	FQIETIDRETSGNLEQLLAV	240
QY	248	VKSIRSIPTALTYAMKAG	TDHLLIRVMVSRSEIDLF	NIRKEFKNFATSLYSMI	307
DB	241	VKSIRSIPTALTYAMKAG	TDHLLIRVMVSRSEIDLF	NIRKEFKNFATSLYSMI	300
QY	308	KGDTSGDYKALLLLSGED	327		
DB	301	KGDTSGDYKALLLLSGED	320		

RESULT 2
 annexin V - bovine
 N:Alternate names: CaBP33; CaBP37
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
 C:Accession: S27214; S27215
 R:Learnmonth, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Glambanco, I.; Blochm. Biophys. Acta 1160, 76-83, 1992
 A:Title: Novel isoforms of CaBP 33/37 (Annexin V) from mammalian brain: structural analysis
 A:Reference number: S27214; MUID:93041974; PMID:1420335
 A:Accession: S27214
 A:Molecule type: protein
 A:Residues: 1-320 <LEA>
 A:Accession: S27215
 A:Molecule type: protein
 A:Residues: 1-35, 'N', 37-124, 'E', 126-320 <LE2>
 A:Note: It is uncertain whether the sequence differences are due to allelic variation or to a different protein.
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipids.
 C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation.
 C:Superfamily: annexin I; annexin repeat homology
 C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin
 F:17-88/Domain: annexin repeat homology <AX1>
 F:28-44/Region: endonexin fold #status predicted
 F:89-160/Domain: annexin repeat homology <AX2>
 F:100-116/Region: endonexin fold #status predicted
 F:172-244/Domain: annexin repeat homology <AX3>
 F:184-200/Region: endonexin fold #status predicted
 F:248-319/Domain: annexin repeat homology <AX4>
 F:259-275/Region: endonexin fold #status predicted
 F:1/Modified site: acetylated amino end (ala) #status experimental
 F:22/Binding site: phosphate (Thr) (covalent) #status experimental
 F:27,29,31,71/Binding site: calcium, high affinity (Met, Gly, Glu) #status predicted
 F:32,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
 F:72,77/Binding site: calcium, low affinity (Leu, Glu) #status predicted
 F:99,101,103,143/Binding site: calcium, high affinity (Leu, Gly, Glu, Asp) #status predicted
 F:258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Glu, Asp) #status predicted

Query Match 93.7%; Score 1536.5; DB 1; Length 320;
Best Local Similarity 96.6%; Pred. No. 2.3e-91;
Matches 309; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 9 AOVLRGTVDGFGDRAETLRKAMKGLGTDDEESTLTLTSSNAQROEISAAPKTLF 68
DB 1 AOVLRGTVDGFGDRAETLRKAMKGLGTDDEESTLTLTSSNAQROEISAAPKTLF 60
QY 69 GRLLDDLSKSELTKGKFKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
DB 61 GRLLDDLSKSELTKGKFKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120
QY 129 LRAIKQVYEEYSGSLEDDVVGDTSGYQYQMLVLLQANRDPAGIDEAQVEDQAALFQ 188
DB 121 LRAIKQVYEEYSGSLEDDVVGDTSGYQYQMLVLLQANRDPAGIDEAQVEDQAALFQ 180
QY 189 AGEKNGTDEKFTITGTRSVSHLRKRVFKYMTISGFQTEETIDRETSGNLQOLLAVV 248
DB 181 AGEKNGTDEKFTITGTRSVSHLRKRVFKYMTISGFQTEETIDRETSGNLQOLLAVV 240
QY 249 KSTRSPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFKRNFATSLYSMIK 308
DB 241 KSTRSPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFKRNFATSLYSMIK 300
QY 309 GDTSGDYKKALLLL-SGEDD 327
DB 301 GDTSGDYKKALLLLCGGEDD 320

RESULT 3

LURTS

annexin V - rat
N:Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; placenta
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C:Accession: C29250; S66680
R:Peplinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning,
J. Biol. Chem. 263, 10799-10811, 1988
A:Title: Five distinct calcium and phospholipid binding proteins share homology with lip
A:Reference number: A92659; MUID:88273202; PMID:2968983
A:Accession: C29250
A:Molecule type: mRNA
A:Residues: 1-319 <PEP>
A:Cross-references: GB:M21730; NID:g205138; PIDN:AAA41512.1; PID:g205139
R:Imai, Y.; Kohsaka, S.
Eur. J. Biochem. 232, 327-334, 1995
A:Title: Structure of rat annexin V gene and molecular diversity of its transcripts.
A:Reference number: S66680; MUID:96035863; PMID:7556178
A:Accession: S66680
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-319 <IMA>
A:Cross-references: EMBL:D42136
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
derstood.
C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula
olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende
C:Genetics:
A:Introns: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/3; 299/3
C:Superfamily: annexin I; annexin repeat homology
F:2-319/Product: annexin V #status predicted <MAT>
F:16-87/Domain: annexin repeat homology <AX1>
F:27-43/Region: endonexin fold #status predicted
F:88-159/Domain: annexin repeat homology <AX2>
F:99-115/Region: endonexin fold #status predicted
F:171-243/Domain: annexin repeat homology <AX3>
F:183-199/Region: endonexin fold #status predicted
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: endonexin fold #status predicted
F:26,28,30,70/Binding site: calcium, high affinity (Met, Gly, Glu) #status predicted
F:31,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status predicted

F:71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F:98,100,102,142/Binding site: calcium, high affinity (Ileu, Gly, Gly, Asp) #status pr
F:257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status p
Query Match 88.8%; Score 1455.5; DB 1; Length 319;
Best Local Similarity 91.8%; Pred. No. 3.6e-86;
Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 12 LRCTVDFGFGDRAETLRKAMKGLGTDDEESTLTLTSSNAQROEISAAPKTLGRD 71
DB 3 LRCTVDFGFGDRAETLRKAMKGLGTDDEESTLTLTSSNAQROEISAAPKTLGRD 62
QY 72 LLDLKLSELTGKFKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPELRA 131
DB 63 LVNDKSELTKGKFKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPELRA 122
QY 132 IKQVYEEYSGSLEDDVVGDTSGYQYQMLVLLQANRDPAGIDEAQVEDQAALFQAGE 191
DB 123 IKQVYEEYSGSLEDDVVGDTSGYQYQMLVLLQANRDPAGIDEAQVEDQAALFQAGE 182
QY 192 LKNGTDEKFTITGTRSVSHLRKRVFKYMTISGFQTEETIDRETSGNLQOLLAVVKS 251
DB 183 LKNGTDEKFTITGTRSVSHLRKRVFKYMTISGFQTEETIDRETSGNLQOLLAVVKS 242
QY 252 RSPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFKRNFATSLYSMIKGD 311
DB 243 RSPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLFNIRKFKRNFATSLYSMIKGD 302
QY 312 SGDYKKALLLL-SGEDD 327
DB 303 SGDYKKALLLLCGGEDD 319

RESULT 4

LUCUS

annexin V - chicken
N:Alternate names: anchorin CII; endonexin II; lipocortin V; placental anticoagulant
C:Species: Gallus gallus (Chicken)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000
C:Accession: A35381; A28623; B40404; S32523; S08771
R:Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaffie, M.; Deutzmann, R.;
J. Biol. Chem. 265, 8344, 1990
A:Reference number: A35381; MUID:90243721; PMID:2159478
A:Contents: erratum
A:Accession: A35381
A:Molecule type: mRNA
A:Residues: 1-321 <PER>
A:Cross-references: GB:M30971; GB:J03194; NID:g211138; PIDN:AAA48591.1; PID:g211139
R:Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaffie, M.; Deutzmann, R.;
J. Biol. Chem. 263, 5921-5925, 1988
A:Title: The structure of anchorin CII, a collagen binding protein isolated from chon
A:Reference number: A28623; MUID:88186917; PMID:2833522
A:Accession: A28623
A:Molecule type: mRNA
A:Residues: 1-118; LKCRILRNQYEAALGRNKITGRHQALFRDWCWCCROIEI'163-167, 'E',169-32
A:Cross-references: GB:M30971; GB:J03194; NID:g211138
R:Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.
J. Biol. Chem. 266, 10678-10685, 1991
A:Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective parti
A:Reference number: A40404; MUID:91244852; PMID:2037607
A:Accession: B40404
A:Molecule type: protein
A:Residues: 188-199 <GEN>
A:Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched mic
R:Boustead, C.M.; Brown, R.; Walker, J.H.
Biochem. J. 291, 601-608, 1993
A:Title: Isolation, characterization and localization of annexin V from chicken liver
A:Reference number: S32523; MUID:93249384; PMID:8484740
A:Accession: S32523
A:Status: preliminary
A:Molecule type: protein
A:Residues: 6-20;85, 'X',87-88, 'X',90-93, 'X',95-96, 'XX',99-100, 'X',102-103, 'XX',106-10
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

derstood.

C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation binding rather than proteolytic inactivation. It does not affect thrombin-dependent C:Superfamily: annexin I; annexin repeat homology
C:Keywords: calcium binding; collagen binding; duplication; endonexin fold; membrane-associated; annexin V #status predicted <MAT>
F:2-321/Product: annexin V #status predicted <AX1>
F:18-69/Domain: annexin repeat homology <AX1>
F:29-45/Region: endonexin fold #status predicted
F:90-161/Domain: annexin repeat homology <AX2>
F:101-117/Region: endonexin fold #status predicted
F:185-245/Domain: annexin repeat homology <AX3>
F:185-245/Region: endonexin fold #status predicted
F:260-276/Domain: annexin repeat homology <AX4>
F:260-276/Region: endonexin fold #status predicted
F:28,30,32,72/Binding site: calcium, high affinity (Thr, Glu, Glu) #status predicted
F:33,35,36/Binding site: calcium, low affinity (Thr, Glu) #status predicted
F:73,78/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F:100,102,104,144/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
F:259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted

Query Match 78.0%; Score 1279; DB 1; Length 321;
Best Local Similarity 78.1%; Pred. No. 7.3e-75;
Matches 250; Conservative 38; Mismatches 32; Indels 0; Gaps 0;

QY 8 MAQLRGTVDPFGPDERADAETLRKAMKGLGTDEESILTLTSRNASQREISAAFKTL 67
DB 1 MAKYTRGVTAFTSPFADADAELKAMKMGMTDEETILKILTSRNASQREISAAFKTL 60
QY 68 FGRDLDDKSELTKGFEKLIKALPKPSRLYDAYELKALKAGTNEKVLTEIIASRTPE 127
DB 61 FGRDLDDKSELTKGFEKLIKALPKPSRLYDAYELKALKAGTNEKVLTEIIASRTPE 120
QY 128 ELRAIKQVYEEYSGSLEDVVDGTSYQYQRMVLVLLQANRPDAGIDQAQVSDQAALF 187
DB 121 EVONIKQVYQVEANLEDKITGETSGHFQRLVLLQANRPDGRVDEALVEKDAQVLF 180
QY 188 QAGELKNGTDEKFTIFGTSVSHLRKVFYKMTYISGFOIBETIDRTSGNLEQULLAV 247
DB 181 RAGELKNGTDEETFTILGTSVSHLRKVFYKMTYISGFOIBETIDRTSGDLEKULLAV 240
QY 248 VKSIRIPALAEYLYAMKAGTDDHTLIRVMSRSEIDLNIRKPRKNTATSIYMI 307
DB 241 VCIKRSVPAYFAETLYSMKAGTDDHTLIRVMSRSEIDLNIRKPRKNTATSIYMI 300
QY 308 KGDTSYDKKALLSGDD 327
DB 301 QKDTSGDYKALLLCGGDD 320

RESULT 5

AQH068
N:Alternate names: calcium-binding protein, 68K; calelectrin; calphobindin II
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C:Accession: J000263; S18519; A31079; JX0091; B34459; B31953; A53507
J:Wasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; Sh
J. Biochem. 106, 43-49, 1989
A:Title: Structure and expression of cDNA for calphobindin II, a human placental coagula
A:Reference number: J00032; MUID:89380132; PMID:2528541
A:Accession: J00032
A:Molecule type: mRNA
A:Residues: 1-673 <TWA>
A:Cross-references: EMBL:D00510; NID:g219550; PIDN:BAA00400.1; PID:g219551
R:Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crompton, M.J.
EMBO J. 7, 21-27, 1988
A:Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p68:
A:Reference number: S00263; MUID:88196081; PMID:3258820
A:Accession: S00263
A:Molecule type: mRNA
A:Residues: 1-618, 'D', 620-673 <CR1>
A:Cross-references: EMBL:Y00097; NID:g35217; PIDN:CAA68286.1; PID:g35218
A:Accession: S18519

A:Molecule type: protein
A:Residues: 103-113;167-172, 'X', 174-177;232-235, 'F', 237-240;251-258;277-281;359-362, '
A:Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-
C:Keywords: eight calcium ions are bound in the presence of phospholipid
R:Suedhof, T.C.; Slaughter, C.A.; Lenicki, I.; Barjon, P.; Reynolds, G.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988
A:Title: Human 67-kDa calelectrin contains a duplication of four repeats found in 35-
A:Reference number: A31079; MUID:88124902; PMID:2563335
A:Accession: A31079
A:Molecule type: mRNA
A:Residues: 1-225, 'MK', 228-554, 'T', 556-673 <SUB>
A:Cross-references: GB:J03578; NID:gl79975; PIDN:AAA35656.1; PID:gl79976
R:Yoshizaki, H.; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Shidara, Y.; Maki, M.
J. Biochem. 107, 43-50, 1990
A:Title: Structure and properties of calphobindin II, an anticoagulant protein from h
A:Reference number: JX0091; MUID:90236978; PMID:2139657
A:Accession: JX0091
A:Molecule type: protein
A:Residues: 2-299;307-314;320-445;447-549;581-673 <YOS>
R:Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T.
J. Biol. Chem. 264, 17222-17230, 1989
A:Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding prot
A:Reference number: A34459; MUID:90008880; PMID:2529258
A:Accession: B34459
A:Molecule type: protein
A:Residues: 10-25;69-75;136-151;192-207;209-220;300-306 <HAY>
A:Experimental source: placenta
R:Ahm, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
A:Reference number: A92696; MUID:89066652; PMID:2974032
A:Accession: B31953
A:Molecule type: protein
A:Residues: 90-108, 'L', 110-126;127,265-276;286-302;626-654 <AHN>
R:Hyatt, S.L.; Liao, L.; Chapline, C.; Jaken, S.
Biochemistry 33, 1223-1228, 1994
A:Title: Identification and characterization of alpha-protein kinase C binding protei
A:Reference number: A53507; MUID:94153907; PMID:8110754
A:Accession: A53507
A:Molecule type: protein
A:Residues: 'X', 473-480, 'DY' <HYA>
C:Comment: This abundant cytosolic protein binds to the inner surface of the cell mem
C:Genetics:
A:Gene: GDB:ANX6
A:Cross-references: GDB:119681; OMIM:114070
A:Map position: 5q32-5q34
C:Superfamily: annexin VI; annexin repeat homology
C:Keywords: acetylated amino end; calcium binding; duplication: endonexin fold; phosph
F:2-673/Product: annexin VI #status experimental <MAT>
F:23-94/Domain: annexin repeat homology <AX1>
F:34-50/Region: endonexin fold #status predicted
F:95-166/Domain: annexin repeat homology <AX2>
F:106-122/Region: endonexin fold #status predicted
F:178-250/Domain: annexin repeat homology <AX3>
F:190-206/Region: endonexin fold #status predicted
F:254-325/Domain: annexin repeat homology <AX4>
F:265-281/Region: endonexin fold #status predicted
F:366-437/Domain: annexin repeat homology <AX5>
F:377-393/Region: endonexin fold #status predicted
F:438-509/Domain: annexin repeat homology <AX6>
F:449-465/Region: endonexin fold #status predicted
F:527-598/Domain: annexin repeat homology <AX7>
F:538-554/Region: endonexin fold #status predicted
F:602-673/Domain: annexin repeat homology <AX8>
F:613-629/Region: endonexin fold #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 56.9%; Score 932; DB 1; Length 673;
Best Local Similarity 58.1%; Pred. No. 3.1e-52;
Matches 193; Conservative 52; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGVTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNASQREISAAFKTLGRDL 72

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Db 11 RGSIHOPGPDNDQDAEALYAMKFGSKDEKALDIITSRNQRQEVQCSYKSLYKDL 70
Qy 73 LDDLSKSLTKFKFKLIVALKMPSRLYDAYELKHALKAGTGNKXVTEIATSRTPPELR 132
Db 71 IADLKVELTKFKFLVGLMRPPAYCDKAKEIKDAISGIGYDEKCLIEILASRTNEQMHQ 130
Qy 133 KQVTEEGSSLEDDVVGDTSGYYQRMVLLQANRPDAGIDEAQVQDAQALFOAGEL 192
Db 131 VAAYKDAYERDLLEADIIIGDTSGHFQKMLVLLQAGTRENDDVSEDVQODVQDYA 190
Qy 193 KWTDEKFTITFTGTRSVSHLRKVFQKMYTISGFQIEETIDRTSGNLEOLLAVKVSIR 252
Db 191 KWTDEAQFYIILGNRSKQHLRVFDEYLTAKTKPIEASIRGELSGDFEKLMLAVKCI 250
Qy 253 SIPAYLAETLYYAMKAGAGTDHLLIRVMVSRSEIDLNFIRKPKNFATSLYSMIKGD 312
Db 251 STEYFAERLFAKMGAGTGLTRDNTLIRIMVSRSELDMLDIRFTRKYSLSYMIKND 310
Qy 313 GDYKALLLLSGEDD 327
Db 311 GEYKTKLLKSGDD 325

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RESULT 6

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annexin VI - mouse
N:Alternate names: calcium-binding protein p68; calelectrin; calphobindin II
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: S01786
R:Moss, S.E.; Crompton, M.R.; Crumpton, M.J.
Eur. J. Biochem. 177, 21-27, 1988
A:Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family.
A:Reference number: S01786; MUID:89030687; PMID:2972541
A:Accession: S01786
A:Molecule type: mRNA
A:Residues: 1-673 <MOS>
A:Cross-references: EMBL:X13460; NID:g53580; PIDN:CAA31808.1; PID:g53581
A:Note: The authors translated the codon GCC for residue 329 as Gly
C:Comment: This abundant cytosolic protein binds to the inner surface of the cell membrane
C:Superfamily: annexin VI; annexin repeat homology
C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phospholipase
F:2-673/Product: annexin VI #status predicted <MAY>
F:23-94/Domain: annexin repeat homology <AX1>
F:34-50/Region: endonexin fold #status predicted
F:95-166/Domain: annexin repeat homology <AX2>
F:106-122/Region: endonexin fold #status predicted
F:178-230/Domain: annexin repeat homology <AX3>
F:190-206/Region: endonexin fold #status predicted
F:254-325/Domain: annexin repeat homology <AX4>
F:265-281/Region: endonexin fold #status predicted
F:366-437/Domain: annexin repeat homology <AX5>
F:377-393/Region: endonexin fold #status predicted
F:438-509/Domain: annexin repeat homology <AX6>
F:449-465/Region: endonexin fold #status predicted
F:527-598/Domain: annexin repeat homology <AX7>
F:538-554/Region: endonexin fold #status predicted
F:603-673/Domain: annexin repeat homology <AX8>
F:613-629/Region: endonexin fold #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

```

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Query Match 56.9%; Score 932; DB 1; Length 673;
Best Local Similarity 59.0%; Pred. No. 3.le-52;
Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

Qy 13 RGVTDFFGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRIEASAFKTLFGKDL 72
Db 11 RGSVDPPEPDANQDAEALYAMKFGSKDKESILELITSRNKKQRIEQCSYKSLYKDL 70
Qy 73 LDDLSKSLTKFKFKLIVALKMPSRLYDAYELKHALKAGTGNKXVTEIATSRTPPELR 132
Db 71 IEDLKVELTKFKFLVGLMRPPAYCDKAKEIKDAISGIGYDEKCLIEILASRTNEQMHQ 130

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Qy 133 KQVTEEGSSLEDDVVGDTSGYYQRMVLLQANRPDAGIDEAQVQDAQALFOAGEL 192
Db 131 VAAYKDAYERDLLEADIIIGDTSGHFQKMLVLLQAGTRENDDVSEDVQODVQDYA 190
Qy 193 KWTDEKFTITFTGTRSVSHLRKVFQKMYTISGFQIEETIDRTSGNLEOLLAVKVSIR 252
Db 191 KWTDEAQFYIILGNRSKQHLRVFDEYLTAKTKPIEASIRGELSGDFEKLMLAVKCI 250
Qy 253 SIPAYLAETLYYAMKAGAGTDHLLIRVMVSRSEIDLNFIRKPKNFATSLYSMIKGD 312
Db 251 STEYFAERLFAKMGAGTGLTRDNTLIRIMVSRSELDMLDIRFTRKYSLSYMIKND 310
Qy 313 GDYKALLLLSGEDD 327
Db 311 GEYKTKLLKSGDD 325

RESULT 7
A42077
annexin IV - human
N:Alternate names: endonexin I; placental anticoagulant protein II; PP4-X protein
C:Species: Homo sapiens (man)
C:Date: 30-Jan-1993 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: A42077; S07434; A31953; A31046
R:Tait, J.F.; Smith, C.; Frankenberg, D.A.; Miao, C.H.; Adler, D.A.; Distèche, C.M.
Genomics 12, 313-318, 1992
A:Title: Chromosomal mapping of the human annexin IV (ANX4) gene.
A:Reference number: A42077; MUID:92155721; PMID:1346776
A:Accession: A42077
A:Molecule type: mRNA
A:Residues: 1-321 <TAI>
A:Cross-references: GB:M82809; NID:g178698; PIDN:AAA51740.1; PID:g178699
A:Accession: B42077
A:Molecule type: DNA
A:Residues: 87-129 <TA2>
R:Grundmann, U.; Amann, E.; Abel, K.J.; Kuepper, H.A.
Behring Inst. Mitt. 82, 59-67, 1988
A:Title: Isolation and expression of cDNA coding for a new member of the phospholipase
A:Reference number: S07434; MUID:88309022; PMID:2970257
A:Accession: S07434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97, 'Q', 99-321 <GRU>
A:Cross-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
R:Ahb, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
inhibitor.
A:Reference number: A92696; MUID:89066652; PMID:2974032
A:Accession: A31953
A:Molecule type: Protein
A:Residues: 29-58, 101-126, 282-310 <AHN>
R:Tait, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E.
Biochemistry 27, 6268-6276, 1988
A:Title: Placental anticoagulant proteins: isolation and comparative characterization
A:Reference number: A90534; MUID:89118212; PMID:2975506
A:Accession: A31046
A:Molecule type: Protein
A:Residues: 4-17, 30-74, 102-146, 283-321 <TA3>
C:Genetics:
A:Gene: GDB:ANX4
A:Cross-references: GDB:I31395; OMIM:106491
A:Map position: 2p13-2p13
A:Introns: 102/3
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; glyco
P:2-321/Product: annexin IV #status predicted <MAY>
F:19-90/Domain: annexin repeat homology <AX1>
F:30-46/Region: endonexin fold #status predicted
F:91-162/Domain: annexin repeat homology <AX2>
F:103-118/Region: endonexin fold #status predicted
F:174-246/Domain: annexin repeat homology <AX3>

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F:186-202/Region: endonexin fold #status predicted
 F:230-321/Domain: annexin repeat homology <AX4>
 F:261-277/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
 F:9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:247/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.3%; Score 923; DB 1; Length 321;
 Best Local Similarity 58.3%; Pred. No. 4.7e-52;
 Matches 183; Conservative 53; Mismatches 78; Indels 0; Gaps 0;

QY 14 GTVDPFGDERADAEATLRKAMKGLGTDEESILTLTSRSNAQRQISAAFTLFGDRL 73
 DB 8 GTVKAASGNAEDAEATLRKAMKGLGTDEDAIISVLAYRSTAQRQIRTAAYKSTIGRDLL 67

QY 74 DLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTIISRTPEELRAIK 133
 DB 68 DLKSELNFGVILGMPTVLYDVQELRRAMKAGTDEGCLIIILASRTPEEIRIN 127

QY 134 QYEEYSGSLEDVVGDTSYGYQYRMVLLQANRDPDAGIDEAQVEQDAQALFOAGELK 193
 DB 128 QYVQOYGRSLDEDIRSDTSEMFQVRLVSLSGAGRDGNYLDDALVRQDAQDLYEAGEKK 187

QY 194 WGTDEKFTITGTRSVSHLRKVFQKYMTISQFQIETDRETSGNLEQLLLAVVKSIRS 253
 DB 188 WGTDEVKFTLVLCSSNRNHLHFVDEYKRIKQDIQSIKSETSGSFEDALLAIVKCMRN 247

QY 254 IPAYLAETIYVAMKAGTDDHTLIRVWVSREIDFNIRKPKNFATSLYSMIKGDTSG 313
 DB 248 KSAFYAEKLYKSKMGLGTDDNTLIRVWVSRAEIDMDIRANFKRLYKGLYSYFIKGDTSG 307

QY 314 DYKALLLSGDD 327
 DB 308 DYRKVLLVLCGGD 321

RESULT 8

LUP64
 annexin IV - pig
 N:Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocortin IV; protein I
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24-Nov-1999
 C:Accession: A27107
 R:Weber, K.; Johansson, N.; Plessmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; Vandekerckh
 EMBL J. 6, 1599-1604, 1987
 A:Title: The amino acid sequence of protein II and its phosphorylation site for protein
 A:Reference number: A27107; MUID:87275850; PMID:2956093
 A:Accession: A27107
 A:Molecule type: protein
 A:Residues: 1-318 <WEB>
 A:Experimental source: intestinal epithelium
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
 derstood.
 C:Superfamily: annexin I; annexin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprotein
 F:16-87/Domain: annexin repeat homology <AX1>
 F:27-43/Region: endonexin fold #status predicted
 F:88-159/Domain: annexin repeat homology <AX2>
 F:99-115/Region: endonexin fold #status predicted
 F:171-243/Domain: annexin repeat homology <AX3>
 F:183-199/Region: endonexin fold #status predicted
 F:247-318/Domain: annexin repeat homology <AX4>
 F:258-274/Region: endonexin fold #status predicted
 F:/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
 F:5/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:124.244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.2%; Score 921; DB 1; Length 318;

Best Local Similarity 58.6%; Pred. No. 6.2e-52;
 Matches 184; Conservative 51; Mismatches 79; Indels 0; Gaps 0;

QY 14 GTVDPFGDERADAEATLRKAMKGLGTDEESILTLTSRSNAQRQISAAFTLFGDRL 73
 DB 8 GTVKAASGNAEDAEATLRKAMKGLGTDEDAIISVLAYRSTAQRQIRTAAYKSTIGRDLL 67

DB 5 GTVKAASGNAEDAEATLRKAMKGLGTDEDAIISVLAYRSTAQRQIRTAAYKSTIGRDLL 64
 QY 74 DLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTIISRTPEELRAIK 133
 DB 65 DLKSELNFGVILGMPTVLYDVQELRRAMKAGTDEGCLIIILASRTPEEIRIN 124

QY 134 QYEEYSGSLEDVVGDTSYGYQYRMVLLQANRDPDAGIDEAQVEQDAQALFOAGELK 193
 DB 125 QYVQOYGRSLDEDIRSDTSEMFQVRLVSLSGAGRDGNYLDDALVRQDAQDLYEAGEKK 184

QY 194 WGTDEKFTITGTRSVSHLRKVFQKYMTISQFQIETDRETSGNLEQLLLAVVKSIRS 253
 DB 185 WGTDEVKFTLVLCSSNRNHLHFVDEYKRIKQDIQSIKSETSGSFEDALLAIVKCMRN 244

QY 254 IPAYLAETIYVAMKAGTDDHTLIRVWVSREIDFNIRKPKNFATSLYSMIKGDTSG 313
 DB 245 KSAFYAEKLYKSKMGLGTDDNTLIRVWVSRAEIDMDIRANFKRLYKGLYSYFIKGDTSG 304

QY 314 DYKALLLSGDD 327
 DB 305 DYRKVLLVLCGGD 318

RESULT 9

S52844
 annexin VI - rat
 N:Alternate names: calcium-binding protein 65/67
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S65683; S52844
 R:Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W.
 Eur. J. Biochem. 230, 741-751, 1995
 A:Title: cDNA cloning and tissue-specific regulation of expression of rat calcium-bin
 A:Reference number: S65683; MUID:95331313; PMID:7607247
 A:Accession: S65683
 A:Molecule type: mRNA
 A:Residues: 1-673 <FAN>
 A:Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181
 A:Experimental source: liver
 C:Superfamily: annexin VI; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associate
 F:2-673/Product: annexin VI #status predicted <MAT>
 F:23-94/Domain: annexin repeat homology <AX1>
 F:34-50/Region: endonexin fold #status predicted
 F:95-166/Domain: annexin repeat homology <AX2>
 F:106-122/Region: endonexin fold #status predicted
 F:178-250/Domain: annexin repeat homology <AX3>
 F:190-206/Region: endonexin fold #status predicted
 F:254-325/Domain: annexin repeat homology <AX4>
 F:265-281/Region: endonexin fold #status predicted
 F:366-437/Domain: annexin repeat homology <AX5>
 F:377-393/Region: endonexin fold #status predicted
 F:438-509/Domain: annexin repeat homology <AX6>
 F:449-465/Region: endonexin fold #status predicted
 F:527-598/Domain: annexin repeat homology <AX7>
 F:538-554/Region: endonexin fold #status predicted
 F:602-673/Domain: annexin repeat homology <AX8>
 F:613-629/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 56.2%; Score 921; DB 1; Length 673;

Best Local Similarity 58.7%; Pred. No. 1.6e-51;
 Matches 185; Conservative 48; Mismatches 82; Indels 0; Gaps 0;

QY 13 RGVTVDPFGDERADAEATLRKAMKGLGTDEESILTLTSRSNAQRQISAAFTLFGDRL 72
 DB 11 RGVHDFADFANQDAEALYTKMGFGSKESILELTSRSNKQRQEQISYKSLGKDL 70

QY 73 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTIISRTPEELRAIK 132
 DB 71 IADLYELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTIISRTPEELRAIK 130

QY 133 KQYEEYSGSLEDVVGDTSYGYQYRMVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 192


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131 VAAYKDAYBROLESIDIGTSGHFQKMLVVLQGTRENDVYSEDVQDVQDLYEAGEL 190
193 KNGTDEERFITFGTRSVSHLRKVDKYMTISGFOIBETIDRETSGNLEQLLAVVKSIR 252
191 KNGTDEAQTYYLGNRSKQHLHFDVDEYKTKTGKPIEASIRGELSGDFEKLMLAVVKIR 250
253 SIPAYLAETLYYAMKAGAGTDDHTLIRVWVSREIDLFNIRKFRKNFATSLYSMTIKGDS 312
251 STPEFAERLFRAMKGLGTRDNTLIRVWVSREIDLFNIRKFRKNFATSLYSMTIKGDS 310
313 GYKKALLLSGDD 327
311 GYKKALLKCGDD 325

RESULT 10
LUBO4
annexin IV - bovine
N:Alternate names: 32K calelectrin; Chromobindin IV; endonexin; lipocortin IV; protein X
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C:Accession: A31578; D45066; S59624; A45066; B45066; F45066; G45066; H45066
R:Hamman, H.C.; Gaffey, L.C.; Lynch, K.R.; Creutz, C.E.
Biochem. Biophys. Res. Commun. 156, 660-667, 1988
A:Title: Cloning and characterization of a cDNA encoding bovine endonexin (chromobindin
A:Reference number: A31578; MUID:89050088; PMID:2847715
A:Accession: A31578
A:Molecule type: mRNA
A:Residues: 1-319 <HAM>
A:Cross-references: GB:X13627; NID:Q215; PIDN:CAA31954.1; PID:Q216; GB:M22248; NID:gl30
R:Kojima, K.; Ogawa, H.K.; Seno, N.; Yamamoto, K.; Irimura, T.; Osawa, T.; Matsumoto, I.
J. Biol. Chem. 267, 20536-20539, 1992
A:Title: Carbohydrate-binding proteins in bovine kidney have consensus amino acid sequen
A:Reference number: A45066; MUID:93015942; PMID:1400371
A:Accession: D45066
A:Molecule type: protein
A:Residues: 10-18,'X',20-22,'X',24-25;29-48;101-107,'X',109-118,'X',194-197,'Y',199,'X',
A:Experimental source: kidney
A:Note: sequence extracted from NCBI backbone (NCBIP:116211, NCBIP:116208, NCBIP:116209,
A:Note: these fragments are derived from a 33k protein that exhibited Ca++-dependent bin
A:Note: 12-Met and 12-Tyr were also found
R:Schma, H.; Matsushima, N.; Watanabe, T.; Hattori, A.; Kuroki, Y.; Akino, T.
Biochem. J. 312, 175-181, 1995
A:Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A and lamellar bod
A:Reference number: S59624; MUID:96077142; PMID:7492310
A:Accession: S59624
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-44;72-77;112-119;163-180;181-190;226-235 <SOH>
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
derstood.
C:Superfamily: annexin I; annexin repeat homology
F:2-319/Product: annexin IV #status predicted <MAT>
F:17-88/Domain: annexin repeat homology <AX1>
F:28-44/Region: endonexin fold #status predicted
F:89-160/Domain: annexin repeat homology <AX2>
F:100-116/Region: endonexin fold #status predicted
F:172-244/Domain: annexin repeat homology <AX3>
F:184-200/Region: endonexin fold #status predicted
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin fold #status predicted
F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:125,245/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.8%; Score 914; DB 1; Length 319;
Best Local Similarity 58.0%; Pred. No. 1.8e-51;
Matches 182; Conservative 51; Mismatches 81; Indels 0; Gaps 0;

14 GTVDFPGFDERADATLRKAMKGLGTDEESILTTSRSNAQORQISAAFKTLFGDRL 73
6 GTVKAASGFNAEDAQTLRKAMKGLGTDEDAIINVLAYRSTAQRQIRTAQKTTIGRDL 65

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74 DLKSELGTCKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPEELRAIK 133
66 DLKSELGNFQVILGHMTPTVLVDVQLRAMKAGAGTDEGCLLEILASRTPPEERRIN 125
134 QYEEYEGSLDEDDVVGDTSGYYQYRMLVLLQANRPDIDAEAOVEQDAQALFQAGEK 193
126 QYQLQYGRSLDEDDIRSDTSEMFQYVLSLSAGGRDESNYLDDALMRQADQDLYEAGEKK 185
194 WGTDEKFTITIGTRSVSHLRKVDKYMTISGFOIBETIDRETSGNLEQLLAVVKSIR 253
186 WGTDEVKFTVLVCSRRNHLHVFDEYKRIAKQDEQSIKSETSGSGFDALLAIVKCMRN 245
254 IPAYLAETLYYAMKAGAGTDDHTLIRVWVSREIDLFNIRKFRKNFATSLYSMTIKGDTSG 313
246 KSAFYAERLYKSMKGLGTDDTLIRVWVSRAEIDMLDIRANFKRLYKGLSYLFIKDTSG 305
314 DYKKALLLSGDD 327
306 DYRKVLLILCGDD 319

RESULT 11
JC2029
annexin - chicken
N:Alternate names: 67K lipid-dependent Ca2+-binding protein
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C:Accession: JC2029
R:Cao, X.; Genge, B.R.; Wu, L.N.Y.; Buzzi, W.R.; Showman, R.M.; Wuthier, R.E.
Biochem. Biophys. Res. Commun. 197, 556-561, 1993
A:Title: Characterization, cloning and expression of the 67-kDa annexin from chicken
A:Reference number: JC2029; MUID:94092130; PMID:8267590
A:Accession: JC2029
A:Molecule type: mRNA
A:Residues: 1-671 <CAO>
C:Superfamily: annexin VI; annexin repeat homology
C:Keywords: calcium binding; phospholipid binding
F:21-92/Domain: annexin repeat homology <AX1>
F:93-164/Domain: annexin repeat homology <AX2>
F:176-248/Domain: annexin repeat homology <AX3>
F:252-323/Domain: annexin repeat homology <AX4>
F:364-435/Domain: annexin repeat homology <AX5>
F:436-507/Domain: annexin repeat homology <AX6>
F:525-597/Domain: annexin repeat homology <AX7>
F:601-671/Domain: annexin repeat homology <AX8>

Query Match 54.7%; Score 896.5; DB 2; Length 671;
Best Local Similarity 57.7%; Pred. No. 5.8e-50;
Matches 184; Conservative 51; Mismatches 83; Indels 1; Gaps 1;

10 QVLRGVTDPPGDERADATLRKAMKGLGTDEESILTTSRSNAQORQISAAFKTLFG 69
6 KYVRGVKPPGPNASODALCNAMKFGSKDRAILDLTTSRSNAQORQISAAFKTLFG 65
70 RDLDDLKSELGTCKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPEEL 129
66 KDLIADLKVELTGKFERLIVSLMRPPAYSDAKIKDAIGTGDEKLEILASRTRNQEI 125
130 RAIKQVYEEYEGSLDEDDVVGDTSGYYQYRMLVLLQANRPDIDAEAOVEQDAQALFQA 189
126 HDLVAAYKDAYERDLEADVVDTSFGHKMLVLLQAGREDDWSEDVLEQDAKDLLEA 185
190 GELKWTGDEKEITIGTRSVSHLRKVDKYMTISGFOIBETIDRETSGNLEQLLAVVVK 249
186 GELKWTGDEAQFTYILGRSKQHLRVFDEYLAIRKPIERSIRLAELSGDFEKLAVK 245
250 SIRSIPAYLAETLYYAMKAGAGTDDHTLIRVWVSREIDLFNIRKFRKNFATSLYSMTIKG 309
246 CVRSTAYFAERYKAMKGLGTDRDNTLIRVWVSREIDMLDIRANFKRLYKGLSYLFIKDTSG 305
310 DTSGDYKKALL-LLSGDD 327

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Db 306 DTSGEYKKALLKLCGGDD 324

RESULT 12

LUBO11

annexin XI form A - bovine

N:Alternate names: calyculin-associated protein peptide, CAP-50

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C:Accession: A42113; #accession B42909; C42909; D42909

R:Towle, C.A.; Treadwell, B.V., 1992

J. Biol. Chem. 267, 5416-5423, 1992

A:Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis.

A:Reference number: A42113; MUID:92184796; PMID:1372001

A:Accession: A42113

A:Molecule type: mRNA

A:Residues: 1-503 <TOW>

A:CROSS-references: GB:M82802; NID:g162673; PIDN:AAA30379.1; PID:g162674

A:Note: The authors did not translate the codon GAC for residue 503

R:Mizutani, A.; Uda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka,

J. Biol. Chem. 267, 13498-13504, 1992

A:Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblast

A:Reference number: A42909; MUID:92317074; PMID:1618851

A:Accession: A42909

A:Molecule type: protein

A:Residues: 213-223, 'X', 225-226; 319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-339; 441-450, 'X',

A:Experimental source: lung

A:Note: sequence modified after extraction from NCBI backbone

C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

derstood.

C:Genetics: 19/1; 56/2

A:Introns: 19/1; 56/2

A:Note: the list of introns is incomplete

C:Superfamily: annexin VII; annexin repeat

C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F:201-272/Domain: annexin repeat homology <AX1>

F:212-228/Region: endonexin fold #status predicted

F:273-344/Domain: annexin repeat homology <AX2>

F:284-300/Region: endonexin fold #status predicted

F:356-428/Domain: annexin repeat homology <AX3>

F:368-384/Region: endonexin fold #status predicted

F:433-503/Domain: annexin repeat homology <AX4>

F:443-459/Region: endonexin fold #status predicted

F:59,111/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.8%; Score 865; DB 1; Length 503;

Best Local Similarity 54.9%; Pred. No. 4.3e-48;

Matches 173; Conservative 58; Mismatches 84; Indels 0; Gaps 0;

QY 13 RGTVDPPGDERADAETLRKAMKGLGTDESIITLLTSRNSAORQETSAAFKTLFGDRL 72

Db 189 RGTITDASGDFPLRDAEVLKAMKGFDTDEQAIICLGSRSNKORQIILLSPKAYGKDL 248

QY 73 LDDLKSELTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132

Db 249 IKDLKSEUSGNFPEKLTILALMKTVPVLDAYEIKKAGTDEACLTIELASRSNEHREL 308

QY 133 KQVYEEYSGSLEDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVQDAQALFQAGEL 192

Db 309 NRVYKTEPKTLEEARSDTSQHQRLLISLQGNRDESTNVDMTLVQRDVQELYAAGEN 368

QY 193 KWTDEEKFITIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSNLEQLLAVVKSIR 252

Db 369 RLGTDESKFNAILCSRAHLVAVFNEYQRTGDIKSIKRENSGDLLEQGLAVVVKCLK 428

QY 253 SIPAYLAETLYAMKAGCTDDHTLIRVMVSRSELDLNFIRKFRNFATSLYMKIGDTS 312

Db 429 NTPAFFAERLKNKMGAGTKORTLIRIMVSRSELDLIRAEYKRLYKSLYHDITGDS 488

QY 313 GDYKALLLLSGEDD 327

Db 489 GDYKILLKICGGND 503

RESULT 13

S23447

annexin XI form B - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 22-Nov-1993 #sequence_revision 10-Feb-1995 #text_change 22-Jun-1999

C:Accession: S23447; S36136

R:Towle, C.

submitted to the EMBL Data Library, February 1992

A:Reference number: S23447

A:Accession: S23447

A:Molecule type: mRNA

A:Residues: 1-505 <TOW>

A:CROSS-references: EMBL:Z11742; NID:g77; PIDN:CAA77801.1; PID:g78

R:Towle, C.A.; Weissbach, L.; Treadwell, B.V.

Biochim. Biophys. Acta 1131, 223-226, 1992

A:Title: Alternatively spliced annexin XI transcripts encode proteins that differ nea

A:Reference number: S36136; MUID:92305067; PMID:1535225

A:Accession: S36136

A:Molecule type: mRNA

A:Residues: 1-77 <TOW>

A:CROSS-references: EMBL:Z11742

C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

derstood.

C:Genetics: 19/1; 58/2

A:Introns: 19/1; 58/2

A:Note: the list of introns is incomplete

C:Superfamily: annexin VII; annexin repeat

C:Keywords: alternative splicing; calcium binding; duplication; endonexin fold; glyco

F:203-274/Domain: annexin repeat homology <AX1>

F:214-230/Region: endonexin fold #status predicted

F:275-346/Domain: annexin repeat homology <AX2>

F:286-302/Region: endonexin fold #status predicted

F:358-430/Domain: annexin repeat homology <AX3>

F:370-385/Region: endonexin fold #status predicted

F:434-505/Domain: annexin repeat homology <AX4>

F:445-461/Region: endonexin fold #status predicted

F:61,113/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.8%; Score 865; DB 1; Length 505;

Best Local Similarity 54.9%; Pred. No. 4.3e-48;

Matches 173; Conservative 58; Mismatches 84; Indels 0; Gaps 0;

QY 13 RGTVDPPGDERADAETLRKAMKGLGTDESIITLLTSRNSAORQETSAAFKTLFGDRL 72

Db 191 RGTITDASGDFPLRDAEVLKAMKGFDTDEQAIICLGSRSNKORQIILLSPKAYGKDL 250

QY 73 LDDLKSELTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132

Db 251 IKDLKSEUSGNFPEKLTILALMKTVPVLDAYEIKKAGTDEACLTIELASRSNEHREL 310

QY 133 KQVYEEYSGSLEDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVQDAQALFQAGEL 192

Db 311 NRVYKTEPKTLEEARSDTSQHQRLLISLQGNRDESTNVDMTLVQRDVQELYAAGEN 370

QY 193 KWTDEEKFITIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSNLEQLLAVVKSIR 252

Db 371 RLGTDESKFNAILCSRAHLVAVFNEYQRTGDIKSIKRENSGDLLEQGLAVVVKCLK 430

QY 253 SIPAYLAETLYAMKAGCTDDHTLIRVMVSRSELDLNFIRKFRNFATSLYMKIGDTS 312

Db 431 NTPAFFAERLKNKMGAGTKORTLIRIMVSRSELDLIRAEYKRLYKSLYHDITGDS 490

QY 313 GDYKALLLLSGEDD 327

Db 491 GDYKILLKICGGND 505

RESULT 14

LUBO11

annexin XI - rabbit

N:Alternate names: calyculin-associated annexin protein CAP-50

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
 C/Accession: JH0694; PH0950; A38250; PS0263
 R/Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 186, 1227-1235, 1992
 A/Title: Molecular cloning of rabbit CAP-50, a calyculin-associated annexin protein.
 A/Reference number: JH0694; MUID:92378579; PMID:1380798

A/Accession: JH0694

A/Molecule type: mRNA

A/Residues: 1-503 <OK>

A/Cross-references: DDBJ:DJ0883; NID:g471147; PIDN:BAA01705.1; PID:g471148

A/Experimental source: lung

A/Accession: PH0950

A/Molecule type: protein

A/Residues: 104-141;213-231;254-262;270-280;285-309;319-337;429-448;478-492 <TK2>

R/Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.

J. Biol. Chem. 267, 8919-8924, 1992

A/Title: A calyculin-associated protein is a newly identified member of the Ca(2+)/phospholipid binding protein family.
 A/Reference number: A38250; MUID:92250478; PMID:1333622

A/Accession: A38250

A/Molecule type: protein

A/Residues: 104-141;213-223,'X',225-231;254-263;271-280;285-291,'X',293-300,'X',302-309;

C/Comment: This protein binds specifically to calyculin in a Ca2+ dependent manner.

C/Superfamily: annexin VII; annexin repeat homology

C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid binding

F:201-272/Domain: annexin repeat homology <AX1>

F:212-228/Region: endonexin fold #status predicted

F:284-300/Region: annexin repeat homology <AX2>

F:356-428/Domain: annexin repeat homology <AX3>

F:368-384/Region: endonexin fold #status predicted

F:432-503/Domain: annexin repeat homology <AX4>

F:443-459/Region: endonexin fold #status predicted

F:58/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.7%; Score 863; DB 1; Length 503;

Best Local Similarity 54.3%; Pred. No. 5.7e-48;

Matches 171; Conservative 60; Mismatches 84; Indels 0; Gaps 0;

Qy 13 RGTVTDPGDFDERADAEATLRKAMKGLTDEESTLTLTSRSNAQROEISAFAKTLFGRLD 72

Db 189 RGTITDASGDFPDRDAEVLKAMKGGTDEQAIDCLGSRNQRQOILLSPFYATYKGLD 248

Qy 73 LDKLSELTKFKFKLIVALKMPSRLYDAYELKHALKAGTNEKVLTEIATSRTPPEELRAI 132

Db 249 IKDLKSELNGFEKTLALMKTPLFDAYEIKAEIKAGTDEACLTIELASRSNEHREL 308

Qy 133 KQVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 192

Db 309 NKAYTEFKTLEEAINDSTSGHFQRLLSLSQGNRDESTNVDMSLVQRDVQVLYAAGEN 368

Qy 193 KWGTDEEKFITIFGTRSVSHLRKVFKYMTISGFOETETDRETSGNLEOLLAVVKSIR 252

Db 369 RLGTDESKFNVLCSRSRAHLVAVFNEYQRTGDIKSTCREMSGDLEQGLAVVVKCLX 428

Qy 253 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFKNFATSLYSMIKGDT 312

Db 429 NTPAFFAERLNARMGAGTKDRTLIRIMVSRSEIDLLDIRSEYKRMYSGLYHDSIGDTS 488

Qy 313 GDYKKALLLSGDEDD 327

Db 489 GDYRKILLKTCGGND 503

RESULT 15

A53152

annexin XI - human

C/Species: Homo sapiens (man)

C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 13-Aug-1999

C/Accession: A53152

R/Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; van Venrooij, W.J.

J. Biol. Chem. 269, 4240-4246, 1994

A/Title: The 56k autoantigen is identical to human annexin XI.

A/Reference number: A53152; MUID:94140847; PMID:7508441

A/Accession: A53152

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-505 <MIS>

A/Cross-references: GB:119605; NID:g457128; PIDN:AAA19734.1; PID:g457129

C/Genetics:

A/Gene: GDB:ANX11

A/Cross-references: GDB:313076

A/Map position: 9q11-q9q22

C/Superfamily: annexin VII; annexin repeat homology

C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid

F:203-274/Domain: annexin repeat homology <AX1>

F:275-346/Domain: annexin repeat homology <AX2>

F:358-430/Domain: annexin repeat homology <AX3>

F:434-505/Domain: annexin repeat homology <AX4>

Query Match 52.2%; Score 855; DB 2; Length 505;

Best Local Similarity 53.3%; Pred. No. 1.9e-47;

Matches 168; Conservative 61; Mismatches 86; Indels 0; Gaps 0;

Qy 13 RGTVTDPGDFDERADAEATLRKAMKGLTDEESTLTLTSRSNAQROEISAFAKTLFGRLD 72

Db 191 RGTITDASGDFPDRDAEVLKAMKGGTDEQAIDCLGSRNQRQOILLSPFYATYKGLD 250

Qy 73 LDKLSELTKFKFKLIVALKMPSRLYDAYELKHALKAGTNEKVLTEIATSRTPPEELRAI 132

Db 251 IKDLKSELNGFEKTLALMKTPLFDAYEIKAEIKAGTDEACLTIELASRSNEHREL 310

Qy 133 KQVEEYSGSLEDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 192

Db 311 NRAYKAEFKTLEEAINDSTSGHFQRLLSLSQGNRDESTNVDMSLAQRDAQELYAAGEN 370

Qy 193 KWGTDEEKFITIFGTRSVSHLRKVFKYMTISGFOETETDRETSGNLEOLLAVVKSIR 252

Db 371 RLGTDESKFNVLCSRSRAHLVAVFNEYQRTGDIKSTCREMSGDLEQGLAVVVKCLX 430

Qy 253 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFKNFATSLYSMIKGDT 312

Db 431 NTPAFFAERLNARMGAGTKDRTLIRIMVSRSEIDLLDIRSEYKRMYSGLYHDSIGDTS 490

Qy 313 GDYKKALLLSGDEDD 327

Db 491 GDYRKILLKTCGGND 505

Search completed: August 22, 2003, 21:36:12

Job time : 17 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2003, 21:28:42 ; Search time 8.66667 Seconds
(without alignments)
1774.354 Million cell updates/sec

Title: US-09-970-969-2

Perfect score: 1639

Sequence: 1 MACGGCHMAQVLRGTVDTP.....KGDTSYKALLLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1585	96.7	319	1 ANX5_HUMAN	P08758 homo sapien
2	1536.5	93.7	320	1 ANX5_BOVIN	P81287 bos taurus
3	1479.5	90.3	319	1 ANX5_MOUSE	P48036 mus musculus
4	1455.5	88.8	318	1 ANX5_RAT	P14668 rattus norv
5	1279	78.0	321	1 ANX5_CHICK	P17153 gallus gall
6	1090.5	66.5	323	1 ANX5_CYNPY	P70075 cynops pyrr
7	932	56.9	672	1 ANX6_HUMAN	P08133 homo sapien
8	932	56.9	672	1 ANX6_MOUSE	P14824 mus musculus
9	923	56.3	318	1 ANX4_HUMAN	P09525 homo sapien
10	921	56.2	318	1 ANX4_PIG	P08132 sus scrofa
11	921	56.2	672	1 ANX6_RAT	P48037 rattus norv
12	916	55.9	318	1 ANX4_MOUSE	P37429 mus musculus
13	914	55.8	318	1 ANX4_BOVIN	P13214 bos taurus
14	901	55.0	318	1 ANX4_CANFA	P50994 canis fami
15	896.5	54.7	671	1 ANX6_CHICK	P51901 gallus gall
16	891	54.4	318	1 ANX4_RAT	P55260 rattus norv
17	865	52.8	503	1 ANXB_BOVIN	P27214 bos taurus
18	863	52.7	503	1 ANXB_HUMAN	P33477 oryctolagus
19	855	52.2	505	1 ANXB_HUMAN	P50995 homo sapien
20	847	51.7	503	1 ANXB_MOUSE	P37384 mus musculus
21	841.5	51.3	327	1 ANXB_MOUSE	O35640 mus musculus
22	831.5	50.7	327	1 ANXB_HUMAN	P13928 homo sapien
23	802.5	49.0	323	1 ANX3_HUMAN	P12429 homo sapien
24	799	48.7	323	1 ANX3_MOUSE	O35639 mus musculus
25	779	47.5	466	1 ANX7_HUMAN	P20073 homo sapien
26	777	47.4	466	1 ANX7_MOUSE	Q07076 mus musculus
27	771	47.0	324	1 ANX3_RAT	P14669 rattus norv
28	761	46.4	618	1 ANX6_BOVIN	P79134 bos taurus
29	718	43.8	316	1 ANXC_HYDAT	P26256 hydra atten
30	711	43.4	512	1 ANX7_XENLA	Q92125 xenopus lae
31	701	42.8	324	1 ANX9_DROME	P22464 drosophila
32	698.5	42.6	338	1 ANX2_HUMAN	P07355 homo sapien
33	694.5	42.4	338	1 ANX2_BOVIN	P04272 bos taurus

Q07936 rattus norv
P07356 mus musculus
P22465 drosophila
P27216 homo sapien
P27006 xenopus lae
Q29471 canis fami
P17785 gallus gall
P24801 xenopus lae
P21662 oryctolagus
P51662 oryctolagus
P14087 canis cutle
P04083 homo sapien
P46193 bos taurus

34 693.5 42.3 338 1 ANX2_RAT
35 691.5 42.2 338 1 ANX2_MOUSE
36 685.5 41.8 320 1 ANX2_DROME
37 679 41.4 315 1 ANXD_HUMAN
38 675.5 41.2 339 1 ANXB_XENLA
39 671 40.9 315 1 ANXD_CANFA
40 666.5 40.7 338 1 ANX2_CHICK
41 662.5 40.4 339 1 ANX2_XENLA
42 649 39.6 346 1 ANX1_RABIT
43 648 39.5 346 1 ANX1_CAVCO
44 643 39.2 345 1 ANX1_HUMAN
45 643 39.2 346 1 ANX1_BOVIN

ALIGNMENTS

RESULT 1
ANX5_HUMAN STANDARD; PRT; 319 AA.
AC P08758;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchoring C1r).
GN ANX5 OR ANX5 OR ENX2 OR PP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88234495; PubMed=2967495;
RA Grundmann U., Abel K.-J., Bohn H., Loebermann H., Lottspeich F., Kuepper H.;
RT "Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88271329; PubMed=2455636;
RA Maurer-Fogy I., Reutlingsperger C.F.M., Pieters J., Bodo G., Stratowa C., Hauptmann R.;
RT "Cloning and expression of cDNA for human vascular anticoagulant, a Ca2+-dependent phospholipid-binding protein.";
RL Eur. J. Biochem. 174:585-592(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88273202; PubMed=2968983;
RA Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
RT "Five distinct calcium and phospholipid binding proteins share homology with lipocortin I.";
RL J. Biol. Chem. 263:10799-10811(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88139278; PubMed=2964863;
RA Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;
RT "Primary structure of human placental anticoagulant protein.";
RL Biochemistry 26:8087-8092(1987).
RN [5]
RP SEQUENCE FROM N.A., AND SEQUENCE.
RX MEDLINE=88139278; PubMed=2963810;
RA Iwasaki A., Suda M., Nakao H., Nagoya T., Saino Y., Arai K., Mizoguchi T., Sato F., Yoshizaki H., Hirata M., Miyata T., Shidara Y., Murata M., Maki M.;
RT "Structure and expression of cDNA for an inhibitor of blood coagulation isolated from human placenta: a new lipocortin-like protein.";

RL J. Biochem. 102:1261-1273(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228020; PubMed=2967291;
RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
RT "Cloning and expression of cDNA for human endonexin II, a Ca²⁺ and
RT phospholipid binding protein.";
RL J. Biol. Chem. 263:8037-8043(1988).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047484; PubMed=7958998;
RA Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
RT "The gene encoding human annexin V has a TATA-less promoter with a
RT high G+C content.";
RL Gene 149:253-260(1994).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94307733; PubMed=8034319;
RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
RA Tait J.F.;
RT "Organization of the human annexin V (ANX5) gene.";
RL Genomics 20:463-467(1994).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Bask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzowski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=90088443; PubMed=2532007;
RA Rothhut R., Comerla C., Cortial S., Haumont P.-Y., Diep Le K.H.,
RA Cavadore J.-C., Conard J., Russo-Marie F., Lederer F.;
RT "A 32 kDa lipocortin from human mononuclear cells appears to be
RT identical with the placental inhibitor of blood coagulation.";
RL Biochem. J. 263:929-935(1989).
RN [11]
RP SEQUENCE OF 85-130; 258-296 And 299-319.
RX MEDLINE=87317598; PubMed=2957692;
RA Schlaepfer D.D., Mehman T., Burgess W.H., Haigler H.T.;
RT "Structural and functional characterization of endonexin II, a
RT calcium- and phospholipid-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
RN [12]
RP SEQUENCE OF 84-92.
RX MEDLINE=89066652; PubMed=2974032;
RA Ahn N.G., Teller D.C., Blenkowski M.J., McMullen B.A., Lipkin E.W.,
RA de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
RT phospholipase A2 inhibitors from human placenta. Evidence against a
RT mechanistically relevant association between enzyme and inhibitor.";
RL J. Biol. Chem. 263:18657-18663(1988).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=91065314; PubMed=2147412;
RA Huber R., Roemisch J., Paques E.-P.;
RT "The crystal and molecular structure of human annexin V, an
RT anticoagulant protein that binds to calcium and membranes.";
RL EMBO J. 9:3867-3874(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91085549; PubMed=2148156;
RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
RT "The calcium binding sites in human annexin V by crystal structure
RT analysis at 2.0-A resolution. Implications for membrane binding and
RT calcium channel activity.";
RL FEBS Lett. 275:15-21(1990).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92177413; PubMed=1311770;
RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
RA Luecke H., Roemisch J., Paques E.-P.;
RT "Crystal and molecular structure of human annexin V after refinement.
RT Implications for structure, membrane binding and ion channel
RT formation of the annexin family of proteins.";
RL J. Mol. Biol. 223:683-704(1992).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=98062349; PubMed=9398511;
RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
RT "Crystal structure of annexin V with its ligand K-201 as a calcium
RT channel activity inhibitor.";
RL J. Mol. Biol. 274:16-20(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=98118533; PubMed=9435213;
RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
RT "Residue-specific bioincorporation of non-natural, biologically
RT active amino acids into proteins as possible drug carriers: structure
RT and stability of the per-thioproline mutant of annexin V.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
CC -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
CC -1- SUBUNIT: MONOMER. BINDS ATP (BY SIMILARITY).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
CC -1- CAUTION: THIS PROTEIN HAS BEEN INDEPENDENTLY SEQUENCED BY AT LEAST
CC SEVEN GROUPS UNDER DIFFERENT NAMES!
CC -1- DATABASE: NAME-RED Systems' cytokine source book: Annexin 5;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=185".
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12454; CAA30985.1; -
DR EMBL: M19384; AAB59545.1; -
DR EMBL: M18366; AAB35570.1; -
DR EMBL: M21731; AAA36166.1; -
DR EMBL: D00172; BAA00122.1; -
DR EMBL: J03745; AAA52386.1; -
DR EMBL: U01691; AAB40047.1; -
DR EMBL: U01681; AAB40047.1; JOINED.
DR EMBL: U01682; AAB40047.1; JOINED.
DR EMBL: U01683; AAB40047.1; JOINED.
DR EMBL: U01685; AAB40047.1; JOINED.
DR EMBL: U01686; AAB40047.1; JOINED.
DR EMBL: U01687; AAB40047.1; JOINED.
DR EMBL: U01689; AAB40047.1; JOINED.
DR EMBL: U01690; AAB40047.1; JOINED.

Query Match 96.7%; Score 1585; DB 1; Length 319;
 Best Local Similarity 99.7%; Pred. No. 1.5e-95;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 AQLRGVTPPPGDERADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFTLF 68
 Db 1 AQLRGVTPPPGDERADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFTLF 60

Qy 69 GRLLDDKSLTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
 Db 61 GRLLDDKSLTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120

Qy 129 LRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEQDAALFQ 188
 Db 121 LRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEQDAALFQ 180

Qy 189 AGELKWTGDEKFTITFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAV 248
 Db 181 AGELKWTGDEKFTITFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAV 240

Qy 249 KSIRSIAPYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKFNATSLYSMIK 308
 Db 241 KSIRSIAPYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKFNATSLYSMIK 300

Qy 309 GDTSGDYKKALLLGGEDD 327
 Db 301 GDTSGDYKKALLLGGEDD 319

RESULT 2
 ANX5_BOVIN
 ID ANX5_BOVIN STANDARD; PRT; 320 AA.
 AC P81287;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93041974; PubMed=1420335;
 RA Learmonth M.P., Howell S.A., Harris A.C.M., Amess B., Patel Y.,
 RA Giambanco I., Bianchi R., Pula G., Ceccarelli P., Donato R.,
 RA Green B.N., Aitken A.;
 RT "Novel isoforms of CaBP 33/37 (annexin V) from mammalian brain:
 RT structural and phosphorylation differences that suggest distinct
 RT biological roles.";
 RL Biochim. Biophys. Acta 1160:76-83(1992).
 CC -|- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 CC -|- SUBUNIT: MONOMER. BINDS AFPR (By similarity).
 CC -|- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -|- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -|- SIMILARITY: Contains 4 annexin repeats.
 DR PIR: S27214; S27214.
 DR HSSP: P08758; 1ANW.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SM000335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Acetylation.
 FT INIT_MET 0 0
 FT REPEAT 23 83 ANNEXIN 1.
 FT REPEAT 95 155 ANNEXIN 2.
 FT REPEAT 179 239 ANNEXIN 3.
 FT REPEAT 254 314 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT VARIANT 36 36 S -> T.
 FT VARIANT 125 125 K -> E.
 SQ SEQUENCE 320 AA; 35942 MW; 50FCE18E95F19C80 CRC64;

Query Match 93.7%; Score 1536.5; DB 1; Length 320;
 Best Local Similarity 96.6%; Pred. No. 2.1e-92;
 Matches 309; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 9 AQLRGVTPPPGDERADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFTLF 68
 Db 1 AQLRGVTPPPGDERADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFTLF 60

Qy 69 GRLLDDKSLTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
 Db 61 GRLLDDKSLTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120

Qy 129 LRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEQDAALFQ 188
 Db 121 LRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEQDAALFQ 180

Qy 189 AGELKWTGDEKFTITFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAV 248
 Db 181 AGELKWTGDEKFTITFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAV 240

Qy 249 KSIRSIAPYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKFNATSLYSMIK 308
 Db 241 KSIRSIAPYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKFRKFNATSLYSMIK 300

Qy 309 GDTSGDYKKALLLGGEDD 327
 Db 301 GDTSGDYKKALLLGGEDD 320

RESULT 3
 ANX5_MOUSE
 ID ANX5_MOUSE STANDARD; PRT; 319 AA.
 AC P48036;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal cavity;
 RX MEDLINE=96422179; PubMed=8824796;
 RA Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
 RT "Mouse annexin V chromosomal localization, cDNA sequence
 RT conservation, and molecular evolution.";
 RL Genomics 31:151-157(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adachi T., Kojima K., Fukuoaka S.-I., Ogawa H., Matsumoto I.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;

RX MEDLINE-99072820; PubMed-9854034;
RA Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,
RA Fernandez M.P.;
RT "Mouse annexin V genomic organization includes an endogenous
retrovirus".
RL J. Biochem. 337:125-131(1999).
CC -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
CC -1- SUBUNIT: MONOMER. BINDS ATRX (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U29395; AAC2530.1; .
DR EMBL: D63423; BAA09728.1; .
DR EMBL: AJ230108; CAA13092.1; JOINED.
DR EMBL: AJ230110; CAA13092.1; JOINED.
DR EMBL: AJ230111; CAA13092.1; JOINED.
DR EMBL: AJ230114; CAA13092.1; JOINED.
DR EMBL: AJ230116; CAA13092.1; JOINED.
DR EMBL: AJ230118; CAA13092.1; JOINED.
DR EMBL: AJ230119; CAA13092.1; JOINED.
DR EMBL: AJ230120; CAA13092.1; JOINED.
DR EMBL: AJ230121; CAA13092.1; JOINED.
DR EMBL: AJ230122; CAA13092.1; JOINED.
DR EMBL: AJ230123; CAA13092.1; JOINED.
DR EMBL: AJ230124; CAA13092.1; JOINED.
DR HSSP: P14668; 1A8B.
DR SWISS-2DPAGE: P48036; MOUSE.
DR MGD: MGI:106008; Anxa5.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
DR KX Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
KW Placenta.
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
SQ SEQUENCE 319 AA; 35752 MW; 55055BAP2E1C3687 CRC64;

Query Match 90.3%; Score 1479.5; DB 1; Length 319;
Best Local Similarity 93.7%; Pred. No. 9.9e-89;
Matches 296; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 13 RGVTFDPGFRADAEATLRKAMKGLGCTDEESTLTLTSRNSAOROEISAAPKTLFGRDL 72
Db 4 RGVTFDPGFRADAEATLRKAMKGLGCTDEESTLTLTSRNSAOROEISAAPKTLFGRDL 63

QY 73 LDDLKSELGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
Db 64 VDDLKSELGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELSAI 123

QY 133 KQVEEYECSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVDAQALFQAGEL 192
Db 124 KQVEEYECSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVDAQALFQAGEL 183

QY 193 KWTDEKTIITFGTSVSHLRKRVFKYMTISGFQIEETIDRTSNGNLEQLLAVVKSIR 252
Db 184 KWTDEKTIITFGTSVSHLRKRVFKYMTISGFQIEETIDRTSNGNLEQLLAVVKSIR 243

QY 253 SIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKNFATSLYSIMIKGDT 312
Db 244 SIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKNFATSLYSIMIKGDT 303

QY 313 GDYKKALLLL-SGEDD 327
Db 304 GDYKKALLLLCGGEDD 319

RESULT 4
ANX5_RAT
ID ANX5_RAT STANDARD; PRT; 318 AA.
AC P14668;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (GBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchoring CII).
GN ANXA5 OR ANX5
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88273202; PubMed-2968983;
RA Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K.,
RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
RA Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
RT "Five distinct calcium and phospholipid binding proteins share
RT homology with lipocortin I".
RL J. Biol. Chem. 263:10799-10811(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar;
RX MEDLINE-96035863; PubMed-7556178;
RA Imai Y., Kohsaka S.;
RT "Structure of rat annexin V gene and molecular diversity of its
RT transcripts".
RL Eur. J. Biochem. 232:327-334(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-93369587; PubMed-8362244;
RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
RT "Rat annexin V crystal structure: Ca(2+)-induced conformational
RT changes".
RL Science 261:1321-1324(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC TISSUE-Kidney;
RX MEDLINE-96089783; PubMed-7583670;
RA Swaijjo M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
RT "Ca(2+)-bridging mechanism and phospholipid head group recognition in
RT the membrane-binding protein annexin V".
RL Nat. Struct. Biol. 2:968-974(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
RX MEDLINE-98272673; PubMed-9609693;
RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swaijjo M.A., Balch C.,
RA Head J.F., Rettinger G., Dedman J.R., Seaton B.A.;
RT "Mutational and crystallographic analyses of interfacial residues in
RT annexin V suggest direct interactions with phospholipid membrane
RT components".
RL Biochemistry 37:8004-8010(1998).
RN [6]
RP INTERACTION WITH DNMT1.
RC STRAIN-Wistar; TISSUE-Brain;
RX MEDLINE-96301899; PubMed-8667030;
RA Ohnawa K., Imai Y., Ito D., Kohsaka S.;
RT "Molecular cloning and characterization of annexin V-binding proteins

with highly hydrophilic peptide structure.*;
 J. Neurochem. 67:89-97(1996).
 -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 -1- SUBUNIT: MONOMER. Binds ATRX and DNMT1.
 -1- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.
 -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 -1- SIMILARITY: Contains 4 annexin repeats.

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 or send an email to license@isb-sib.ch).

 DR EMBL; M21730; AAA41512.1; -;
 DR EMBL; D42137; BAA07708.1; -;
 DR EMBL; D42129; BAA07708.1; JOINED.
 DR EMBL; D42130; BAA07708.1; JOINED.
 DR EMBL; D63337; BAA07708.1; JOINED.
 DR EMBL; D42131; BAA07708.1; JOINED.
 DR EMBL; D42132; BAA07708.1; JOINED.
 DR EMBL; D42133; BAA07708.1; JOINED.
 DR EMBL; D42134; BAA07708.1; JOINED.
 DR EMBL; D42135; BAA07708.1; JOINED.
 DR EMBL; D42136; BAA07708.1; JOINED.
 DR PIR; C29250; L0RT5.
 DR PDB; 2RAN; 30-NOV-94.
 DR PDB; 1A8A; 17-JUN-98.
 DR PDB; 1A8B; 17-JUN-98.
 DR PDB; 1BC0; 13-JAN-99.
 DR PDB; 1BC1; 13-JAN-99.
 DR PDB; 1BC3; 13-JAN-99.
 DR PDB; 1BCW; 13-JAN-99.
 DR PDB; 1BCY; 13-JAN-99.
 DR PDB; 1BC2; 13-JAN-99.
 DR PDB; 1G5N; 13-MAR-02.
 DR PDB; 1N41; 04-FEB-03.
 DR PDB; 1N42; 04-FEB-03.
 DR PDB; 1N44; 04-FEB-03.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR PRODOM; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 Placenta; Acetylation; 3D-structure.
 FT INIT_MET 0
 FT REPEAT 20 80 ANNEXIN 1.
 FT REPEAT 92 152 ANNEXIN 2.
 FT REPEAT 176 236 ANNEXIN 3.
 FT REPEAT 251 311 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION.
 FT TURN 10 11
 FT HELIX 14 25
 FT HELIX 32 39
 FT TURN 40 41
 FT HELIX 44 58
 FT HELIX 62 69
 FT HELIX 72 82
 FT HELIX 85 97
 FT HELIX 104 113
 FT HELIX 116 130
 FT HELIX 134 141
 FT HELIX 144 154
 FT TURN 155 156
 FT HELIX 166 179
 FT TURN 180 182

FT HELIX 188 197
 FT HELIX 200 214
 FT HELIX 218 225
 FT HELIX 228 242
 FT HELIX 244 256
 FT HELIX 263 273
 FT TURN 274 277
 FT HELIX 278 289
 FT HELIX 293 300
 FT HELIX 303 313
 SQ SEQUENCE 318 AA; 35613 MW; 1A755A7C11FALICE CRC64;
 Query Match 88.8%; Score 1455.5; DB 1; Length 318;
 Best Local Similarity 91.8%; Pred. No. 3.5e-87;
 Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
 QY 12 LRGVTVPFDFDEADAEIIRKAMKGLGTDDESLTLLTSRSNAORQEISAAFKTLFGRD 71
 DB 2 LRGVTVPFDFGDRADAELVRKAMKGLGTDDESLTLLTSRSNAORQOIAEEFKTLFGRD 61
 QY 72 LLDLKSGLTGKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 131
 DB 62 LVNDKMSGLTGKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 121
 QY 132 IKQYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEODAQAALFOAGE 191
 DB 122 IKQAYEEYEGSNLEDDVVGDTSGYYQRMVLVLLQANRDPDPAIDDAQVELDAQAALFOAGE 181
 QY 192 LKWTDEKFTITFGTRSVSHLRKVPDKYMTISFGQIEETIDRETSGNLELLAVVKS 251
 DB 182 LKWTDEKFTITLGTTRSVSHLRVFDKYMISGFIQIEETIDRETSGNLELLAVVKS 241
 QY 252 RSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKFRKFNATSLYSNIKGD 311
 DB 242 RSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKFRKFNATSLYSNIKGD 301
 QY 312 SGDYKKALLL-SGEDD 327
 DB 302 SGDYKKALLLGGGEDD 318
 RESULT 5
 ANX5_CHICK STANDARD; PRT; 321 AA.
 AC P17153;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANXA5 OR ANX5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88186917; PubMed=2833522;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
 RA Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of anchoring CII, a collagen binding protein isolated
 RT from chondrocyte membrane.";
 RL J. Biol. Chem. 263:5921-5925(1988).
 RN [2]
 RP SUGGEST SEQUENCING ERROR.
 RX MEDLINE=90020458; PubMed=2552626;
 RA Moss S.E., Crumpton M.J.;
 RT "Alternative splicing or cloning artefact?";
 RL Trends Biochem. Sci. 14:325-325(1989).
 RN [3]

RP REVISIONS.
 RX MEDLINE-90243721; PubMed-2159478;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaffle M.,
 RA Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of annexin CII, a collagen binding protein isolated
 RT from chondrocyte membrane.";
 RL J. Biol. Chem. 265:8344-8344(1990).
 RN [4]
 RP REVISIONS.
 RA Pfaffle M., Ruggiero F., Hofmann H., Fernandez M.P., Selmin O.,
 RA Yamada Y., Garrone R., von der Mark K.;
 RL EMBO J. 9:1336-1336(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-White leghorn; TISSUE=Liver;
 RX MEDLINE-94215900; PubMed-8163186;
 RA Fernandez M.P., Fernandez M.R., Morgan R.O.;
 RT "Structure of the gene encoding annexin CII (chick annexin V).";
 RL Gene 141:179-186(1994).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE-93249384; PubMed-8484740;
 RA Boustead C.M., Brown R., Walker J.H.;
 RT "Isolation, characterization and localization of annexin V from
 RT chicken liver.";
 RL Biochem. J. 291:601-608(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-93229489; PubMed-8471604;
 RA Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.;
 RT "Structure of chicken annexin V at 2.25-A resolution.";
 RL Biochemistry 32:3923-3929(1993).
 CC -1- FUNCTION: COLLAGEN-BINDING PROTEIN.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M30971; AAA48591.1; ALT_SEQ.
 DR EMBL; U01680; AAB39917.1;
 DR EMBL; U01671; AAB39917.1; JOINED.
 DR EMBL; U01672; AAB39917.1; JOINED.
 DR EMBL; U01673; AAB39917.1; JOINED.
 DR EMBL; U01675; AAB39917.1; JOINED.
 DR EMBL; U01676; AAB39917.1; JOINED.
 DR EMBL; U01677; AAB39917.1; JOINED.
 DR EMBL; U01678; AAB39917.1; JOINED.
 DR EMBL; U01679; AAB39917.1; JOINED.
 DR PIR; A35381; LUCHS.
 DR PDB; 1ALA; 31-OCT-93.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 FT REPEAT 24 84
 FT REPEAT 96 156 ANNEXIN 1.
 FT REPEAT 180 240 ANNEXIN 2.
 FT REPEAT 255 315 ANNEXIN 3.
 FT CONFLICT 168 168 ANNEXIN 4.
 FT TURN 13 14 D -> E (IN REF. 1).
 FT HELIX 17 28

FT HELIX 35 44
 FT HELIX 47 61
 FT HELIX 65 72
 FT HELIX 75 85
 FT TURN 88 90
 FT HELIX 91 100
 FT HELIX 107 116
 FT HELIX 119 133
 FT HELIX 137 144
 FT HELIX 147 157
 FT TURN 158 158
 FT HELIX 169 184
 FT TURN 185 187
 FT HELIX 191 200
 FT HELIX 203 217
 FT HELIX 221 224
 FT HELIX 232 245
 FT HELIX 247 259
 FT HELIX 266 275
 FT TURN 276 280
 FT HELIX 281 292
 FT HELIX 296 303
 FT HELIX 306 316
 SQ SEQUENCE 321 AA; 36198 MW; 43E2983F86797025 CRC64;
 Query Match 78.0%; Score 1279; DB 1; Length 321;
 Best Local Similarity 78.1%; Pred. No. 8.6e-76;
 Matches 250; Conservative 38; Mismatches 32; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVDPFGFDERADAETLRKAMKGLGTDEESILTLTSRNAQOEISAAFKTL 67
 DB 1 MAKYTRGTVTAFSPFDARADAEALRKAMKMGMTDEETILKILTSRNAQOEISAAFKTL 60
 QY 68 FGRDLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHLKAGTNEKVLTEIASRTPE 127
 DB 61 FGRDLVDDLKSELTGAFETLWLSMRPARIFADHAKHLKAGTNEKVLTEIASRTPA 120
 QY 128 ELRAIKQVYEEYSSLEDDVWGDTSGYYORMLVLLQANRPDAGIDEAQVDDAQLF 187
 DB 121 EVQNIQVYQVEANLEKIDTSGHFORLLVLLQANRPDPGRVDEALVEKDAQVLF 180
 QY 188 OAGELKNGDEEFITFGTSVSHLRKVPDKYMTISGQIEETIDRETSGNLEOLLAV 247
 DB 181 RAGELKNGDEEFITLGTTSVSHLRVDFKVTISGQIEETIDRETSGDLEKLLAV 240
 QY 248 VKSIRSIAPYLAETLYYAMKAGCTDDHTLIRVWVSSEIDLFNIRKFRKNFATSLYSMI 307
 DB 241 VKCIRSVPAYFAETLYYSKMGACTDDDTLIRVWVSSEIDLLDIRHFRKNFAKSLYQMI 300
 QY 308 KGDTSGDYKALLLSGEDD 327
 DB 301 QKDTSGDYRKALLLSGGDD 320
 RESULT 6
 ANX5_CYNPY STANDARD; PRT; 323 AA.
 AC P70075;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Yamamoto T., Hikono T., Abe S.I.;
 RT "Differential expression of annexin V during spermatogenesis in the
 RT newt Cynops pyrrhogaster.";
 RL Dev. Genes Evol. 206:64-71(1996).

CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D64134; BAA11012.1; -
 DR HSSP: P08758; IAVH
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 FT REPEAT 26 86 ANNEXIN 1.
 FT REPEAT 98 158 ANNEXIN 2.
 FT REPEAT 182 242 ANNEXIN 3.
 FT REPEAT 257 317 ANNEXIN 4.
 FT REPEAT 323 331 ANNEXIN 4.
 SO SEQUENCE 323 AA; 35981 MW; 044B31AC28164CE2 CRC64;
 Query Match 66.5%; Score 1090.5; DB 1; Length 323;
 Best Local Similarity 66.7%; Pred. No. 1.3e-63;
 Matches 218; Conservative 45; Mismatches 59; Indels 5; Gaps 1;
 QY 1 MACGGGMAQVLRGTVDTPGDFERADAETLRKAMKGLGTDSILTLTSRNSAQKQEI 60
 Db 1 MACLKG-----AKGTQVADPDFDKDAETLRAMKGLGTDEDTILKLLSRNKQKQEI 55
 QY 61 SAAFKTLFGRDLDDKLSLTGFEKLVLMKPSRLYDAVEKLHAKLGAGTNEKVLTEI 120
 Db 56 ALTYKTLFGRDLDDKLSLGSFGFETLLVALMPAHLYDACELRNALKGLTLENVIEI 115
 QY 121 IASRTPEELRAIKQVVEEYEGSSLEDDVDGDTGYGYQRMVLVLLQANRDPDAGIDEAQVE 180
 Db 116 MASRTAAEVKNIKETKYKPEFDSLEKIDVGTSGNFERLLVSLVQANRDPGVKDEQVE 175
 QY 181 ODAQALFOAGELKNGTDEEKFIIFGTGRSVSHLRKPKVDKTYTSGFQIETIDRETSGNL 240
 Db 176 NDAKALFDAGENKNGTDEETFIILSTRGVHLRKVDQYMTISGYQIEESIQSTGGHF 235
 QY 241 EQLLAVVKSIRSPAYLAETLYYAMKAGTDDHTLIRVSVSRSEIDLNFIRKFKNEA 300
 Db 236 EKULLAVVKSIRSIQGVLAELVLYNSMKAGTDQTLIRVLSRSEIDLNFIRQTFKHYG 295
 QY 301 TSLYSMTKGTSDGYKALLLLSGEDD 327
 Db 296 KSLHAMIQSDTSGDYRNALLLCGEID 322
 RESULT 7
 ANX6_HUMAN STANDARD; PRT; 672 AA.
 AC P08133;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANX6 OR ANX6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
 RP MEDLINE=88196081; PubMed=3258820;
 RA Crompton M.R., Owens R.J., Totty N.F., Moss S.E., Waterfield M.D.,
 RA Crumpton M.J.;
 RT "Primary structure of the human, membrane-associated Ca²⁺-binding
 RL protein p68 a novel member of a protein family.";
 RL EMBO J. 7:21-27(1988).
 RN [2]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=88124902; PubMed=2963335;
 RA Suedhof T.C., Slaughter C.A., Leznicki I., Barjon P., Reynolds G.A.;
 RT "Human 67-kDa calelectrin contains a duplication of four repeats
 RL found in 35-kDa lipocortins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89380132; PubMed=2528541;
 RA Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya T.,
 RA Saino Y., Shidara Y., Maki M.;
 RT "Structure and expression of cDNA for calphobindin II, a human
 RL placental coagulation inhibitor.";
 RL J. Biochem. 106:43-49(1989).
 RN [4]
 RP SEQUENCE.
 RX MEDLINE=90236978; PubMed=2139657;
 RA Yoshizaki H., Mizoguchi T., Arai K., Shiratsuchi M., Shidara Y.,
 RA Maki M.;
 RT "Structure and properties of calphobindin II, an anticoagulant
 RL protein from human placenta.";
 RL J. Biochem. 107:43-50(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzay D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Halton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 RX MEDLINE=96326697; PubMed=8709144;
 RA Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann S.,
 RA Huber R., Voges D.;
 RT "The structure of recombinant human annexin VI in crystals and
 RL membrane-bound.";
 RL J. Mol. Biol. 260:638-643(1996).
 CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF
 CC CA(2+) FROM INTRACELLULAR STORES.
 CC -1- INDUCTION: BY BBV.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- PTM: PHOSPHORYLATED IN RESPONSE TO GROWTH FACTOR STIMULATION.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----

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DR EMBL: D00510; BAA00400.1; -;
 DR EMBL: Y00057; CAA68286.1; -;
 DR EMBL: J03578; AAA35656.1; -;
 DR EMBL: BC017046; AAI17046.1; -;
 DR PIR: J00032; AOHU68.
 DR PDB: 1M9I; 07-AUG-02.
 DR Genew: HGNC:544; ANXA6.
 DR MIM: 114070; -;
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 8.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 8.
 DR SMART: SM00335; ANX; 8.
 DR PROSITE: PS00223; ANNEXIN; 8.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Acetylation;
 KW Phosphorylation; 3D-structure.
 FT INIT_MET 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 FT MOD_RES 1 1 ACETYLATION.
 FT CONFLICT 225 226 IE -> MK (IN REF. 2).
 FT CONFLICT 554 554 S -> T (IN REF. 2).
 FT CONFLICT 618 618 E -> D (IN REF. 1).
 SQ SEQUENCE 672 AA; 75742 MW; 2829237029BDIDCB CRC64;

Query Match 56.9%; Score 932; DB 1; Length 672;
 Best Local Similarity 58.1%; Pred. No. 5.2e-53;
 Matches 183; Conservative 52; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGVTVDFPGFDRADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTLFGRDL 72
 DB 10 RGSIHDFPGFDPNQAALYATAMKFGSGDKAEILDIITSRNRQROEVQCSYKSLYKDL 69
 QY 73 LDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
 DB 70 IADLYELTKFERLIVGLMRPAYCDAKEIKDAISGIGTDEKCLTEILASRTNEQMHO 129
 QY 133 KOVYEEYSGSLEDVVGDTSCYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 192
 DB 130 VAAKYDAVERDEADIIIGDTSQHFQKMLVLLQGTREDDVVSDELVQDVQDLYEAGEL 189
 QY 313 GDYKKALLSGEDD 327
 DB 310 GEYKTKLLKSGDD 324
 RESULT 8
 ANX6_MOUSE
 ID ANX6_MOUSE
 AC P14824; STANDARD; PRT; 672 AA.
 DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANXA6 OR ANX6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c;
 RX MEDLINE=89030687; PubMed=2972541;
 RA Moss S.E., Crompton M.R., Crompton M.J.;
 RT "Molecular cloning of murine p68, a Ca2+-binding protein of the
 RT lipocortin family";
 RL Eur. J. Biochem. 177:21-27(1988).
 CC -!- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF
 CC CA(2+) FROM INTRACELLULAR STORES.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -!- SIMILARITY: Contains 8 annexin repeats.
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DR EMBL: X13450; CAA31808.1; -;
 DR PIR: S01786; S01786.
 DR HSP: P79134; IAVC.
 DR MGD: MGI:88255; Anxa6.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 8.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 8.
 DR SMART: SM00335; ANX; 8.
 DR PROSITE: PS00223; ANNEXIN; 8.
 KW Annexin; calcium/phospholipid-binding; Repeat.
 FT INIT_MET 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 SQ SEQUENCE 672 AA; 75755 MW; 2D85C1DD235FC76 CRC64;

Query Match 56.9%; Score 932; DB 1; Length 672;
 Best Local Similarity 59.0%; Pred. No. 5.2e-53;
 Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGVTVDFPGFDRADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTLFGRDL 72
 DB 10 RGSVHDFPGFDPNQAALYATAMKFGSGDKSEILELITSRNRQROEIQCSYKSLYKDL 69
 QY 73 LDDLKSELTKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
 DB 70 IEDLYELTKFERLIVGLMRPAYCDAKEIKDAISGIGTDEKCLTEILASRTNEQMHO 129
 QY 133 KOVYEEYSGSLEDVVGDTSCYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 192
 DB 130 VAAKYDAVERDEADIIIGDTSQHFQKMLVLLQGTREDDVVSDELVQDVQDLYEAGEL 189
 QY 193 KMGTDDEEFPITIFGTRSVSHLRKVKYMTISGFOIETIDRETSGNLEBQLLAVVVKSTR 252
 DT 01-APR-1990 (Rel. 14, Created)

Db 190 KWGTDAQFIYILGNRSKQHLRLVDEYLTKTGPTEASIRGSLSGDFEKMLAVVKCIR 243

QY 253 SIPAYLAETLYAMKGAGCTDDHTLIRVMVSRESDLEINRKEFRKNFATSLYSIMIKGDTS 312
I : I I I I I I I I .
Db 250 STPEYFAERALLKGLTGRTDNTLIRMWSELDMDIREIFTRKYKSLSYMIKNDIS 309
SIPAYLAETLYAMKGAGCTDDHTLIRVMVSRESDLEINRKEFRKNFATSLYSIMIKGDTS 312

QY 313 GPTYEKAIIILSGEDD 327
I : I I I I I I I I I I
Db 310 GEYKALKLCGGDD 324
I : I I I I I I I I I I

RESULT 9

ANX4_HUMAN

ID ANX4_HUMAN STANDARD; PRT; 318 AA.

AC P09525; Q96F33; Q9BWK1;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PPA-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/P41).
DE DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88309022; Pubmed=2970257;
RA Grundmann U., Amann E., Abel K.-J., Kuepper H.A.;
RT "Isolation and expression of cDNA coding for a new member of the phospholipase A2 inhibitor family."; Behring Inst. Mitt. 82:59-67(1988).
RL [2]
RN RP
RP SEQUENCE FROM N.A.
RX MEDLINE=92155721; Pubmed=1346776;
RA Tait J.F., Smith C., Frankenberry D.A., Miao C.H., Adler D.A., Distèche C.M.;
RA "Chromosomal mapping of the human annexin IV (ANX4) gene."; Genomics 12:313-318(1992).
RL [3]
RN RP
RP SEQUENCE FROM N.A.
RX MEDLINE=97239215; Pubmed=9084877;
RA Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T., Matsumoto I.;
RA "Characterization of human p33/41 (annexin IV), a Ca2+ dependent carbohydrate-binding protein with monoclonal anti-annexin IV antibodies, AS11 and AS17."; Biol. Pharm. Bull. 20:224-229(1997).
RL [4]
RN RP
RP SEQUENCE FROM N.A.
RC TISSUE=Eye, and Uterus;
RX MEDLINE=22388257; Pubmed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J.N., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5] SEQUENCE OF 26-55; 98-123 AND 279-307.
MEDLINE=89066652; PubMed=2974032;
RA Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
RT phospholipase A2 inhibitors from human placenta. Evidence against a
RT mechanistically relevant association between enzyme and inhibitor.";
J. Biol. Chem. 263:18657-18663(1988).
[6] SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
MEDLINE=89118212; PubMed=2975506;
RA Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
Hendrickson L.B., Fujikawa K.;
RA "Placental anticoagulant proteins: isolation and comparative
RT characterization of four members of the lipocortin family";
Biochemistry 27:6268-6276(1988).
[7] X-RAY CRYSTALLOGRAPHY.
MEDLINE=91073383; PubMed=2254922;
RA Freemont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;
RT "Crystallization and preliminary X-ray crystallographic studies of
RT human placental annexin IV.";
J. Mol. Biol. 216:219-221(1990).
CC -!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: Contains 4 annexin repeats.
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@lsb-sib.ch).
DR EMBL; M19383; AAC41689.1; ALT_INIT.
DR EMBL; M82809; AAA51740.1; -
DR EMBL; D78152; BAA11227.1; ALT_INIT.
DR EMBL; BC000182; AAH0182.1; ALT_INIT.
DR EMBL; BC011659; AAH11659.1; ALT_INIT.
DR HSSP; P13214; 1ANN.
DR SWISS-2DPAGE; P09525; HUMAN.
DR PMMA-2DPAGE; P09525; -
DR Genew; HGNC:542; ANXA4.
DR MIM; 106491; -
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INIT_MET 0
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
FT CONFLICT 95 95 R -> Q (IN REF. 1).
SQ SEQUENCE 318 AA; 35751 MW; 16B19E01500350F7 CRC64;
Query Match 56.3%; Score 923; DB 1; Length 318;
Best Local Similarity 58.3%; Pred. No. 8e-53;
Matches 183; Conservative 53; Mismatches 78; Indels 0; Gaps 0;
Qy 14 GTVDFPGFDERADAETLRKAMGLGTDDESIILTLTSRSNAQRQETISAAFKTLFGDLL 73
Db 5 GTVKAAQSGFNAMDAOTLRKAMGLGTDDESIILTSVLAQRTAQRQETIRYAKSTIGRDLI 64

	Query Match	56.3%	Score 923;	DB 1;	Length 318;
	Best Local Similarity	58.3%;	Pred. No. 8e-53;		
	Matches 183;	Conservative	53;	Mismatches	78;
			Indels	0;	Gaps
QY	14	GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSRNAQRQETISAQKTLFGDILL	73		
Db	5	GTVKAAAGFNAMEDAOTLRKAMKGLGTDEDAITLSTLAYRNTAQROEIRTAAYKSTIGRDLLI	64		

EMBL; F14682; CAA23194.1; -.

Matches	184;	Conservative	51;	Mismatches	79;	Indels	0;	Gaps	0;
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CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF

CA(2+) FROM INTRACELLULAR STORES.
 -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 -1- SIMILARITY: Contains 8 annexin repeats.

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 EMBL; X86086; CAA60040.1; --
 PIR; S65683; S52844.
 HSP; P79134; IAVC.
 InterPro; IPR001464; Annexin.
 Pfam; PF00191; annexin; 8.
 PRINTS; PR00196; ANNEXIN.
 ProDom; PD000143; Annexin; 8.
 SMART; SM00335; ANX; 8.
 ProSITE; PS00223; ANNEXIN; 7.
 Annexin; Calcium/phospholipid-binding; Repeat.
 INIT_MET 0 BY SIMILARITY.
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 SQ SEQUENCE 672 AA; 75622 MW; BBEE798A9CAB1511 CRC64;

 Query Match 56.2%; Score 921; DB 1; Length 672;
 Best Local Similarity 58.7%; Pred. No. 2.7e-52;
 Matches 185; Conservative 48; Mismatches 82; Indels 0; Gaps 0;

 QY 13 RGTVDPPGDFERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTLFGDRL 72
 DB 10 RGSVHPADFDANQDAALYATKMGFGSDRESILTLTSRSNAQOEISAAFKTLFGDRL 69
 QY 73 LDKSELTKGFEKLIYALVMPKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
 DB 70 IADLYELTKFELIYALVMPKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 129
 QY 133 KQVEEYGSLSDDVVDGTSYQYQRMVLLVLANRDPDAGIDEAQVEQDAQALFOAGEL 192
 DB 130 VAAYKDAYERDLESIIIGDTSYQYQRMVLLVLANRDPDAGIDEAQVEQDAQALFOAGEL 189
 QY 193 KWTDEEKFITICTRSVSHLKFVDEKYMVTISGFOIETIDRETSGNLEQLLAVVKSIR 252
 DB 190 KWTDEEKFITICTRSVSHLKFVDEKYMVTISGFOIETIDRETSGNLEQLLAVVKSIR 249
 QY 253 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRNFATSLYSMIKGDT 312
 DB 250 STEYFAERLYKSMKGLGTDDNTLIRVMVSRSEIDLFNIRKFRNFATSLYSMIKGDT 309
 QY 313 GDYKALLLSGDD 327
 DB 310 GEYKALLKLCGGDD 324

 RESULT 12
 ANX4_MOUSE ID ANX4_MOUSE STANDARD; PRT; 318 AA.
 AC P97429;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV).

GN ANX4 OR ANX4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HeJ;
 RA Sable C.L., Shannon J., Riches D.W.H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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 EMBL; U72941; AAB40697.1; --
 HSP; P13214; IANN.
 MGD; MGI:88030; Anxa4.
 InterPro; IPR001464; Annexin.
 Pfam; PF00191; annexin; 4.
 PRINTS; PR00196; ANNEXIN.
 ProDom; PD000143; Annexin; 4.
 SMART; SM00335; ANX; 4.
 ProSITE; PS00223; ANNEXIN; 4.
 Annexin; Calcium/phospholipid-binding; Repeat.
 INIT_MET 0 BY SIMILARITY.
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 SQ SEQUENCE 318 AA; 35858 MW; 53FAC7AD8006BC0D CRC64;

 Query Match 55.9%; Score 916; DB 1; Length 318;
 Best Local Similarity 57.3%; Pred. No. 2.3e-52;
 Matches 180; Conservative 58; Mismatches 76; Indels 0; Gaps 0;

 QY 14 GTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTLFGDRL 73
 DB 5 GTVKAASGFNATEDAOTLRKAMKGLGTDEDAIIGILAYRNTAQRQETRSAYKSTIGRDLI 64
 QY 74 LDKSELTKGFEKLIYALVMPKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 133
 DB 65 EDLKESSLPFQVILGLMTPTVLYDVOELRRAMKAGTDEGCLEILASRTPEELRIN 124
 QY 134 QVYEEYGSLSDDVVDGTSYQYQRMVLLVLANRDPDAGIDEAQVEQDAQALFOAGEL 193
 DB 125 QTYQQQYGRSLEEDICSDTSFWMFORVLFVLSAQRDEGNLYDDALMKQDAQELVGEKR 184
 QY 194 WGTDEEKFITICTRSVSHLKFVDEKYMVTISGFOIETIDRETSGNLEQLLAVVKSIR 253
 DB 185 WGTDEVKFLSLCSRNHLLHVFDEYKRIQSKDIEQISQKSETSGSPEDALLAIVKCMRS 244
 QY 254 IPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRNFATSLYSMIKGDTSG 313
 DB 245 KPSYFAERLYKSMKGLGTDDNTLIRVMVSRSEIDLFNIRKFRNFATSLYSMIKGDTSG 304
 QY 314 DYKALLLSGDD 327
 DB 305 DYKVVLLILCGDD 318

Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.	
KW	INIT_MET 0 0
FT	REPEAT 22 82 ANNEXIN 1.
FT	REPEAT 94 154 ANNEXIN 2.
FT	REPEAT 178 238 ANNEXIN 3.
FT	REPEAT 253 313 ANNEXIN 4.
FT	CONFLICT 94 94 L -> V (IN REF. 2).
FT	CONFLICT 210 210 E -> K (IN REF. 2).
FT	HELIX 15 26
FT	HELIX 33 40
FT	TURN 41 42
FT	HELIX 45 59
FT	HELIX 63 70
FT	HELIX 73 83
FT	HELIX 86 98
FT	HELIX 105 114
FT	HELIX 117 131
FT	HELIX 135 142
FT	HELIX 145 155
FT	TURN 156 156
FT	HELIX 167 182
FT	TURN 183 185
FT	HELIX 189 198
FT	HELIX 201 215
FT	HELIX 219 226
FT	HELIX 229 257
FT	HELIX 264 274
FT	TURN 275 278
FT	HELIX 279 290
FT	HELIX 294 301
FT	HELIX 304 314
SEQ	SEQUENCE 318 AA; 35757 MW; 866BDF349D774FD CRC64;

Query Match	
Best Local Similarity 55.8%; Score 914; DB 1; Length 318;	
Matches 182; Conservative 51; Mismatches 81; Indels 0; Gaps 0;	

Qy	14	GTVTDFPGFERADAETLRKAMKGLGTDEESILTLTTSRNASQROEISAAFKTLFGRDLL 73
Db	5	GTVKAASGFNAEDACTLRKAMKGLGTDEDAIINVLAYRSTAQOEIRTAKTITGRDLM 64
Qy	74	DDLKSELTGFKPEKLIVALKPRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
Db	65	DDLKSELSSGFNEQVILGMMTPTVLYDQELRKAMKAGTDEGCLIEILASRTPEEIRRN 124
Qy	134	QVTEEEYGSLEDDVVGDTSGYGYQRMVLVLLQANRDPDAGIDEAOVEDAQAALFOAGELK 193
Db	125	QTQLQVGRSLEDDIRSDTSFMFORVLVLSAGCRDESINLDDALMQDAQDLYEAGEKK 184
Qy	194	WGTDEEKFIPTFQTRSVSHLRKVFQKMTISGFQIETIDRETSGNLEQLLLAVVKSIRS 253
Db	185	WGTDEVKFLTVLCNRNHLHVDFEYKRIAKQDIEQSIKSETSGSPEDALLAIVKCMRN 244
Qy	254	IPAYLAETLYYKMGAGTDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMIKGDTSG 313
Db	245	KSAFYAERLYKSMKGLGTDDDTLIRVMVSRAEIDMLDIRANFRKLYGKSLYSPIKGDTSG 304
Qy	314	DYRKALLLSGEDD 327
Db	305	DYRKVLLILCGDD 318

RESULT 14	
ANX4_CANFA	ID ANX4_CANFA STANDARD; PRT; 318 AA.
AC	P50994;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Annexin A4 (Annexin IV) (lipocortin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).
GN	ANXA4 OR ANXA.
OS	Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP STRAIN=Mongrel; TISSUE=Pancreas;
 RC Fukuoka S.-I.;
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D38223; BAA07398.1; -;
 DR HSP; P13214; IANN.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT SEQUENCE 318 AA; 35681 MW; 42EF5B89179B4863 CRC64;
 SQ
 Query Match 55.0%; Score 901; DB 1; Length 318;
 Best Local Similarity 57.0%; Pred. No. 2.1e-51;
 Matches 179; Conservative 54; Mismatches 81; Indels 0; Gaps 0;
 QY 14 GTVDPFGDERADAETLRKAMKGLGDEESILTLTSRNSAORQETSAAFKTLFGDGL 73
 DB 5 GTVKPAGFSATEDAQTLRKAMKGLGDEDAISVLAPRNTSQRQETRTAYKSTIGRDL 64
 QY 74 DLKSELTKGFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEELRAIK 133
 DB 65 DLKSELSGNFERIVGMITPTVLYDVQELRRAMKSGTDEGCLIELASRTPEELRCIN 124
 QY 134 QVTEEEYSGSLEDVVDGTSYGYRMVLVLLQANRPDAGIDEAQVBDQAALFQAGELK 193
 DB 125 QTYQLQGRSLDEIVRSDFMFQRLVLSAGRDGDFNLDDALMRQADQDLYEAGEKK 184
 QY 194 WGTDEERFLIFGTRSVSHLRKVDKYMTISGQIETIDRTSGNLEQLLAVVKIRS 253
 DB 185 WGDEKFLVLCSSRNHLLHVFDEYKRISQDKIEQIKSESGSFEDALLAIVKCMRN 244
 QY 254 IPAYLAETLYAMKAGDTHITLRVMVSRSEIDLFNIRKFNATISLYMIKGTSG 313
 DB 245 KSAYFAERLYKSMKGLGTDDNTLLRVMSRAEIDMDIRSFRELYKSLSYFKGDTSG 304
 QY 314 DYKALLLLSGDD 327
 DB 305 DYRKVLILAGDD 318
 RESULT 15
 ANX6_CHICK
 ID ANX6_CHICK STANDARD; PRT; 671 AA.

AC P51901;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANX6 OR ANX6.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94092130; PubMed=8267590;
 RA Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthier R.E.;
 RT "Characterization, cloning and expression of the 67-kDa annexin from
 RT chicken growth plate cartilage matrix vesicles.";
 RL Biochem. Biophys. Res. Commun. 197:556-561(1993).
 CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF
 CC CA(2+) FROM INTRACELLULAR STORES (BY SIMILARITY).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S67466; AAB29337.2; -;
 DR PIR; JC2029; JC2029.
 DR HSP; P79134; IAVC.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 8.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 8.
 DR SMART: SM00335; ANX; 8.
 DR PROSITE: PS00223; ANNEXIN; 5.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 KW REPEAT 27 87 ANNEXIN 1.
 FT REPEAT 99 159 ANNEXIN 2.
 FT REPEAT 183 243 ANNEXIN 3.
 FT REPEAT 258 318 ANNEXIN 4.
 FT REPEAT 370 430 ANNEXIN 5.
 FT REPEAT 442 502 ANNEXIN 6.
 FT REPEAT 531 592 ANNEXIN 7.
 FT REPEAT 607 666 ANNEXIN 8.
 FT SEQUENCE 671 AA; 75218 MW; D0E02F4311A93D98 CRC64;
 Query Match 54.7%; Score 896.5; DB 1; Length 671;
 Best Local Similarity 57.7%; Pred. No. 1e-50;
 Matches 184; Conservative 51; Mismatches 83; Indels 1; Gaps 1;
 QY 10 QVLRGTVDTPGDERADAETLRKAMKGLGDEESILTLTSRNSAORQETSAAFKTLFG 69
 DB 6 KVRGYSVKDFPGFNASQDADALCNAMKFGSKDAILDLITSRNKQRLCTQAYKSYQ 65
 QY 70 RDLDDLKSELTKGFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEEL 129
 DB 66 KDLIADUKYELTGKFERLIVSLMRPPAYSADAKETDAIGTGTEKCLIELASRTNQEI 125
 QY 130 RAIKQVVEEYSGSLEDVVDGTSYGYRMVLVLLQANRPDAGIDEAQVBDQAALFQA 189
 DB 126 HDLVAAYKDAYERDLEADVVDGTSYGHFKMLVLQAGAREDDVVSDELVDQAKDLLEA 185
 QY 190 GELKWTGDEEKFTIFGTRSVSHLRKVDKYMTISGQIETIDRTSGNLEQLLAVVK 249
 DB 186 GELKWTGDEAQFYILGRRSKQHLRMVWFDEYKLTSGKPIERSIRAEISGDEKELAVVK 245

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:29:22 ; Search time 31.6667 Seconds
(without alignments)
2664.733 Million cell updates/sec

Title: US-09-970-969-2

Perfect score: 1639

Sequence: 1 MACGGHMAQLRGTVTDFP.....KGDTSYKALILLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPREMBL_23:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1585	96.7	320	4 Q8WV69	Q8WV69 homo sapien
2	1475.5	90.0	319	11 Q98LA1	Q98LA1 mus musculus
3	1390	84.8	302	11 Q70371	Q70371 rattus norv
4	1042	63.6	317	13 Q93445	Q93445 oryzias lat
5	932	56.9	476	11 Q8CEX0	Q8CEX0 mus musculus
6	932	56.9	667	11 Q99JX6	Q99JX6 mus musculus
7	930	56.7	673	11 Q8BS54	Q8BS54 bos taurus
8	866	52.8	320	13 Q93444	Q93444 oryzias lat
9	856	52.2	508	13 Q93447	Q93447 oryzias lat
10	849	51.8	321	13 Q90X16	Q90X16 xenopus lae
11	847	51.7	503	11 Q921F1	Q921F1 mus musculus
12	840.5	51.3	327	11 Q8K2N9	Q8K2N9 mus musculus
13	836.5	51.0	327	6 Q95L54	Q95L54 bos taurus
14	822.5	50.2	327	6 Q97529	Q97529 oryctolagus
15	799	48.7	323	11 Q8C1X9	Q8C1X9 mus musculus
16	773	47.2	463	11 Q922A2	Q922A2 mus musculus

17	770	47.0	463	11 Q8VIN2	Q8vin2 rattus norv
18	769	46.9	463	11 Q8BP75	Q8bp75 mus musculus
19	752	45.9	324	5 Q9NL61	Q9nl61 bombyx mori
20	752	45.9	324	5 Q8IGJ8	Q8igj8 drosophila
21	743.5	45.4	301	11 Q921D0	Q921d0 mus musculus
22	729	44.5	323	5 Q9NL59	Q9nl59 bombyx mori
23	720	43.9	324	5 Q9NG55	Q9ng55 drosophila
24	715	43.6	321	5 Q8WFG9	Q8wp99 bombyx mori
25	714	43.6	486	5 Q8WPH0	Q8wph0 bombyx mori
26	709	43.3	497	5 Q27512	Q27512 caenorhabdi
27	705	43.0	323	5 Q9NGG6	Q9ngg6 bombyx mori
28	701	42.8	323	5 Q9NL60	Q9nl60 bombyx mori
29	701	42.8	324	5 Q969D3	Q969d3 drosophila
30	694.5	42.4	339	11 Q8TBV2	Q8tbv2 homo sapien
31	686.5	41.9	339	11 Q9GZ17	Q9gz17 mus musculus
32	685	41.8	315	5 Q95V57	Q95v57 artemia san
33	680	41.5	317	11 Q99UG3	Q99ug3 mus musculus
34	673	41.1	357	6 Q8MJB5	Q8mj55 oryctolagus
35	661	40.3	511	5 Q9VXG3	Q9vxg3 drosophila
36	657	40.1	337	13 Q93446	Q93446 oryzias lat
37	655	40.0	322	5 Q9VXG4	Q9vxg4 drosophila
38	646	39.4	316	13 Q98SH7	Q98sh7 brachydanio
39	643	39.2	346	6 Q8HZM6	Q8hzm6 equus cabal
40	625.5	38.2	314	13 Q92128	Q92128 xenopus lae
41	582	35.5	322	5 Q27864	Q27864 caenorhabdi
42	573.5	35.0	415	11 Q8CCV9	Q8ccv9 mus musculus
43	572	34.9	209	11 Q8BSL2	Q8bsl2 mus musculus
44	540	32.9	317	5 Q27473	Q27473 caenorhabdi
45	528	32.2	365	5 Q9XY89	Q9xy89 schistosoma

ALIGNMENTS

RESULT 1

ID	Q8WV69	PRELIMINARY;	PRT;	320 AA.
AC	Q8WV69;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Annexin A5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.			
CC	-1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.			
DR	EMBL; BC018671; AAH18671.1; -			
DR	InterPro; IPR001464; Annexin.			
DR	Pfam; PF00191; annexin; 4.			
DR	PRINTS; PR00196; ANNEXIN.			
DR	ProDom; PD000143; Annexin; 4.			
DR	SMART; SM00335; ANK; 4.			
DR	PROSITE; PS00223; ANNEXIN; 4.			
KW	Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding; Repeat.			
SQ	SEQUENCE 320 AA; 35924 MW; 45FAC411DDBA4D1A CRC64;			

Query Match	96.7%;	Score	1585;	DB 4;	Length	320;			
Best Local Similarity	99.4%;	Pred. No.	2.3e-103;						
Matches	318;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	8	MAQVLRGTVTDFPQGFDERADAETLRKAMKGLGTDDEESILTLTLLSRNAQROEISAAFKTL	67						
Db	1	MAQVLRGTVTDFPQGFDERADAETLRKAMKGLGTDDEESILTLTLLSRNAQROEISAAFKTL	60						

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QY 68 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
Db 61 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
QY 128 ELRAIKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 187
Db 121 ELRAIKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
QY 188 QAGELKWTGDEKFTIFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAV 247
Db 181 QAGELKWTGDEKFTIFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAV 240
QY 248 VKSIRSIPAYLAETIYAMKAGTDDHTLIRVWVSSEIDLNIKEFRKNFATSLYSMI 307
Db 241 VKSIRSIPAYLAETIYAMKAGTDDHTLIRVWVSSEIDLNIKEFRKNFATSLYSMI 300
QY 308 KGDTSQDYKKALLLGGEDD 327
Db 301 KGDTSQDYKKALLLGGEDD 320

RESULT 2
Q99LA1 PRELIMINARY; PRT; 319 AA.
AC Q99LA1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Annexin A5.
GN ANXA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC003716; AA03716.1; -.
DR HSSP; PI4668; IAB8.
DR MGD; MGI:106008; Anxa5.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 319 AA; 35738 MW; 52B2C7CCEA386917 CRC64;

Query Match 90.0%; Score 1475.5; DB 11; Length 319;
Best Local Similarity 93.4%; Pred. No. 1.1e-95;
Matches 295; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 13 RGTVTDFPGFDRADAETLRKAMKGLGTDEESILTLTSRSNAQROETSAAFKTLFGRLD 72
Db 4 RGTVTDFPGFDRADAETLRKAMKGLGTDEESILTLTSRSNAQROETSAAFKTLFGRLD 63
QY 73 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPELRAI 132
Db 64 VDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPELSAI 123
QY 133 KQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQAGEL 192
Db 124 KQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQAGEL 183
QY 193 KMGTEDEKFTIFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAVVKSIR 252

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Db 184 KMGTEDEKFTIFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAVVKSIR 243
QY 253 SIPAYLAETIYAMKAGTDDHTLIRVWVSSEIDLNIKEFRKNFATSLYSMIKGDTS 312
Db 244 SIPAYLAETIYAMKAGTDDHTLIRVWVSSEIDLNIKEFRKNFATSLYSMIKGDTS 303
QY 313 GDYKKALLL-SGEDD 327
Db 304 GDYKKALLLGGEDD 319

RESULT 3
Q70371 PRELIMINARY; PRT; 302 AA.
AC Q70371;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Lipocortin V (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99362163; PubMed=10329451;
RA Wen Y., Edelman J L., Kang T., Sachs G.;
RT "Lipocortin V may function as a signaling protein for vascular
RT endothelial growth factor receptor-2/Fik-1.";
RL Biochem. Biophys. Res. Commun. 258:713-721(1999).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF051895; AAC06290.1; -.
DR HSSP; PI4668; IAB8.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 3.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
FT NON_TER 302 302
SQ SEQUENCE 302 AA; 33965 MW; AB9FB40934A3D007 CRC64;

Query Match 84.8%; Score 1390; DB 11; Length 302;
Best Local Similarity 92.0%; Pred. No. 1e-89;
Matches 276; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 12 LRGTVTDFPGFDRADAETLRKAMKGLGTDEESILTLTSRSNAQROETSAAFKTLFGRLD 71
Db 3 LRGTVTDFPGFDRADAETLRKAMKGLGTDEESILTLTSRSNAQROETSAAFKTLFGRLD 62
QY 72 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPELRA 131
Db 63 LVNDKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPELRA 122
QY 132 IKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQAGE 191
Db 123 IKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQAGE 182
QY 192 LKMGTEDEKFTIFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAVVKSIR 251
Db 183 LKMGTEDEKFTIFGTRSVSHLRKVFQKYMISGFOIETIDRETSGNLEQLLAVVKSIR 242
QY 252 RSIPAYLAETIYAMKAGTDDHTLIRVWVSSEIDLNIKEFRKNFATSLYSMIKGD 311
Db 243 RSIPAYLAETIYAMKAGTDDHTLIRVWVSSEIDLNIKEFRKNFATSLYSMIKGD 302

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ID	Q93445	PRELIMINARY;	PRT;	317 AA.
AC	Q93445;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Annexin max2.			
OS	Oryzias latipes (Medaka fish) (Japanese ricefish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;			
OC	Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.			
OX	NCBI_TaxID=8090;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99025617; PubMed=9809745;			
RT	Osterloh D., Wittbrodt J., Gerke V.;			
RT	"Characterization and developmentally regulated expression of four			
RT	annexins in the killifish medaka.";			
RL	DNA Cell Biol. 17:835-847(1998).			
CC	-1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR			
CC	CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.			
CC	-1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.			
DR	EMBL; Y11253; CAAY2123.1; -.			
DR	RSSP; P1153; IALA.			
DR	InterPro: IPR001464; Annexin.			
DR	Pfam: PF00191; annexin; 4.			
DR	PRINTS: PR00196; ANNEXIN.			
DR	ProDom: PD000143; Annexin; 4.			
DR	SMART: SM00335; ANX; 4.			
DR	PROSITE: PS00223; ANNEXIN; 4.			
DR	Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;			
KW	Repeat.			
SK	SEQUENCE 317 AA; 34765 MW; AFD618681BAFFOPE CRC64;			
QY	Query Match	53.6%;	Score 1042;	DB 13; Length 317;
Db	Best Local Similarity	64.4%;	Pred. No. 2.9e-65;	
Db	Matches 203; Conservative 48; Mismatches 62; Indels 2; Gaps 1;			
QY	13 RGVTVDPFGDERADAEILRKAMKGLGTDEESITLILTSRNAQRQEISAFTLFGKDL 72			
Db	4 KGTVKAANEKASADAEVLHKAMKGGTDEDAILQLVCARNAQRQEIKATYKTLFGKDL 63			
QY	73 LDKLSKLGKFEKLIVALKMPRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132			
Db	64 INDLKSELGKFEKLIVALTPTTAYDVVSLRNAIKAGTDEKVLVEILASRTPEQVKDI 123			
QY	133 KQVYEEYSGSLEDVVGGTSGVYQRMVLVLLQANRPDAGIDEAQVEQDAQLFQAGEL 192			
Db	124 IAAKREYDADLEEDICGGTSGHFKRLVLLVLLQANR--QTGVQEGDITENDAQVLFKAGEQ 181			
QY	193 KMGTDKEKFTITGTRSVSLRLRVFKYMTISGFOIETIDRTSGNLEQLLLAVVKSR 252			
Db	182 KFGTDSQTFVTLGNRSQAHLRVFVDAYMKLSGVEIEESIKRETSGSKOLLAVVKAR 241			
QY	253 SPAYLAETLYYAMKAGGTDHDLIRVWVSRSEIDLFNIRKEFRKNPATSLYSIKGDTG 312			
Db	242 SVPAYFAETLYNAMKAGGTDHDLIRVWVTRGEVMDLIRAEFRKLFARSLFSIKGDTG 301			
QY	313 GDYKALLLLSGDD 327			
Db	302 GDYKALLLLCGDD 316			
RESULT 5				
ID	Q8CEX0	PRELIMINARY;	PRT;	476 AA.
AC	Q8CEX0;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			

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DR PRINTS: PR00196; ANNEXIN.
DR PRODOM: PD000143; ANNEXIN; 8.
DR SMART: SM00335; ANX; 8.
DR PROSITE: PS00223; ANNEXIN; 8.
KW ANNEXIN: Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 667 AA; 75260 MW; 363088A2A55CFF34 CRC64;

Query Match
Best Local Similarity 56.9%; Score 932; DB 11; Length 667;
Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQISAAFKTLFGRL 72
DB 11 RGVHDFPEFDAQDAALYATAMKFGSKESILELITSRNQRQICQYKSLYKGL 70
QY 73 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
DB 71 IEDUKVELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 130
QY 133 KQVVEEYSSLEDVVDGTSYGYQRMVLVLLQANRPDPDAGIDEAQVBDQAALFOAGEL 192
DB 131 VAAKYDAYERDLESDIIGDTSGHFKMLVLLQGTRENDVVDVSEDVQDDLYEAGEL 190
QY 193 KWTDEKFTITFGRSVSHLRKVDKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252
DB 191 KWTGDEAQFIYILGNRSKQHLRVDFEYLVKTTGPKPIEASIRGELSGDFEKLMLAVVKCIR 250
QY 253 SIPAYLAETLYAMKAGTDHTTLIRVMVSRSEIDLENIRKFRKNFATSLYSIMKGDTS 312
DB 251 STPEYFAERLFPKAMKGLGTRNTLIRVMVSRSEIDLENIRKFRKNFATSLYSIMKNDTS 310
QY 313 GDYKALLLGGDD 327
DB 311 GEYKALLKGGDD 325

RESULT 7
Q8BSS4
ID Q8BSS4 PRELIMINARY; PRT: 673 AA.
AC Q8BSS4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Annexin A6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RM EMBL: AK030728; BAC27101.1; .
SQ SEQUENCE 673 AA; 75885 MW; DCC5FC56CB088809 CRC64;

Query Match
Best Local Similarity 56.7%; Score 930; DB 11; Length 673;
Matches 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;

QY 13 RGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQISAAFKTLFGRL 72
DB 11 RGVHDFPEFDAQDAALYATAMKFGSKESILELITSRNQRQICQYKSLYKGL 70
QY 73 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
DB 71 IEDUKVELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 130

QY 133 KQVVEEYSSLEDVVDGTSYGYQRMVLVLLQANRPDPDAGIDEAQVBDQAALFOAGEL 192
DB 131 VAAKYDAYERDLESDIIGDTSGHFKMLVLLQGTRENDVVDVSEDVQDDLYEAGEL 190
QY 193 KWTDEKFTITFGRSVSHLRKVDKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252
DB 191 KWTGDEAQFIYILGNRSKQHLRVDFEYLVKTTGPKPIEASIRGELSGDFEKLMLAVVKCIR 250
QY 253 SIPAYLAETLYAMKAGTDHTTLIRVMVSRSEIDLENIRKFRKNFATSLYSIMKGDTS 312
DB 251 STPEYFAERLFPKAMKGLGTRNTLIRVMVSRSEIDLENIRKFRKNFATSLYSIMKNDTS 310
QY 313 GDYKALLLGGDD 327
DB 311 GEYKALLKGGDD 325

RESULT 8
Q93444
ID Q93444 PRELIMINARY; PRT: 320 AA.
AC Q93444;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Annexin max1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphs; Acanthopterygii; Perciformes; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93025617; PubMed=9809745;
RA Osterloh D., Wittbrodt J., Gerke V.;
RT "Characterization and developmentally regulated expression of four
RT annexins in the killifish medaka."
RT DNA Cell Biol. 17:835-847(1998).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL: Y11252; CAA72122.1; .
DR HSSP: P13214; IANN.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin. 4.
DR PRINTS: PR00196; ANNEXIN.
DR PRODOM: PD000143; Annexin; 4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
DR ANNEXIN: Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 320 AA; 35424 MW; D2EED32C8676777D CRC64;

Query Match
Best Local Similarity 52.8%; Score 866; DB 13; Length 320;
Matches 170; Conservative 59; Mismatches 83; Indels 0; Gaps 0;

QY 13 RGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQISAAFKTLFGRL 72
DB 7 RGTVTEASGNPDODDAOKLRAMKAGTDEAIIKLAHRTIAQRQIKLAYKQVSGKDL 66
QY 73 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
DB 67 AEDLSSELSGHFQSVVGLLMPAPVYDAYELKAMKAGTDEAIIKLAHRTIAQRQIKLAYKQVSGKDL 126
QY 133 KQVVEEYSSLEDVVDGTSYGYQRMVLVLLQANRPDPDAGIDEAQVBDQAALFOAGEL 192
DB 127 NEVYKKEYTGLTLEAVCGDTSQGMFQVRLVSLTAGRDESKVDQAQVKAQKDFEAGEA 186
QY 193 KWTGDEKFTITFGRSVSHLRKVDKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252
DB 187 RWTGDEVKFLTVLCVRNRHLLRVDFEYLVKTTGPKPIEASIRGELSGDFEKLMLAVVKCIR 246

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QY	313	GDYKKALLLSGDD	327		
Db	494	GDYKNLLLCGSSD	508		
RESULT 10					
Q90X16		PRELIMINARY;	PRT;	321	AA.
ID	Q90X16				
AC	Q90X16;				
DT	01-DEC-2001 (T-EMBLrel. 19, Created)				
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)				
DT	01-MAR-2003 (T-EMBLrel. 23, Last annotation update)				
DE	Anexin 4.				
OS	Xenopus laevis (African clawed frog).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
ON	[1]				
RP	SEQUENCE FROM N.A.				
RA	Seville R.A., Nijjar S., Barnett M.W., Jones E.A.;				
RT	"Anexin 4 (Xanx-4) has a role in the development of the pronephric				
RT	tubules in Xenopus laevis.";				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- DOMAIN: A PAIR OF ANEXIN REPEATS MAY FORM ONE BINDING SITE FOR				
CC	CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE ANEXIN FAMILY.				
CC	-1- SIMILARITY: CONTAINS 4 ANEXIN REPEATS.				
DR	EMBL; AY039235; AAK83461.1; -				
DR	InterPro: IPR001464; Annexin.				
DR	Pfam: PF00191; annexin; 4.				
DR	PRINTS; PR00196; ANNEXIN.				
DR	ProDom; PD0001143; Annexin; 4.				
DR	SMART; SM00335; ANX; 4.				
DR	PROSITE; PS00223; ANNEXIN; 4.				
KW	Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;				
KW	Repeat.				
SQ	SEQUENCE 321 AA; 35801 MW; 5C28CAFAC17687D CRC64;				
Query Match 51.8%; Score 849; DB 13; Length 321;					
Best Local Similarity 54.0%; Pred. No. 1e-51;					
Matches 170; Conservative 55; Mismatches 90; Indels 0; Gaps 0;					
QY	13	RGVTFPPGDERADAEITLKAKKGLGTDEESILTTLTSRSNAQRQEISAAFKITLGRDL	72		
Db	7	KGTIKYPNFAADVDQKLKAKMGATDEDAVIDIANRTLSQRQEIKTAYKTTVGKDL	66		
QY	73	LDDLKSELTGKFEKLVALMKPSRLVDAYELKHALKGAGTNEKVLTEIASRTPEELRAI	132		
Db	67	DDDLKSELTGFKVILGLTSTLYDVEELKAMKGAGTDEGLIEILASRAEELKNI	126		
QY	133	KQYVEEYGSLEDDVVGDTSGYVQRMLVLLQANRPDAGIDFAQVEQDAQALFQAGEL	192		
Db	127	NITYKIKYKGSLEDDICSDTSFVFQVILVSLAAGGRDQSSTVNEDLAKDANDLYEAGEK	186		
QY	193	KWGTDEKFTITIGTSRVSHLRVDFDKYMTISGQIEETIDRTSGNLEQLLAVVKSIR	252		
Db	187	KWGTDEKFTILCSRRNHLKVFEEYKIAKDLKLEASIKSEMSGHLEDSLLAIVKCIK	246		
QY	253	SIPAYLAETIYKAMKGATDDHTLIRVWVSREIDLENIRKEFRKNFATSLYSNIKGDTS	312		
Db	247	SRPAYFAERLYKMGKGLGTDKDTLIRVWVSREIDMLEIRCEPKFKMYGKLSHFIGDCS	306		
QY	313	GDYKKALLLSGDD	327		
Db	307	GDYKRVLLLCGGED	321		
RESULT 11					
Q921F1		PRELIMINARY;	PRT;	503	AA.
ID	Q921F1				
AC	Q921F1;				
DT	01-DEC-2001 (T-EMBLrel. 19, Created)				

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DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to annexin A11.
GN ANX11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC012875; A012875.1; -.
DR MGI; MGI:108481; Annexin.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 503 AA; 54079 MW; 33F3471EE21A0D32 CRC64;

Query Match 51.7%; Score 847; DB 11; Length 503;
Best Local Similarity 53.7%; Pred. No. 2.7e-51;
Matches 169; Conservative 59; Mismatches 87; Indels 0; Gaps 0;

QY 13 RGVTVDFPGDERADAEIIRKAMKGLGTDEESILTLTSSNAORQEISAAPKTLFGRDL 72
DB 189 RGVTAASGFDPLRDRAEVLKAMKGFGEQAIIDCLGRSNKQROQIILSFATGKDL 248
QY 73 LDDKSELGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAI 132
DB 249 IKDLKSELGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAI 132
QY 133 KOVVEEYSGSLEDDVGGTSGYQRMVLLQANRPDAGIDEAQVEQDAQALFOAGEL 192
DB 309 SRAKTEFQKLEEARSTSGHFRQLLSLSOGNDESTNVDMSLVORDVOELYAAGEN 368
QY 193 KMTDEKFTITIGTRSVSHLRKVFQKMTISGFOIEETIDRETSGNLEQLLAVVKSIR 252
DB 369 RLGTDESKENAILCSRAHLVAVFNQYQRTGRDIEKSTCRMSGDLQGLAVVCKLK 428
QY 253 SIPAYLAETLYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKFNATSLYSMIKGTSGDYK 312
DB 429 NTPAFPAERLNKAMRGAGTKDRTLIRIMVSRSEIDLNFIRKFNATSLYSMIKGTSGDYK 488
QY 313 GDYKALLLSGDD 327
DB 489 GDYRKILLKICGND 503

RESULT 12
Q8K2N9 PRELIMINARY; PRT; 327 AA.
ID Q8K2N9
AC Q8K2N9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to annexin A8.
GN ANX8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
```

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RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030407; A030407.1; -.
DR MGI; MGI:1201374; Annex8.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
SQ SEQUENCE 327 AA; 36724 MW; 56DB9CFAFA8C2B21 CRC64;

Query Match 51.3%; Score 840.5; DB 11; Length 327;
Best Local Similarity 57.8%; Pred. No. 4.2e-51;
Matches 177; Conservative 49; Mismatches 79; Indels 1; Gaps 1;

QY 22 FDERADAETLRKAMKGLGTDEESILTLTSSNAORQEISAAPKTLFGRDLDDKSEL 81
DB 21 FNPDPDAETLYKAMKGLGTNEQAIIDVTLKRSVQROQIAKSPKAGKDLTETLKSEL 80
QY 82 GKPEKLIVALKPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAIKOVYEEY 141
DB 81 GKFERLIVALKYPPSYEAKELHDMKGLGTKEGVIEILASRTKQLRIMKAYEDYG 140
QY 142 SSLEDDVGGTSGYQRMVLLQANRPDAGIDEAQVEQDAQALFOAGELKMGTDDEK 200
DB 141 STLEEDIQGTSGYLERILVCLLQSGRSDVSGFVDPGLVLDQAALHEAGEKIMGTD 200
QY 201 FTFIFGTRSVSHLRKVFQKMTISGFOIEETIDRETSGNLEQLLAVVKSIRIPAYLAE 260
DB 201 FTFILTRSATHLRMVFEYKIEKNCIEDSIKSTHGSLEEAMLTGVKTRNVHSYFAE 260
QY 261 TLYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKFNATSLYSMIKGTSGDYKALL 320
DB 261 RLYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKFNATSLYSMIKGTSGDYKALL 320
QY 321 LLSGED 326
DB 321 NLVGT 326

RESULT 13
Q95L54 PRELIMINARY; PRT; 327 AA.
ID Q95L54
AC Q95L54;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Annexin VIII.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA White A.H., Wallis G.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF417637; AAL13308.1; -.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 327 AA; 36787 MW; 2EB178E13738CF22 CRC64;

Query Match 51.0%; Score 836.5; DB 6; Length 327;
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Db 309 GDYRTVLLKICGEDD 323

Search completed: August 22, 2003, 21:35:24
Job time : 37.6667 secs

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgebcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 26 Row: f Column: 11
 This clone has the following problem: no 5' EST match.

FEATURES

source

Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3924873"
 /issue_type="Skin, melanotic melanoma."
 /clone_lib="NIH_MGC_72"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 BASE COUNT 449 a 337 c 364 g 452 t
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Query Match 97.7%; Score 958; DB 11; Length 1602;

Best Local Similarity 99.5%; Pred. No. 6.5e-246;

Matches 961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 16 GCCATATGGCACAGTCTTCAGAGCACTGTGACTTCCCTGGATTGATGACGG 75
DB 149 GTCGTATGGCACAGTCTTCAGAGCACTGTGACTTCCCTGGATTGATGACGG 208
QY 76 GCTGATGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 135
DB 209 GCTGATGCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATC 268
QY 136 CTGACTCTGTTGACATCCGGAAGTATGCTCAGCGCCAGGAATCTCTCGAGCTTTAAG 195
DB 269 CTGACTCTGTTGACATCCGGAAGTATGCTCAGCGCCAGGAATCTCTCGAGCTTTAAG 328
QY 196 ACTCTGTTGGCAGGATCTCTCGATGACCTGAATCAGACTACTCGAAATTTGAA 255
DB 329 ACTCTGTTGGCAGGATCTCTCGATGACCTGAATCAGACTACTCGAAATTTGAA 388
QY 256 AAATTAATTTGGCTCTGTATGAACCCCTCTCGCTTTATGATGCTTTATGAACCTGAACAT 315
DB 389 AAATTAATTTGGCTCTGTATGAACCCCTCTCGCTTTATGATGCTTTATGAACCTGAACAT 448
QY 316 GCCTTGAGGGAGCTGGAAACAATGAAGAAGTACTGACAGAAATTTATGCTTCAAGGACA 375
DB 449 GCCTTGAGGGAGCTGGAAACAATGAAGAAGTACTGACAGAAATTTATGCTTCAAGGACA 508
QY 376 CTTGAAGAACTCAGAGCCATCAACAAGTTTATGAAGAAGTATGGCTCAAGCCCTGGAA 435
DB 509 CTTGAAGAACTCAGAGCCATCAACAAGTTTATGAAGAAGTATGGCTCAAGCCCTGGAA 568
QY 436 GATGACGTGGTGGGGACACTTCAGGGTACTACCGCGGATGTGGTGGTCTTCCTTCAG 495
DB 569 GATGACGTGGTGGGGACACTTCAGGGTACTACCGCGGATGTGGTGGTCTTCCTTCAG 628
QY 496 GCTACAGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGTCTCAGGCT 555
DB 629 GCTACAGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGTCTCAGGCT 688
QY 556 TTATTTCAGCTGGAGAACTTAAATGGGGCAGAGATGAAGAAAGTTTATCACCATCTTT 615
DB 689 TTATTTCAGCTGGAGAACTTAAATGGGGCAGAGATGAAGAAAGTTTATCACCATCTTT 748
QY 616 GGAACACAGAGTGTCTCTCATTTGAGAAAGGCTTTGACAAGTACATGACTATATCAGGA 675
DB 749 GGAACACAGAGTGTCTCTCATTTGAGAAAGGCTTTGACAAGTACATGACTATATCAGGA 808
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DB 809 TTTCAAATTTAGAGAAACCAATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTT 868
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QY 796 ATGAAGGGAGCTGGGACAGATGATACCCCTCATCAGAGTATGTTTCCAGGAGTGAAG 855
DB 929 ATGAAGGGAGCTGGGACAGATGATACCCCTCATCAGAGTATGTTTCCAGGAGTGAAG 988
QY 856 ATGATGCTGTTTAAACATCAGAGAGGAGTTTAGGAAGAATTTGCCACCTCTCTTTATTC 915
DB 989 ATGATGCTGTTTAAACATCAGAGAGGAGTTTAGGAAGAATTTGCCACCTCTCTTTATTC 1048
QY 916 ATGATTAAAGGAGATACATCTGGGACTATAGAAAGCTCTTCTGCTGCTCTCCGAGAA 975
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DB 1109 GATGAC 1114

RESULT 2
BM464122
LOCUS
DEFINITION BM464122 1076 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6445585 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5540173
5', mRNA sequence.
ACCESSION BM464122
VERSION BM464122.1 GI:18513164
SOURCE EST.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCPD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Distribution by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12235 row: n column: 14
High quality sequence stop: 708.
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/db_xref="taxon:9606"
/clone="IMAGE:5540173"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 296 a 229 c 273 g 274 t 4 others
ORIGIN
Query Match 89.1%; Score 874.4; DB 12; Length 1076;
Best Local Similarity 96.9%; Pred. No. 1.5e-223;
Matches 932; Conservative 0; Mismatches 25; Indels 5; Gaps 4;
QY 22 ATGGCACAGTCTTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
DB 105 ATGGCACAGTCTTCAGAGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 164
  
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QY 496 GCTAACAGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAGATGCTCAGGCT 555
 DDb 663 GCTAACAGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAGATGCTCAGGCT 722
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 DDb 723 TTATTTCAGGCTGGAGAACCTTAATGCGGACAGATGAAGAAAGTTTATCAGCATCTTT 782
 QY 616 GGAACACGAGTGTGCTCTATTGAGAAAGTCTTTGACAAGTACATGACTATATCAGGA 675
 DDb 783 GGAACACGAGTGTGCTCTATTGAGAAAGTCTTTGACAAGTACATGACTATATCAGGA 842
 QY 676 TTTCAAATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTAGAGCAACTACTCCTT 735
 DDb 843 TTTCAAATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTAGAGCAACTACTCCTT 902
 QY 736 GCTGTTGTGAATCTATTGGAAGTATACCTGCTACCTCCAGAGACCTCTATTATGCT 795
 DDb 903 GCTGTTGTGAATCTATTGGAAGTATACCTGCTACCTCCAGAGACCTCTATTATGCT 962
 QY 796 ATGAAGGAGCTGGGACAGATGATACCTCTCATCAGACTGATGTTCCAGAGTGAG 855
 DDb 963 ATGAAGGAGCTGGGACAGATGATACCTCTCATCAGACTGATGTTCCAGAGTGAG 1022
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 DDb 1023 ATTGATCTGTTTAACTATCAGGAAGGAGTTTATGGAAGAAATTT 1063

RESULT 4
 BX379189
 LOCUS
 DEFINITION
 BX379189 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI030YL18 5-PRIME, mRNA sequence.
 BX379189
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2353.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DI030DF09QPlcluster=2353.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI030DF09QPl.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI030YL18"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR v
 sites of the pCMVSPORT 6 vector. Library was normalized."
 307 a 263 c 295 g 294 t 42 others

BASE COUNT
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 RESULT 5
 BX417429
 LOCUS
 DEFINITION
 BX417429 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009Y116
 linear EST 13-MAY-2003

Query Match 87.5%; Score 858.4; DB 13; Length 1201;
 Best Local Similarity 94.9%; Pred. No. 3.1e-219;
 Matches 892; Conservative 15; Mismatches 27; Indels 6; Gaps 2;
 QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTGATGAGCGGGCTGAT 81
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 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCTCTGACT 141
 DDb 263 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGACATCTCTGACT 322
 QY 142 CTGTTGACATCCCGAAGTAAATGCTCAGCGCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201
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 QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
 DDb 383 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 442
 QY 262 ATTGTGCTCTGATGAAGCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTTG 321
 DDb 443 ATTGTGCTCTGATGAAGCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTTG 502
 QY 322 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 DDb 503 AAGGAGCTGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 562
 QY 382 GAAGTACAGGACCAATCAACAACTTTATGAAGAGATATGGCTCAAGCCTGGAAGATGAC 441
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 DDb 683 AGAGACCTCTGATGCTGGAATTTGAAAGTCAAGTTGAACAAGATGCTCAGGCTTTATTT 742
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 QY 742 GTCAAACTATTTCGAAAGTATACCTGCTACCTTTCAGAGACCTCTATTATGCTATGAAG 801
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 DDb 983 GGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGGAGTGAATGAT 1042
 QY 862 CTGTTTAACTATCAGGAAGGATTTAGAGAAATTTTGGCAACCTCTCTTTATTCATGATT 921
 DDb 1043 CTGTTTAACTATCAGGAAGGATTTAGAGAAATTTTGGCAACCTCTCTTTTATTCATGATT 1099
 QY 922 AAGGAGATACATCTCGGGACTATAGAAGCTCTCTTCG 961
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5-PRIME, mRNA sequence.
BX4117429
VERSION BX4117429.1 GI:30654405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0D09BE08QPL&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D09BE08QPL.
Location/Qualifiers
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/note="vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 310 a 260 c 297 g 295 t 39 others
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Best Local Similarity 95.0%; Pred. No. 2.3e-218;
Matches 893; Conservative 10; Mismatches 30; Indels 7; Gaps 2;

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Db 206 ATGCACAGGTTCTCAGAGGCTGTGACTGCTCCCTGGATTGTGATGCGGGCTGAT 265
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Qy 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
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Db 266 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 325
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Qy 142 CTGTTGACATCCCGAAGTAATGCTCAGGCCAGGAATCTGCAAGCTTTTAAAGCTCTG 201
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Db 326 CTGTTGACATCCCGAAGTAATGCTCAGGCCAGGAATCTGCAAGCTTTTAAAGCTCTG 385.
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Qy 202 TTTCGGCAGGATCTCTCGATGACCTGAATCAGAACTAACTGGAATTTGAAAATTA 261
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Db 386 TTTCGGCAGGATCTCTCGATGACCTGAATCAGAACTAACTGGAATTTGAAAATTA 445
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Qy 262 ATTGTGGCTCTGATGAACACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCGCTTG 321
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Db 446 ATTGTGGCTCTGATGAACACCTCTCGGCTTTATGATGCTTTATGAACCTGAACATGCGCTTG 505
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Qy 322 AAGGAGCTGGAACAATGAAAAGTACTGACGAAATTTATGCTTCAAGGACACCTGAA 381
|||||
Db 506 AAGGAGCTGGAACAATGAAAAGTACTGACGAAATTTATGCTTCAAGGACACCTGAA 565
|||||

Qy 382 GAATGAGAGCCATCAACAGATTATGAAGAAGTATGCTCAAGCTTGAAGATGAC 441
|||||
Db 566 GAATGAGAGCCATCAACAGATTATGAAGAAGTATGCTCAAGCTTGAAGATGAC 625
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Qy 442 GTGGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTTCCTCTCAGGCTAAC 501
|||||

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626 GTGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 685
|||||
Qy 502 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGCTTGAACAAGATGCTCAGGCTTTATTT 561
|||||
Db 686 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGCTTGAACAAGATGCTCAGGCTTTATTT 745
|||||
Qy 562 CAGGCTGGAGAACCTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGACA 621
|||||
Db 746 CAGGCTGGAGAACCTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGACA 805
|||||
Qy 622 CGAAGTGTCTCTATTGAGAAAGGTTTGCACAACTACATGATATATCAGGATTTCAA 681
|||||
Db 806 CGAAGTGTCTCTATTGAGAAAGGTTTGCACAACTACATGATATATCAGGATTTCAA 865
|||||
Qy 682 ATTGAGAAACCTTGAACCGGACACTTCTGGCAATTTAGAGCAACTACTCTTGGCTCTT 741
|||||
Db 866 ATTGAGAAACCTTGAACCGGACACTTCTGGCAATTTAGAGCAACTACTCTTGGCTCTT 925
|||||
Qy 742 GTGAAATCTATTTCGAAGTATACCTGACCTTTCGAGAGCCCTCTATTATGCTATGAAG 801
|||||
Db 926 GTGAAATCTATTTCGAAGTATACCTGACCTTTCGAGAGCCCTCTATTATGCTATGAAG 985
|||||
Qy 802 GGAGCTGGGACAGATGATACCTCTCATCAGATCATGGTTTCAGGAGTGAGATGAT 861
|||||
Db 986 GGAGCTGGGACAGATGATACCTCTCATCAGATCATGGTTTCAGGAGTGAGATGAT 1045
|||||
Qy 862 CTGTTTAAATCAGGAGGAGGTTTGAAGAAATTTGCGACCTCTCTTTATTCATGAT 921
|||||
Db 1046 CTGTTTAAATCAGGAGGAGGTTTGAAGAAATTTGCGACCTCTCTTTATTCATGAT 1101
|||||
Qy 922 AAGGAGATACATCTGGGACTATAGAAGACCTCTTCTGTC 961
|||||
Db 1102 RGRGAWA---MWTGGGACWATAAAACCTCTCTCTCTSY 1138
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RESULT 6
BX398791 996 bp mRNA linear EST 13-MAY-2003
LOCUS BX398791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION BX398791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX398791
VERSION BX398791.1 GI:30613780
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 996)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0D1064CD10QPL&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1064CD10QPL.
Location/Qualifiers
1..996
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1064YH19"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)

```

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 282 a 192 c 248 g 256 t 18 others

ORIGIN

Query Match 86.8%; Score 851.6; DB 13; Length 996;
Best Local Similarity 97.6%; Pred. No. 1.9e-217;
Matches 856; Conservative 15; Mismatches 5; Indels 1; Gaps 1;

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QY 22 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTTATGAGCGGGCTGAT 81
Db 121 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTTATGAGCGGGCTGAT 180
QY 82 GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 141
Db 181 GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 240
QY 142 CTGTTGACATCCGGAAGTAACTGTCAGCCAGGAAATCTCTGACGCTTTTAAGACTCTG 201
Db 241 CTGTTGACATCCGGAAGTAACTGTCAGCCAGGAAATCTCTGACGCTTTTAAGACTCTG 300
QY 202 TTGGCAGGATCTCTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 261
Db 301 TTGGCAGGATCTCTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 360
QY 262 ATTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAAACATGCTTG 321
Db 361 ATTGGCTCTGATGAACCCCTCTCGGCTTTTATGATGCTTATGAACCTGAAACATGCTTG 420
QY 322 AAGGAGCTGGAAACAAATGAAAGTACTGACGAAATTTATGCTTCAAGGACACCTGAA 381
Db 421 AAGGAGCTGGAAACAAATGAAAGTACTGACGAAATTTATGCTTCAAGGACACCTGAA 480
QY 382 GAAGTGGAGCACTCAACAAAGTTTATGAAGAGATATGGCTCAAGCTGGAAGATGAC 441
Db 481 GAAGTGGAGCACTCAACAAAGTTTATGAAGAGATATGGCTCAAGCTGGAAGATGAC 540
QY 442 GTGGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCTCAGGCTAAC 501
Db 541 GTGGTGGGGACACTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCTCAGGCTAAC 600
QY 502 AGAGACCTTGATCGGAAATGATGAAGCTCAAGTTGACAGATGCTCAGGCTTATT 561
Db 601 AGAGACCTTGATCGGAAATGATGAAGCTCAAGTTGACAGATGCTCAGGCTTATT 660
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCAACCATCTTTGGAACA 621
Db 661 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCAACCATCTTTGGAACA 720
QY 622 CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAGTACATGACTATATCAGGATTTCAA 681
Db 721 CGAAGTGT-NCTCATTTGAGAAAGTGTGTTGACAGTACATGACTATATCAGGATTTCAA 779
QY 682 ATTGAGGAACCAATGACCGGAGACTCTGCGCAATTTAGACCACTACTCTCTGCTTT 741
Db 780 ATTGAGGAACCAATGACCGGAGACTCTGCGCAATTTAGACCACTACTCTCTGCTTT 839
QY 742 GTGAATCTATTTCGAAGTATAGCTGCTACCTTGCAGAGACCTCTTATTATGCTATGAAG 801
Db 840 GTGAATCTATTTCGAAGTATAGCTGCTACCTTGCAGAGACCTCTTATTATGCTATGAAG 899
QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGATCATGTTTCCAGGAGTGAATGAT 861
Db 900 GGAGCTGGGACAGATGATCATACCTCATCAGAGATCATGTTTCCAGGAGTGAATGAT 959
QY 862 CTGTTTAAATCAGGAGGAGTTAGGAAGATTTTG 898
Db 960 YTKTTTAAATWAGRGAGGTTTGGGAAATTTTK 996
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RESULT 7
BX396240

LOCUS BX396240 1062 bp mRNA linear EST 13-MAY-2003
DEFINITION BX396240 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI014YI09 5-PRIME, mRNA sequence.
ACCESSION BX396240
VERSION BX396240.1 GI:30624830
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91060 EVRY cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI014AE05QP1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI014AE05QP1.
Location/Qualifiers
1. 1062
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI014YI09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 285 a 234 c 272 g 270 t 1 others

Query Match 86.5%; Score 848.2; DB 13; Length 1062;
Best Local Similarity 99.4%; Pred. No. 1.6e-216;
Matches 850; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 22 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTTATGAGCGGGCTGAT 81
Db 208 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTTATGAGCGGGCTGAT 267
QY 82 GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 141
Db 268 GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 327
QY 142 CTGTTGACATCCGGAAGTAACTGTCAGCCAGGAAATCTCTGACGCTTTTAAGACTCTG 201
Db 328 CTGTTGACATCCGGAAGTAACTGTCAGCCAGGAAATCTCTGACGCTTTTAAGACTCTG 387
QY 202 TTGGCAGGATCTCTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 261
Db 388 TTGGCAGGATCTCTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTCGACT 447
QY 262 ATGTTGGCTCTGAGGAAACCTCTCGGCTTTTATGATGCTTATGAACTGAAACATGCTTG 321
Db 448 ATGTTGGCTCTGAGGAAACCTCTCGGCTTTTATGATGCTTATGAACTGAAACATGCTTG 507
QY 322 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
Db 508 AAGGAGCTGGAAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 567
QY 382 GAAGTGGAGCACTCAACAAAGTTTATGAAGAGAAATATCGCTCAAGCTGGAAGATGAC 441
Db 568 GAAGTGGAGCACTCAACAAAGTTTATGAAGAGAAATATCGCTCAAGCTGGAAGATGAC 627
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AL542496      1201 bp      mRNA      linear      EST 12-MAY-2003
LOCUS      AL542496 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YI14
DEFINITION      5-PRIME, mRNA sequence.
ACCESSION      AL542496
VERSION      AL542496.2 GI:30547699
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12874598.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE012BE070P1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DE012BE070P1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YI14"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      310 a 243 c 293 g 307 t 48 others
ORIGIN
Query Match      85.5%; Score 838.4; DB 9; Length 1201;
Best Local Similarity 98.2%; Pred. No. 7.3e-214;
Matches 875; Conservative 3; Mismatches 10; Indels 3; Gaps 3;
QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTCCCTGGATTGATGAGCGGGCTGAT 81
DB 167 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTCCCTGGATTGATGAGCGGGCTGAT 226
QY 82 GCAGAACTCTCGGAGGCTATGAAGGCTTGGCCACAGATGAGGAGCATCCTGACT 141
DB 227 GCAGAACTCTCGGAGGCTATGAAGGCTTGGCCACAGATGAGGAGCATCCTGACT 286
QY 142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 201
DB 287 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 346
QY 202 TTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAATTTGAAAATTA 261
DB 347 TTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAATTTGAAAATTA 406
QY 262 ATTGTGGCTCTGATGAACCCCTCTGGCTTTTATGATGCTTATGAACATGAACCTGTG 321
DB 407 ATTGTGGCTCTGATGAACCCCTCTGGCTTTTATGATGCTTATGAACATGAACCTGTG 466
QY 322 AAGGAGCTGGGAACAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB 467 AAGGAGCTGGGAACAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 526
QY 382 GAACTGAGAGCCATCAACAAGTTTATGAAGAAGAAATATGGCTCAAGCCTGGAAGATGAC 441

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527 GAACTGAGAGCCATCAACAAGTTTATGAAGAAGAAATATGGCTCAAGCCCTGGAAGATGAC 586
QY 442 GTGGTGGGGGACACTTCAGGCTACTACCAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 501
DB 587 GTGGTGGGGGACACTTCAGGCTACTACCAGCGGATGTTGGTGGTCTCTCCTCAGGCTAAC 646
QY 502 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTTGAACAAGATGCTCAGGCTTTATTT 561
DB 647 AGAGACCCCTGATGCTGGAATTTGATGAAGCTCAAGTTTGAACAAGATGCTCAGGCTTTATTT 706
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATACCAATCTTTTGAACA 621
DB 707 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATACCAATCTTTTGAACA 766
QY 622 CGAAGTGTCTCTCA-TTTGAGAAGGTTTTCACAAGTACATGACTATATCAGGATTTCA 680
DB 767 CGAAGTGTCTCTCA-TTTGAGAAGGTTTTCACAAGTACATGACTATATCAGGATTTCA 826
QY 681 AATTGAGGAAGC-ATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGGCTG 739
DB 827 AATTGAGGAAGCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGGCTG 886
QY 740 TTGTTGAATCTATTTCGAAGTATACCTGCTACCTTCGACAGACCCCTCTATTATGCTATGA 799
DB 887 TTGTTGAATCTATTTCGAAGTATACCTGCTACCTTCGACAGACCCCTCTATTATGCTATGA 946
QY 800 AGGAGCTGGGACAGATGATACCTCATCAGAGTATGTTTCCAGAGTGCAGATTG 859
DB 947 AGGAGCTGGGACAGATGATACCTCATCAGAGTATGTTTCCAGAGTGCAGATTG 1006
QY 860 ATCTGTTTAACTCAGGAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTT 910
DB 1007 ATCTGTTT-ACATCAGGAAGGTTTAGGAAGAAATTTGCCACCTCTCTTTAT 1056

RESULT 10
LOCUS      BX358605
DEFINITION      BX358605 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI041YI02 5-PRIME, mRNA sequence.
ACCESSION      BX358605
VERSION      BX358605.1 GI:30382268
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI041BE01QP1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI041BE01QP1.
Location/Qualifiers
1. .1076
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI041YI02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)

```

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

```
BASE COUNT      287 a   233 c   274 g   278 t
ORIGIN
Query Match      85.2%; Score 835.8; DB 13; Length 1076;
Best Local Similarity 97.4%; Pred. No. 3.4e-213;
Matches 866; Conservative 4; Mismatches 16; Indels 3; Gaps 2;
Qy 22 ATGCGACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGACGGCGGTGAT 81
Db 191 ATGCGACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGACGGCGGTGAT 250
Qy 82 GCAGAACTCTCGGAGGCTATGAAGGCTTGGGCACAGATCAGAGAGCATCCTGACT 141
Db 251 GCAGAACTCTCGGAGGCTATGAAGGCTTGGGCACAGATCAGAGAGCATCCTGACT 310
Qy 142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 201
Db 311 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 370
Qy 202 TTTGGCAGGATCTTCGGATGACTTGAATCAGAACTAATCTGCTGAAATTTGAAAATTA 261
Db 371 TTTGGCAGGATCTTCGGATGACTTGAATCAGAACTAATCTGCTGAAATTTGAAAATTA 430
Qy 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG 321
Db 431 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG 490
Qy 322 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTAATGCTTCAAGGACACCTGAA 381
Db 491 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTAATGCTTCAAGGACACCTGAA 550
Qy 382 GAAGTGAAGCCATCAACAACTTTATGAAGAGATATGGCTCAGCCCTGGAAGATGAC 441
Db 551 GAAGTGAAGCCATCAACAACTTTATGAAGAGATATGGCTCAGCCCTGGAAGATGAC 610
Qy 442 GTGTGGGGGACACTTCAGGGTACTACAGCGGATGTGGTGTCTCCCTTCAGGCTAAC 501
Db 611 GTGTGGGGGACACTTCAGGGTACTACAGCGGATGTGGTGTCTCCCTTCAGGCTAAC 670
Qy 502 AGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 561
Db 671 AGAGACCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 730
Qy 562 CAGCTGGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAA 621
Db 731 CAGCTGGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAA 790
Qy 622 CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 681
Db 791 CGAAGTGT-TCTCATTTGAGAAAGTGTGTTGACAAGTACATGACTATATCAGGATTTCAA 849
Qy 682 ATTGAGAAACCATGACCGGAGACTCTGGAATTTAGAGCAACTACTCCTTGCTGTT 741
Db 850 ATTGAGAAACCATGACCGGAGACTCTGGAATTTAGAGCAACTACTCCTTGCTGTT 909
Qy 742 GTGAATCTATTGCAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 801
Db 910 GTGAATCTATTGCAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 969
Qy 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGAGTGGAGATGAT 861
Db 970 GGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTTCCAGAGTGGAGATGAT 1029
Qy 862 CTGTTTAACATCAGGAAGGATTTAGGAAGATTTTGGCCACCTCTCTTT 910
Db 1030 CTGTTTA--CATCAGGAGGATTTAGGAGRATTTKCCACTCTCTTTT 1076

RESULT 11
BX402751
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LOCUS      BX402751      1007 bp      mRNA      linear      EST 13-MAY-2003
DEFINITION BX402751 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS001084YA05 5-PRIME, mRNA sequence.
ACCESSION  BX402751
VERSION     BX402751.1      GI:30607254
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1007)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished
COMMENT     Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2353.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIAI0212G03QPl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSIAI0212G03QPl.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS001084YA05"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo (dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      277 a   216 c   257 g   256 t   1 others
ORIGIN
Query Match      84.8%; Score 832.2; DB 13; Length 1007;
Best Local Similarity 99.6%; Pred. No. 3.1e-212;
Matches 834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 22 ATGCGACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGACGGCGGTGAT 81
Db 171 ATGCGACAGTTCTCAGAGCACTGTGACTTCCCTGGATTTGATGACGGCGGTGAT 230
Qy 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATCAGAGAGCATCCTGACT 141
Db 231 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATCAGAGAGCATCCTGACT 290
Qy 142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 201
Db 291 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAGACTCTG 350
Qy 202 TTTGGCAGGATCTTCCTGATGACTTGAATCAGAACTAATCTGGAATTTGAAAATTA 261
Db 351 TTTGGCAGGATCTTCCTGATGACTTGAATCAGAACTAATCTGGAATTTGAAAATTA 410
Qy 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG 321
Db 411 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTG 470
Qy 322 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTAATGCTTCAAGGACACCTGAA 381
Db 471 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTAATGCTTCAAGGACACCTGAA 530
Qy 382 GAAGTGAAGCCATCAACAACTTTATGAAGAGATATGCTCAGCCCTGGAAGATGAC 441
Db 531 GAAGTGAAGCCATCAACAACTTTATGAAGAGATATGCTCAGCCCTGGAAGATGAC 590
```

QY 442 GTGGTGGGGACACTTCAGGGTACTACACGCGATGTTGGTGGTCTCTCTCAGGCTAAC 501
Db 591 GTGGTGGGGACACTTCAGGGTACTACACGCGATGTTGGTGGTCTCTCTCAGGCTAAC 650
QY 502 ACAGACCCCTGATGCTGGAAATTCATGAGCTCAAGTTGAACAAGTCTCAGGCTTTATTT 561
Db 651 ACAGACCCCTGATGCTGGAAATTCATGAGCTCAAGTTGAACAAGTCTCAGGCTTTATTT 710
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QY 622 CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACATATATCAGGATTTCAA 681
Db 771 CGAAGTGTCTCATTTGAGAAAGTGTGTTGACAAGTACATGACATATATCAGGATTTCAA 830
QY 682 ATTGAGGAACCATTCAGCGGACAGACTCTGCGCAATTTAGACAACACTACTCTCTGTT 741
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QY 742 GTGAATCTATTTCGAAGTATACCTGCTACCTTGCGAGAGACCCCTCTATTATGCTATGAAG 801
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QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAAT 858
Db 951 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAAT 1007

RESULT 12

AL547761

LOCUS

DEFINITION AL547761 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI017YJ11 5-PRIME, mRNA sequence.

ACCESSION

AL547761

VERSION

AL547761.2

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12882128.

Contact: Genoscope

Genoscope Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2353.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgl-bin/cluster.cgi?seq=CS0DI017CE060P1&cluster=2353.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI017CE06QPI.

Location/Qualifiers

1. :1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI017YJ11"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

311 a 252 c 305 g 306 t 27 others

BASE COUNT

ORIGIN

Query Match 84.8%; Score 831.6; DB 9; Length 1201;
Best Local Similarity 95.0%; Pred. No. 4.9e-212;
Matches 911; Conservative 11; Mismatches 26; Indels 11; Gaps 6;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTCATGATGAGCGGGCTGAT 81
Db 208 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTCATGATGAGCGGGCTGAT 267
QY 82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCCTGACT 141
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QY 142 CTGTTGACATCCGGAAGTAAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201
Db 328 CTGTTGACATCCGGAAGTAAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 387
QY 202 TTTGSCAGGATCTTCTGGATGACCTGAATCAGAACTAACTGGAAATTTGAAAAATTA 261
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QY 262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCTTGG 321
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QY 322 AAGGAGCTGGGAACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
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QY 382 GAACCTGAGAGCCATCAACAAGTTTATGAAGAATATGGCTCAAGCCTGGAAAGTAC 441
Db 568 GAACCTGAGAGCCATCAACAAGTTTATGAAGAATATGGCTCAAGCCTGGAAAGTAC 627
QY 442 GTGGTGGGGACACTTCAGGGTACTACACGCGATGTTGGTGGTCTCTCTCAGGCTAAC 501
Db 628 GTGGTGGGGACACTTCAGGGTACTACACGCGATGTTGGTGGTCTCTCTCAGGCTAAC 687
QY 502 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGTCTCAGGCTTTATTT 561
Db 688 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGTCTCAGGCTTTATTT 747
QY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA 621
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QY 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGGTTTCCAGGAGTGAATTTAT 861
Db 987 GGAGCTGGGACAGATGATCAT-CCTCATCAGTCACTGG-TTCCAGGAGTGAATTTAT 1044
QY 862 CTGTTTAAATCAGGAAGGAGTTTAGGAAGAAATTTGGCACTCTCTCTCTCTCTCTCTCT 921
Db 1045 CTGTTT-ACMTTCAGGAAGGAGTTTAGGA--GAATTTGGCACCTCTCTCTCTCTCTCTCT 1101
QY 922 AAGGAGATACATCTGGGAGCTATGAAGAAGCTCTCTGCTCTCTCTCTCGGGAAGATGA 980
Db 1102 AAGGAGATACATCTGGGAGCTATGAAGAAGCTCTCTGCTCTCTCTCTCGGGAAGATGA 1155

RESULT 13

AL517516

LOCUS

DEFINITION AL517516 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone

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CS0DA003YF05 5-PRIME, mRNA sequence.
AL517516
AL517516.2 GI:30534896
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12781009.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DA003CC03QPl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DA003CC03QPl.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
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/clone="CS0DA003YF05"
/tissue_type="NEUROBLASTOMA"
/notes="Vector: pcMVSPORT.6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 317 a 257 c 303 g 297 t 27 others
ORIGIN
Query Match 84.5%; Score 828.6; DB 9; Length 1201;
Best Local Similarity 93.5%; Pred. No. 3.1e-211;
Matches 880; Conservative 14; Mismatches 20; Indels 7; Gaps 3;

QY 22 ATGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCTCGATTGATGAGCGGCTGAT 81
DDB 204 ATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCTCGATTGATGAGCGGCTGAT 263
QY 82 GCAGAACTCTTCGAGAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DDB 264 GCAGAACTCTTCGAGAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 323
QY 142 CTGTTGACATCCGAGCAATGCTCAGCGCCAGGAATCTCGAGCTTTTAAGACTCTG 201
DDB 324 CTGTTGACATCCGAGCAATGCTCAGCGCCAGGAATCTCGAGCTTTTAAGACTCTG 383
QY 202 TTGGGAGGATCTTCGGATGACTGAAATCAGAACTAACTGGAATTTGAAAAATTA 261
DDB 384 TTGGGAGGATCTTCGGATGACTGAAATCAGAACTAACTGGAATTTGAAAAATTA 443
QY 262 ATTGTGCTCTGATGAAACCTCTCGGCTTTATGATGCTTTATGAACTGAACATGCTTG 321
DDB 444 ATTGTGCTCTGATGAAACCTCTCGGCTTTATGATGCTTTATGAACTGAACATGCTTG 503
QY 322 AAGGAGCTGGAACAAATGAAAGTACTGACGAAATTTATGCTTCAAGGACACCTGAA 381
DDB 504 AAGGAGCTGGAACAAATGAAAGTACTGACGAAATTTATGCTTCAAGGACACCTGAA 563
QY 382 GAATGAGAGCCATCAACAGTTTATGAGAGAAATATGCTCAAGCTTGGAGATGAC 441
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442 GTGGTGGGGACACTTTCAGGGTACTACAGCGGATGTTGGTGTCTCTCCTTCAGGCTAAC 501
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QY 502 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTTCAGGCTTATTT 561
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QY 562 CAGGCTGGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAAACA 621
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QY 682 ATTGAGGAACCACTTACCCGAGAGCTTCTGGCAATTTAGAGCAACTACTCTTCGCTGTT 741
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DDB 924 GTCAAAATCTATTGCAAGTATACCTGCTACCTTGCAGAGACCCCTCTA-TTATGCTATGAA 983
QY 801 GGGAGCTGGGACAGATGATCATACCTCATCAGAGTATGTTCCAGGAGTGAAGATGA 860
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QY 861 TCTGTTTAAACATCAGGAGGAGTTTAGGAAGATTTTGGCCACTCTCTTTATTCATGAT 920
DDB 1041 ATCTGTTTAAACATCAGGAGGAGTTTAGGAAGATTTTGGCCACTCTCTTTATTCATGAT 1097
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DDB 1098 TSAGGGAGAAACTGGGGCTATAGAAACACTCTCTGCGS 1138

RESULT 14
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LOCUS AL5141412 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE006YJ10
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL5141412
VERSION AL5141412.2 GI:30545565
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12872460.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE006DE05QPl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE006DE05QPl.
Location/Qualifiers
1. .1201
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

BASE COUNT 315 a 256 c 289 g 303 t 38 others
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Query Match 83.8%; Score 822; DB 9; Length 1201;
Best Local Similarity 94.3%; Pred. No. 1.9e-209;
Matches 886; Conservative: 18; Mismatches 29; Indels 7; Gaps 5;

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QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTGGGCACAGATGAGGAGCATCTGACT 141
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QY 142 CTGTTGACATCCGGAAGTAACTGTCAGCGCAGAAATCTCTGCAGCTTTTAAGACTCTG 201
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QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 261
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QY 262 ATTGTGGCTCTGATGAAGCCCTCTCGGCTTTATGATGCTTATGAACATGCAATGCTTGG 321
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Db 436 ATTGTGGCTCTGATGAAGCCCTCTCGGCTTTATGATGCTTATGAACATGCAATGCTTGG 495
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Db 496 AAGGGAGCTGGAACTAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 555
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QY 382 GAACCTGAGAGCCATCAACAAGTTTATGAAGAAATATGGCTCAAGCCCTGGGAAGTAC 441
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QY 442 GTGGTGGGGACACTTCAGGCTACTACACGCGATGTTGGTGGTCTCTCTTCAGGCTAAC 501
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QY 502 AGAGACCTTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGTCTCAGGCTTTATT 561
|||||
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QY 681 AATTGAGGAAACATTGACCGGAGACTT-CTGGCAATTTAGAGCAACTACTCTCTGGTG 739
|||||
Db 856 AATTGAGGAAACATTGACCGGAGACTTCTTGGCAATTTAGAGCAACTACTCTCTGGTG 915
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Db 916 TTGTGAATCTATTCGAAGTATACCTGCTTACCTTCAGAGACCCCTCTATTATGCTATGA 975
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QY 859 GATCTCTTAAACATCAGGAGGTTTGAAGAAATTTTGGCAACCTCTCTTTATTCATG 918
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RESULT 15
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5-PRIME, mRNA sequence.
ACCESSION AL583578
VERSION
KEYWORDS AL583578.2 GI:30606551
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1022)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12952676.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE004CB11Q1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE004CB11Q1.
Location/Qualifiers
I. 1022
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 282 a 219 c 261 g 255 t 5 others
ORIGIN

Query Match 83.6%; Score 820.4; DB 9; Length 1022;
Best Local Similarity 99.1%; Pred. No. 4.6e-209;
Matches 840; Conservative 5; Mismatches 1; Indels 2; Gaps 2;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTGATGAGCGGCTGAT 81
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Db 176 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTCCCTGGATTGATGAGCGGCTGAT 235
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QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTGGGCACAGATGAGGAGCATCTGACT 141
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Db 236 GCAGAACTCTTCGGAAGGCTATGAAGGCTGGGCACAGATGAGGAGCATCTGACT 295
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QY 142 CTGTTGACATCCGGAAGTAACTGTCAGCGCAGAAATCTCTGCAGCTTTTAAGACTCTG 201
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Db 296 CTGTTGACATCCGGAAGTAACTGTCAGCGCAGAAATCTCTGCAGCTTTTAAGACTCTG 355
|||||

QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 261
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Db 356 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAAAAATTTGAAAAATTA 415
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QY 262 ATTGTGGCTCTGATGAAGCCCTCTCGGCTTTATGATGCTTATCAACTGAAACATGCTTGG 321
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Qy	382	GAACTGAGAGCCATCAACAAGTTTATGAAGAGAATATGGCTCAAGCCCTGGAAGATGAC	441
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Qy	502	AGAGACCTCGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	561
Db	656	AGAGACCTCGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	715
Qy	562	CAGGCTGGAGAACTTAANTGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA	621
Db	716	CAGGCTGGAGAACTTAANTGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA	775
Qy	622	CGAAGTGTGTCTCATTTGAGAAAGTCTTTGACAAGTACATGACTATATCAGGATTTCAA	681
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Qy	682	ATTGAGGAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT	741
Db	835	ATTGAGGAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT	894
Qy	742	GTGAATCTATTGAAATATACCTGCTACCTTGCAGAGACCCCTCTATTATGCTATGAAG	801
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2003, 21:27:21 ; Search time 37.6667 Seconds
(without alignments)
1377.971 Million cell updates/sec

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Perfect score: 1639
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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14:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*		
15:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*		
16:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*		
17:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*		
18:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*		
19:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*		
20:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*		
21:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*		
22:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*		
23:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*		
24:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	1639	100.0	327 22	AAB50864 Modified human ann
2	1630	99.5	327 22	AAB50865 Modified human ann
3	1618	98.7	327 22	AAB50863 Modified human ann
4	1590	97.0	320 9	AAP80511 Placental coagulat
5	1590	97.0	320 10	AAP91953 Vascular anti-coag
6	1590	97.0	320 12	AAR13082 PAP-I. Homo sapie
7	1590	97.0	320 20	AAY13923 S65T GFP variant/h
8	1590	97.0	320 21	AAY84788 Amino acid sequenc
9	1590	97.0	320 23	ABG31220 Human annexin V, c

10	1587	96.8	320 10	AAP90053 anticoagulant pp4
11	1587	96.8	600 21	AAV92930 Annexin V/urokinas
12	1586	96.8	320 9	AAP82317 PAP-I isolated fro
13	1585	96.7	319 13	AAR26276 CPB-I. Homo sapie
14	1585	96.7	319 14	AAR41021 Calphobindin I (CP
15	1585	96.7	319 23	ABG32550 Human CPB-I protel
16	1584	96.6	320 9	AAP80714 Sequence vascular
17	1584	96.6	320 9	AAP80714 Sequence vascular
18	1584	96.6	320 12	AAR11910 Vascular anticoagu
19	1580	96.4	319 13	AAR26180 CPB-I. Homo sapie
20	1577	96.2	320 10	AAP91363 Human lipocortin-V
21	1553	94.8	319 13	AAR25718 CPB-I. Homo sapie
22	1479.5	90.3	319 20	AAV13924 S65T GFP variant/h
23	1479.5	90.3	319 23	ABBS7067 Mouse ischaemic co
24	1455.5	88.8	318 20	AAV13925 S65T GFP variant/h
25	1448.5	88.4	319 16	AAR75695 Rat annexin-V. Ra
26	1442.5	88.0	319 24	ABP56248 Human annexin V pr
27	1442.5	88.0	669 24	ABP56249 Modified annexin p
28	1012	61.7	208 21	AAB58393 Lung cancer associ
29	932	56.9	672 11	AAR03725 Human placenta-der
30	931	56.8	786 11	ABU54621 Human NOVX polypep
31	931	56.8	786 11	AAR03726 Human placenta-der
32	923	56.3	321 20	AAV13926 S65T GFP variant/h
33	923	56.3	321 23	ABG96279 Human ovarian canc
34	923	56.3	324 21	AAB43617 Human cancer assoc
35	922	56.3	321 10	AAP91913 Anticoagulative pp
36	906.5	55.3	320 21	AAV84790 Amino acid sequenc
37	872	53.2	736 22	ABG19948 Novel human diagno
38	865	52.8	503 14	AAR34127 Annexin XI type I
39	857	52.3	505 14	AAR34128 Annexin XI type I
40	850	52.2	505 20	AAV07117 Lung cancer associ
41	844	51.5	299 23	ABP69394 Human polypeptide
42	831.5	50.7	327 9	AAP80715 Sequence vascular
43	831.5	50.7	327 10	AAP91954 Vascular anti-coag
44	831.5	50.7	327 14	AAR35754 VAC-beta. Synthet
45	831.5	50.7	327 22	AAW78665 Human protein SEQ

ALIGNMENTS

RESULT 1	
AAAB50864	ID AAB50864 standard; Protein; 327 AA.
XX	AC AAB50864;
XX	DT 16-MAR-2001 (first entry)
XX	DE Modified human annexin, SEQ ID NO: 4.
XX	DE Human: annexin; chelation site; nuclear imaging; apoptosis;
KW	transplant rejection.
XX	OS Homo sapiens.
XX	PN WO200073332-A1.
XX	PD 07-DEC-2000.
XX	PF 25-MAY-2000; 2000WO-US14324.
XX	PR 01-JUN-1999; 99US-0324096.
XX	PA (UNIW) UNIV WASHINGTON.
XX	PI Tait JF, Brown DS;
XX	DR WPI: 2001-080465/09.
XX	DR N-PSDB: AAC91369.
XX	PT Novel modified annexin useful for imaging vascular thrombi and
PT	apoptosis; has N-terminal chelation site comprising amino acid

PT extension which comprises a glycine and a cysteine residue -
XX
PS Claim 15; Page 33-35; 39pp; English.
XX
CC The present sequence is a modified annexin having an N-terminal
CC chelation site, which comprises an amino acid extension including a
CC glycine and a cysteine residue. The modified annexin is useful for
CC imaging vascular thrombi or apoptosis which is associated with response
CC to a chemotherapeutic agent or with rejection as a result of
CC transplantation. The modified annexin can effectively chelate a
CC radionuclide and retain annexin bioactivity. It can be readily prepared
CC in high radiochemical yield and with high radiochemical purity. In
CC contrast to conventional conjugation chemistries that provide a
CC distribution of conjugation products, the modified annexin has a single
CC chelation site remote from the site of biological activity.
XX
SQ Sequence 327 AA;
Query Match 100.0%; Score 1639; DB 22; Length 327;
Best Local Similarity 100.0%; Pred. No. 9.2e-143;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGGCGHMAQVLRGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSSNAORQEI 60
DB |||||
QY 61 SAAFTLFGRODLLDLKSELTKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
DB |||||
QY 121 IASRTPEELRAIKQVTEEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVE 180
DB |||||
QY 121 IASRTPEELRAIKQVTEEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVE 180
DB |||||
QY 181 QDAQALFQAGELKNGTDEEKFTIFGTRSVSHLRKVFDRKVTMTSGFQIETIDRETSGNL 240
DB |||||
QY 181 QDAQALFQAGELKNGTDEEKFTIFGTRSVSHLRKVFDRKVTMTSGFQIETIDRETSGNL 240
DB |||||
QY 241 EQLLAVVKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFIRKFRKNA 300
DB |||||
QY 241 EQLLAVVKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFIRKFRKNA 300
DB |||||
QY 301 TSLSYMIKGTSGDYKKALLLSGDD 327
DB |||||
QY 301 TSLSYMIKGTSGDYKKALLLSGDD 327
DB |||||
RESULT 2
AAB50865
ID AAB50865 standard; Protein; 327 AA.
XX
AC AAB50865;
XX
DT 16-MAR-2001 (first entry)
XX
DE Modified human annexin, SEQ ID NO: 6.
XX
KW Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO200073332-A1.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US14324.
XX
PR 01-JUN-1999; 99US-0324096.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Tait JF, Brown DS;

XX
DR WPI; 2001-080465/09.
DR N-PSDB; AAC91370.
XX
PT Novel modified annexin useful for imaging vascular thrombi and
PT apoptosis, has N-terminal chelation site comprising amino acid
PT extension which comprises a glycine and a cysteine residue -
XX
PS Claim 18; Page 37-38; 39pp; English.
XX
CC The present sequence is a modified annexin having an N-terminal
CC chelation site, which comprises an amino acid extension including a
CC glycine and a cysteine residue. The modified annexin is useful for
CC imaging vascular thrombi or apoptosis which is associated with response
CC to a chemotherapeutic agent or with rejection as a result of
CC transplantation. The modified annexin can effectively chelate a
CC radionuclide and retain annexin bioactivity. It can be readily prepared
CC in high radiochemical yield and with high radiochemical purity. In
CC contrast to conventional conjugation chemistries that provide a
CC distribution of conjugation products, the modified annexin has a single
CC chelation site remote from the site of biological activity.
XX
SQ Sequence 327 AA;
Query Match 99.5%; Score 1630; DB 22; Length 327;
Best Local Similarity 99.7%; Pred. No. 6.2e-142;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAGGCGHMAQVLRGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSSNAORQEI 60
DB |||||
QY 1 MAGGCGHMAQVLRGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSSNAORQEI 60
DB |||||
QY 61 SAAFTLFGRODLLDLKSELTKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
DB |||||
QY 61 SAAFTLFGRODLLDLKSELTKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
DB |||||
QY 121 IASRTPEELRAIKQVTEEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVE 180
DB |||||
QY 121 IASRTPEELRAIKQVTEEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVE 180
DB |||||
QY 181 QDAQALFQAGELKNGTDEEKFTIFGTRSVSHLRKVFDRKVTMTSGFQIETIDRETSGNL 240
DB |||||
QY 181 QDAQALFQAGELKNGTDEEKFTIFGTRSVSHLRKVFDRKVTMTSGFQIETIDRETSGNL 240
DB |||||
QY 241 EQLLAVVKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFIRKFRKNA 300
DB |||||
QY 241 EQLLAVVKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFIRKFRKNA 300
DB |||||
QY 301 TSLSYMIKGTSGDYKKALLLSGDD 327
DB |||||
QY 301 TSLSYMIKGTSGDYKKALLLSGDD 327
DB |||||
RESULT 3
AAB50863
ID AAB50863 standard; Protein; 327 AA.
XX
AC AAB50863;
XX
DT 16-MAR-2001 (first entry)
XX
DE Modified human annexin, SEQ ID NO: 2.
XX
KW Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO200073332-A1.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US14324.

XX 01-JUN-1999; 99US-0324096.
XX (UNIW) UNIV WASHINGTON.
XX Tait JF, Brown DS;
XX WPI; 2001-080465/09.
XX N-PSDB; AAC91368.
XX Novel modified annexin useful for imaging vascular thrombi and
XX apoptosis, has N-terminal chelation site comprising amino acid
XX extension which comprises a glycine and a cysteine residue -
XX
XX Claim 12; Page 30-31; 39pp; English.
XX The present sequence is a modified annexin having an N-terminal
XX chelation site, which comprises an amino acid extension including a
XX glycine and a cysteine residue. The modified annexin is useful for
XX imaging vascular thrombi or apoptosis which is associated with response
XX to a chemotherapeutic agent or with rejection as a result of
XX transplantation. The modified annexin can effectively chelate a
XX radionuclide and retain annexin bioactivity. It can be readily prepared
XX in high radiochemical yield and with high radiochemical purity. In
XX contrast to conventional conjugation chemistries that provide a
XX distribution of conjugation products, the modified annexin has a single
XX chelation site remote from the site of biological activity.
XX
XX Sequence 327 AA;

Query Match 98.7%; Score 1618; DB 22; Length 327;
Best Local Similarity 99.4%; Pred. No. 8e-141;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAGCGHMAQVLRGTVTFDFGDERADAETLRKAMKGLGTDEESILTLTSSNAQROEI 60
DB 1 MACGGHMAQVLRGTVTFDFGDERADAETLRKAMKGLGTDEESILTLTSSNAQROEI 60
QY 61 SAAFKTLFGRDLDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
DB 61 SAAFKTLFGRDLDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
QY 121 IASRTPPELRKQVVEEYEGSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVE 180
DB 121 IASRTPPELRKQVVEEYEGSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVE 180
QY 181 QDAQALFOAGELKMGTDDEEFITIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNL 240
DB 181 QDAQALFOAGELKMGTDDEEFITIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNL 240
QY 241 EQLLLVVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFRNKRKNFA 300
DB 241 EQLLLVVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFRNKRKNFA 300
QY 301 TSLYSMTKGTSGDYKKALLLSGEDD 327
DB 301 TSLYSMTKGTSGDYKKALLLSGEDD 327

RESULT 4
AAP80511
ID AAP80511 standard; protein; 320 AA.
XX AAP80511;
XX
XX 25-MAR-2003 (updated)
XX 10-MAR-2003 (updated)
XX 12-NOV-1990 (first entry)
XX Placental coagulation inhibitor.
XX Placental coagulation inhibitor; disseminated vascular coagulation;
XX thrombosis.

XX Homo sapiens.
XX OS
XX EP279459-A.
XX JP03219875-A.
XX 24-AUG-1988.
XX 19-FEB-1988; 88EP-0102468.
XX 20-FEB-1987; 87JP-0037227.
XX 23-JUL-1987; 87JP-0184428.
XX (KOWA) KOWA CO LTD.
XX Saino Y, Iwasaki A, Suda M;
XX WPI; 1988-236733/34.
XX WPI; 1991-329110/45.
XX N-PSDB; AAN81113.
XX Recombinant placental coagulation inhibitor - useful for the prevention
XX and treatment of thromboses or disseminated intra-vascular coagulation.
XX
XX Disclosure; Page ?; ?pp; English.
XX This polypeptide exhibits strong anticoagulant activities and is useful
XX for the treatment and prevention of e.g. thrombosis or disseminated
XX intravascular coagulation in the brain, heart and peripheral blood
XX vessels, such as cerebral and myocardial infarction. It has no
XX antigenicity against man and can be produced in large amts. using
XX recombinant methods.
XX (Updated on 10-MAR-2003 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PR field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 320 AA;

Query Match 97.0%; Score 1590; DB 9; Length 320;
Best Local Similarity 99.7%; Pred. No. 3e-138;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 MAQVLRGTVTFDFGDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 67
DB 1 MAQVLRGTVTFDFGDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 60
QY 68 FGRDLDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPPE 127
DB 61 FGRDLDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPPE 120
QY 128 ELRAIKOVYEEYEGSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 187
DB 121 ELRAIKOVYEEYEGSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
QY 188 QAGELKMGTDDEEFITIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLQALLAV 247
DB 181 QAGELKMGTDDEEFITIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLQALLAV 240
QY 248 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFRNKRKNFAISLXSMI 307
DB 241 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFRNKRKNFAISLXSMI 300
QY 308 KGDTSGDYKKALLLSGEDD 327
DB 301 KGDTSGDYKKALLLSGEDD 320

RESULT 5
AAP91953
ID AAP91953 standard; protein; 320 AA.
XX AAP91953;
XX

XX 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 30-JUL-1989 (first entry)
XX Vascular anti-coagulating protein-alpha.
DE Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
XX Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
KW Chimeric - Homo sapiens.
OS Chimeric - Mus musculus.
XX Key Location/Qualifiers
FH CDS 1..320
FT /product-VAC-alpha protein
XX DE3810331-A.
PN 05-OCT-1989.
XX 26-MAR-1988; 88DE-3810331.
XX 26-MAR-1988; 88DE-3810331.
XX (BOEH) BOEHRINGER INGELHEIM.
XX Gunther A;
XX WPI; 1989-293724/41.
DR N-PSDB; AAN91353.
XX Monoclonal antibodies to vascular anti-coagulating proteins - and
PT hybridomas producing such antibodies.
XX Disclosure; fig 1; lipp; German.
XX This vascular anti-coagulating protein (VAC)-alpha is used in the
CC preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected
CC into a host animal, in conjugation with eg keyhole limpet haemocyanin,
CC and the B-cells from immunised hosts are then fused with myeloma cells.
CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-
CC alpha. Abs can be used as immunoassay reagents to detect VAC proteins,
CC as affinity ligands for protein purificn. and as medicaments for binding
CC and/or neutralising VAC proteins in vivo. See also AAN91354 and
CC EP-181465.
CC (Updated on 10-MAR-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 320 AA;
Query Match 97.0%; Score 1590; DB 10; Length 320;
Best Local Similarity 99.7%; Pred. No. 3e-138; Mismatches 1; Indels 0; Gaps 0;
Matches 319; Conservative 0;
QY 8 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQETSAFRTL 67
DB 1 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQETSAFRTL 60
QY 68 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
DB 61 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 128 ELRAIKQVYEEYEGSSLEDVVDGTSYQYQRMVLLVLLQANRPDPDAGIDEAQVEQDAQALF 187
DB 121 ELRAIKQVYEEYEGSSLEDVVDGTSYQYQRMVLLVLLQANRPDPDAGIDEAQVEQDAQALF 180
QY 188 QAGELKWGTDDEKFTIFGTRSVSHLRKVFVKYMTISGQIETIDRETSGNLEQLLLAV 247
DB 248 VKSIRSIPLAETLYAMKAGTDDHTLIRVWVSRSEIDLNIKRFKNFATSLSYMI 307
DB 241 VKSIRSIPLAETLYAMKAGTDDHTLIRVWVSRSEIDLNIKRFKNFATSLSYMI 300

QY 308 KGDTSGDYKKALLLSGEDD 327
DB 301 KGDTSGDYKKALLLSGEDD 320
RESULT 6
AAR13082
ID AAR13082 standard; Protein; 320 AA.
AC AAR13082;
XX 25-MAR-2003 (updated)
DT 30-SEP-1991 (first entry)
XX PAP-I.
XX Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;
KW gla-domain; VKDP.
XX Homo sapiens.
OS WO9109953-A.
PN 11-JUL-1991.
XX 13-DEC-1990; 90WO-US07335.
XX 29-DEC-1989; 89US-0459082.
XX (ZYMO) ZYMOGENETICS INC.
PA Foster DC;
PI WPI; 1991-222905/30.
XX N-PSDB; AAQ12679.
DR Recombinant prodn. of hybrid phospholipid-binding proteins -
XX comprising lipocortin phospholipid-binding domain and
PT vitamin K-dependent protein
XX Disclosure; Fig 7; 57pp; English.
XX This sequence, or a fragment of it, is used in the construction of
CC hybrid phospholipid-binding proteins (PBP) comprising at least one
CC lipocortin phospholipid binding domain (PBD), e.g. of PAP-I, joined
CC to a gla-domainless vitamin K-dependent protein, e.g. protein C or
CC activated protein C. See also AAQ12678-81.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 320 AA;
Query Match 97.0%; Score 1590; DB 12; Length 320;
Best Local Similarity 99.7%; Pred. No. 3e-138; Mismatches 1; Indels 0; Gaps 0;
Matches 319; Conservative 0;
QY 8 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQETSAFRTL 67
DB 1 MAQVLRGTVTDPPGDERADAETLRKAMKGLGTDEESILTLTSRNAQRQETSAFRTL 60
QY 68 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
DB 61 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 128 ELRAIKQVYEEYEGSSLEDVVDGTSYQYQRMVLLVLLQANRPDPDAGIDEAQVEQDAQALF 187
DB 121 ELRAIKQVYEEYEGSSLEDVVDGTSYQYQRMVLLVLLQANRPDPDAGIDEAQVEQDAQALF 180
QY 188 QAGELKWGTDDEKFTIFGTRSVSHLRKVFVKYMTISGQIETIDRETSGNLEQLLLAV 247
DB 181 QAGELKWGTDDEKFTIFGTRSVSHLRKVFVKYMTISGQIETIDRETSGNLEQLLLAV 240

QY 248 VKSIRIPAYLAETLYAMKAGCTDDHTLIRVMSRSEIDLFNIRKEFRNFATSLYSMI 307
 Db 241 VKSIRIPAYLAETLYAMKAGCTDDHTLIRVMSRSEIDLFNIRKEFRNFATSLYSMI 300

QY 308 KGDTSGDYKKALLLLSGEDD 327
 Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 7
 AAY13923
 ID AAY13923 standard; protein; 320 AA.
 AC AAY13923;
 XX
 DT 13-JUL-1999 (first-entry)
 XX
 DE S65T GFP variant/hannexin V protein.
 XX
 KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KW fluorescent intensity; anionic phospholipid binding affinity;
 KW asymmetric distribution; plasma membrane phospholipid;
 KW apoptotic cell detection.
 XX
 OS Aequorea victoria.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W09919470-A2.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO-US21444.
 XX
 PR 09-OCT-1997; 97US-0948276.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Ernst JD;
 XX
 DR WPI; 1999-277634/23.
 XX
 PT Bifunctional fusion protein useful for the detection of apoptotic
 cells
 PS
 PS Claim 2; Page 14-15; 23pp; English.
 XX
 CC This sequence represents an example of a protein of the invention.
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labelled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes.
 XX
 SQ Sequence 320 AA;
 Query Match 97.0%; Score 1590; DB 20; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 MAQVLRGTVDFFGFDERADAETLRKAMKGLGTDEESILTLTSSRQAQRQISAAFKTL 67
 Db 1 MAQVLRGTVDFFGFDERADAETLRKAMKGLGTDEESILTLTSSRQAQRQISAAFKTL 60

QY 68 FGRLDLDLSELTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
 Db 61 FGRLDLDLSELTGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120

QY 128 ELRAIKQVYEEYGGSSLEDDVVGDTSGYYORMLVLLQANRDPDAGIDEAQVSDQAALF 187
 Db 121 ELRAIKQVYEEYGGSSLEDDVVGDTSGYYORMLVLLQANRDPDAGIDEAQVSDQAALF 180

QY 188 QAGELKWTDEKFTIFGTRSVSHLRKVKFDKVTISGFOIETIDRETSGNLEQLLAV 247
 Db 181 QAGELKWTDEKFTIFGTRSVSHLRKVKFDKVTISGFOIETIDRETSGNLEQLLAV 240

QY 248 VKSIRIPAYLAETLYAMKAGCTDDHTLIRVMSRSEIDLFNIRKEFRNFATSLYSMI 307
 Db 241 VKSIRIPAYLAETLYAMKAGCTDDHTLIRVMSRSEIDLFNIRKEFRNFATSLYSMI 300

QY 308 KGDTSGDYKKALLLLSGEDD 327
 Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 8
 AAY84788
 ID AAY84788 standard; peptide; 320 AA.
 XX
 AC AAY84788;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Amino acid sequence of annexin V.
 KW Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory;
 KW coating; thrombogenic biomaterial; labelling compound; negative charge.
 XX
 OS Unidentified.
 XX
 FH Key
 FT Domain
 FT Location/Qualifiers
 FT 16..91
 FT /note= "domain 1"
 XX
 PN FR2784106-A1.
 XX
 PD 07-APR-2000.
 XX
 PF 02-OCT-1998; 98FR-0012366.
 XX
 PR 02-OCT-1998; 98FR-0012366.
 XX
 CC (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 CC (UYPA-) UNIV CURIE PARIS VI P & M.
 XX
 PI Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerois R;
 XX
 DR WPI; 2000-320664/28.
 XX
 CC Chemical structure having affinity for phospholipid comprises chemical
 CC platform comprising six residues supporting set of chemical functions
 CC that are capable of binding to phospholipid
 XX
 PS Claim 13; Fig 6b; 63pp; French.
 XX
 CC The present sequence represents an annexin polypeptide. The domain of
 CC annexin, which may be modified, is used to construct the chemical
 CC compounds of the invention. The specification describes chemical
 CC compounds which have an affinity for a phospholipid. The chemical
 CC compounds comprise at least one chemical platform comprising six
 CC residues supporting a set of chemical functions that are capable of
 CC binding to the phospholipid and at least partly define the affinity
 CC of the structure for the phospholipid. The compounds act as
 CC phospholipid sequestrers. The compounds are useful for preparing
 CC antithrombotic, antitumor and antiinflammatory medicaments, for
 CC making coatings for thrombogenic biomaterials, and for preparing
 CC labelling compounds useful for analysing and detecting negative

CC charges on cell surfaces and microvesicles in blood.
 XX Sequence 320 AA;
 SQ Query Match 97.0%; Score 1590; DB 21; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 MAQVLRGVTDPFGDERADAETLRKAMKGLGTDEESILTLTSRSNAQRQETSAAFKTL 67
 DB 1 MAQVLRGVTDPFGDERADAETLRKAMKGLGTDEESILTLTSRSNAQRQETSAAFKTL 60

QY 68 FGRDLLDLKSELTKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRDLLDLKSELTKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

QY 128 ELRAIKQVVEEYSGSLEDVVDGTSYQYQRMVLLVLLQANRPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVVEEYSGSLEDVVDGTSYQYQRMVLLVLLQANRPDAGIDEAQVEQDAQALF 180

QY 188 QAGELKKGTDDEKFTIFGTRSVSHLRKVFDMYMTISGFQIETIDRETSGNLEQLLLAV 247
 DB 181 QAGELKKGTDDEKFTIFGTRSVSHLRKVFDMYMTISGFQIETIDRETSGNLEQLLLAV 240

QY 248 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVWVSERSEIDLNFIRKPKNFATSLYSMI 307
 DB 241 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVWVSERSEIDLNFIRKPKNFATSLYSMI 300

QY 308 KGDTSQDYKAKALLLGGEDD 327
 DB 301 KGDTSQDYKAKALLLGGEDD 320

RESULT 9
 ABC31220
 ID ABC31220 standard; Protein; 320 AA.
 XX
 AC ABC31220;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human annexin V, containing a delta RACK binding site.
 XX
 KW Human; annexin V; delta RACK; delta protein kinase C; deltaPKC;
 KW V1 domain; vasotropic; cerebroprotective; deltaV1-1; deltaV1-2; RACK;
 KW pseudo-delta RACK; pseudo-delta receptor for activated C-kinase;
 KW deltaV1-5; PKC; protein kinase C; signal transduction; cell growth;
 KW gene expression; ion channel activity; translocation; hypoxia; stroke;
 KW ischaemic damage; creatine kinase.
 OS Homo sapiens.
 XX
 PN WO200257413-A2.
 XX
 XX 25-JUL-2002.
 XX
 PF 09-NOV-2001; 2001WO-US47556.
 XX
 PR 18-JAN-2001; 2001US-262060P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Mochly-Rosen D;
 XX
 DR WPI; 2002-599715/64.
 XX
 PT New delta protein kinase C peptide for reducing or enhancing damage to
 PT cells or tissues exposed to ischemic or hypoxic event caused by stroke,
 PT or for protecting tissue from damage due to ischemia -
 XX
 PS Claim 45; Page 64-65; 65pp; English.
 XX
 CC The invention discloses peptides comprising deltaV1-1, deltaV1-2,

CC pseudo-delta receptors for activated C-kinase (RACK), deltaV1-5 or their
 CC derivatives or fragments. Protein kinase C (PKC) is a key enzyme in
 CC signal transduction involved in a variety of cellular functions including
 CC cell growth, regulation of gene expression and ion channel activity. The
 CC localisation of different PKC isozymes to different areas of the cell in
 CC turn appears due to binding of the activated isozymes to the specific
 CC anchoring molecules (RACKs). Peptides that mimic either the PKC-binding
 CC site on RACKs or the RACK-binding site on PKC are isozyme specific
 CC translocation inhibitors of PKC. The disclosed peptides are useful in
 CC activating or inhibiting translocation or function of deltaPKC. The
 CC deltaPKC agonists or antagonists are useful in reducing, enhancing or
 CC protecting against damage to cells or tissues due to ischaemic or hypoxic
 CC event caused by stroke. Acute administration of the peptides, conjugated
 CC to a carrier peptide or a Tat-derived peptide, protected hearts against
 CC ischaemic damage as shown by decreased release of creatine kinase. The
 CC data indicate that in an intact heart, inhibition of deltaPKC conferred
 CC greater than 50% protection against ischaemic damage. The sequence
 CC presented is human annexin V, which contains a delta RACK binding site.
 XX
 SQ Sequence 320 AA;
 Query Match 97.0%; Score 1590; DB 23; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3e-138;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 MAQVLRGVTDPFGDERADAETLRKAMKGLGTDEESILTLTSRSNAQRQETSAAFKTL 67
 DB 1 MAQVLRGVTDPFGDERADAETLRKAMKGLGTDEESILTLTSRSNAQRQETSAAFKTL 60

QY 68 FGRDLLDLKSELTKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRDLLDLKSELTKFKFKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

QY 128 ELRAIKQVVEEYSGSLEDVVDGTSYQYQRMVLLVLLQANRPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVVEEYSGSLEDVVDGTSYQYQRMVLLVLLQANRPDAGIDEAQVEQDAQALF 180

QY 188 QAGELKKGTDDEKFTIFGTRSVSHLRKVFDMYMTISGFQIETIDRETSGNLEQLLLAV 247
 DB 181 QAGELKKGTDDEKFTIFGTRSVSHLRKVFDMYMTISGFQIETIDRETSGNLEQLLLAV 240

QY 248 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVWVSERSEIDLNFIRKPKNFATSLYSMI 307
 DB 241 VKSIRSIAPYLAETLYYAMKAGTDDHTLIRVWVSERSEIDLNFIRKPKNFATSLYSMI 300

QY 308 KGDTSQDYKAKALLLGGEDD 327
 DB 301 KGDTSQDYKAKALLLGGEDD 320

RESULT 10
 AAP90053
 ID AAP90053 standard; protein; 320 AA.
 XX
 AC AAP90053;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE antioagulant PP4 protein.
 XX
 KW Anticoagulant; PP4 protein; thromboplastin.
 XX
 OS Homo sapiens (human).
 XX
 PN EP318703-A.
 XX
 PD 07-JUN-1989.
 XX
 PF 29-OCT-1988; 88EP-0118039.
 XX
 PR 03-NOV-1987; 87DE-3737239.
 XX

PA (BEHW) BEHRINGWERKE AG.

XX PI Grundmann U, Abel KJ, Kupper H;

XX DR WPI; 1989-166767/23.

XX PT New DNA sequence encoding anticoagulant P4 protein

XX PT - and new recombinant protein, vectors, antibodies, etc.,

XX PT useful therapeutically and diagnostically.

XX PS Claim 1; page 11 and Table 1; 12pp; German.

XX CC Amino acid sequence of anticoagulant P4 protein. This

XX CC inhibits blood coagulation at the thromboplastin stage.

XX CC (Updated on 25-MAR-2003 to correct PF field.)

XX CC (Updated on 25-MAR-2003 to correct PR field.)

XX CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 320 AA;

Query Match 96.8%; Score 1587; DB 10; Length 320;

Best Local Similarity 99.4%; Pred. No. 5.6e-138;

Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MAQVLRGTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROETSAAPKTL 67

Db 1 MAQVLRGTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROETSAAPKTL 60

Qy 68 FGRDLLDLKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127

Db 61 FGRDLLDLKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120

Qy 128 ELRAIKQVYEEYGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODAQLF 187

Db 121 ELRAIKQVYEEYGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODAQLF 180

Qy 188 QAGELKNGTDEEKPTITFGTRSVSHLRKRVFDKYMTISGFQIEETIDRETSGNLEQLLAV 247

Db 181 QAGELKNGTDEEKPTITFGTRSVSHLRKRVFDKYMTISGFQIEETIDRETSGNLEQLLAV 240

Qy 248 VKSTRSIPAYLAETLYYAMKAGGDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI 307

Db 241 VKSTRSIPAYLAETLYYAMKAGGDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI 300

Qy 308 KGDTSGDYKKALLLGGEDD 327

Db 301 KGDTSGDYKKALLLGGEDD 320

RESULT 11

AA92930

ID AA92930 standard; Protein; 600 AA.

XX AC AA92930;

XX DT 25-OCT-2000 (first entry)

XX DE Annexin V/urokinase fusion protein.

XX KW Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;

XX KW urokinase; insect cell; fibrinolysis.

XX OS Unidentified.

XX PN CNI247195-A.

XX PD 15-MAR-2000.

XX PF 12-MAR-1999; 99CN-0113524.

XX PR 12-MAR-1999; 99CN-0113524.

XX PA (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.

XX PI Wu X, Sun J, Yang G;

XX DR WPI; 2000-413098/36.

XX DR N-PSDB; AAA11241.

XX PT New thrombolytic fusion protein for targetting thrombus - comprises

XX PT fusion of Annexin V and urokinase

XX PS Claim 2; Page 2-4; 20pp; Chinese.

XX CC Annexin V, which has high affinity for active thrombocytes, is used

XX CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion

XX CC protein. The protein (this sequence) is the result of expression of a

XX CC fusion gene comprising the Annexin V gene and a low-molecular urokinase

XX CC gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed

XX CC in insect cell strain Tn-5B1-4, has high affinity for active thrombocytes

XX CC and has the fibrinolytic activity of urokinase.

XX SQ Sequence 600 AA;

Query Match 96.8%; Score 1587; DB 21; Length 600;

Best Local Similarity 99.4%; Pred. No. 1.4e-137;

Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MAQVLRGTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROETSAAPKTL 67

Db 281 MAQVLRGTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROETSAAPKTL 340

Qy 68 FGRDLLDLKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127

Db 341 FGRDLLDLKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 400

Qy 128 ELRAIKQVYEEYGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODAQLF 187

Db 401 ELRAIKQVYEEYGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODAQLF 460

Qy 188 QAGELKNGTDEEKPTITFGTRSVSHLRKRVFDKYMTISGFQIEETIDRETSGNLEQLLAV 247

Db 461 QAGELKNGTDEEKPTITFGTRSVSHLRKRVFDKYMTISGFQIEETIDRETSGNLEQLLAV 520

Qy 248 VKSTRSIPAYLAETLYYAMKAGGDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI 307

Db 521 VKSTRSIPAYLAETLYYAMKAGGDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI 580

Qy 308 KGDTSGDYKKALLLGGEDD 327

Db 581 KGDTSGDYKKALLLGGEDD 600

RESULT 12

AA92317

ID AA92317 standard; protein; 320 AA.

XX AC AA92317;

XX DT 25-MAR-2003 (updated)

XX DT 13-NOV-1990 (first entry)

XX DE PAP-I isolated from biological fluid, used as anticoagulant.

XX DE PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;

XX KW phospholipase A2; disseminated intravascular coagulation;

XX KW deep vein thrombosis.

XX OS Homo sapiens.

XX PN WO8805659-A.

XX PD 11-AUG-1988.

XX PF 05-FEB-1988; 88WO-US00340.

PR 06-FEB-1987; 87US-0011782.
 PR 05-JUN-1987; 87US-0059355.
 XX (ZYMO) ZYMOGENETICS INC.
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Fujikawa K, Irani MH, Carter BLA;
 XX WPI; 1988-235049/33.
 DR DR N-PSDB; AAN82107.
 XX
 PT Human proteins having anticoagulant and antiinflammatory activity -
 PT isolated from biological fluid by anion-exchange chromatographoc media.
 XX
 XX Disclosure; Page ?; ?pp; English.
 XX
 CC The protein does not contain a leader peptide sequence,
 CC indicating that PAP-I is probably not constitutively secreted.
 CC The Met residue is removed at in a post-translational event and the
 CC newly formed NH2-terminal Ala residue is blocked by acetylation.
 CC It binds to phospholipid and inhibits phospholipase A2.
 CC The protein can substitute heparin or other anticoagulants in
 CC the treatment of disseminated intravascular coagulation, deep vein
 CC thrombosis, or other disorders. It also has antiinflammatory
 CC properties.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 320 AA;
 Query Match 96.8%; Score 1586; DB 9; Length 320;
 Best Local Similarity 99.4%; Pred. No. 6.9e-138;
 Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 MAQVLGRTVTDFFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEISAAPKTL 67
 DB 1 MAQVLGRTVTDFFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEISAAPKTL 60
 QY 68 FGRLDLDLSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRLDLDLSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYQYORMLVLLQANRPDAGIDEAQVQDAQALF 187
 DB 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYQYORMLVLLQANRPDAGIDEAQVQDAQALF 180
 QY 188 QAGELKAGTDEEKFTITFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKAGTDEEKFTITFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRSTPAVLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 307
 DB 241 VKSIRSTPAVLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
 QY 308 KGTSGDYKKALLLLSGEDD 327
 DB 301 KGTSGDYKKALLLLCGEDD 320
 RESULT 13
 AAR26276
 ID AAR26276 standard; protein; 319 AA.
 XX
 AC AAR26276;
 XX
 DT 10-MAR-2003 (updated)
 DT 04-FEB-1993 (first entry)
 XX
 XX CPB-I.
 XX CPB-I; stabilisation; frozen; molten; processed; activity.
 KW Homo sapiens.
 OS
 XX
 XX

PN JP04198195-A.
 XX 17-JUL-1992.
 XX 28-NOV-1990; 90JP-0328286.
 XX 28-NOV-1990; 90JP-0328286.
 XX (KAGA) KAGAKU OYOBI KESSEI RYOHO.
 PA (KOWA) KOWA CO LTD..
 XX WPI; 1992-288937/35.
 XX Stabilisation of CPB-I for drug compsn. - by adding basic
 PT aminoacid selected from lysine, arginine and/or ornithine
 XX
 XX Disclosure; Page 2; 4pp; Japanese.
 XX
 CC The sequence given is the amino acid sequence of CPB-I. CPB-I was
 CC used within a method which involved adding basic amino acids to it
 CC which resulted in its stabilisation. This lead to the production of
 CC CPB-I which keeps its activity when it is frozen, molten or has been
 CC processed by several procedures.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 319 AA;
 Query Match 96.7%; Score 1585; DB 13; Length 319;
 Best Local Similarity 99.7%; Pred. No. 8.5e-138;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 AQVLGRTVTDFFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEISAAPKTLF 68
 DB 1 AQVLGRTVTDFFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQRQEISAAPKTLF 60
 QY 69 GRDLDDLDLSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 128
 DB 61 GRDLDDLDLSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 129 LRAIKQVYEEYEGSSLEDDVVGDTSGYQYORMLVLLQANRPDAGIDEAQVQDAQALFQ 188
 DB 121 LRAIKQVYEEYEGSSLEDDVVGDTSGYQYORMLVLLQANRPDAGIDEAQVQDAQALFQ 180
 QY 189 AGELKAGTDEEKFTITFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLAVV 248
 DB 181 AGELKAGTDEEKFTITFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLAVV 240
 QY 249 KSTRSTPAVLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMIK 308
 DB 241 KSTRSTPAVLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMIK 300
 QY 309 GDTSGDYKKALLLLSGEDD 327
 DB 301 GDTSGDYKKALLLLCGEDD 319
 RESULT 14
 AAR41021
 ID AAR41021 standard; protein; 319 AA.
 XX
 AC AAR41021;
 XX
 DT 29-MAR-1994 (first entry)
 DT
 DE Calphobindin I (CPB-I).
 XX Calphobindin I; CPB-I; Protein kinase C; PKC; Inhibition; tumour.
 KW Homo sapiens.
 OS
 XX
 PN JP05213769-A.
 XX 24-AUG-1993.

XX 04-FEB-1992; 92JP-0019032.
 XX 04-FEB-1992; 92JP-0019032.
 XX (KOWA) KOWA CO LTD.
 XX (KAGA-) 2H KAGAKU OYOBI KESSEN RYOHO KENKYUSHO.
 XX WPI; 1993-299558/38.
 XX Protein kinase C inhibitor effective against malignant tumours -
 PT contg. (opt. recombinant) calphobindin I
 XX Claim 1; Page 2-3; 6pp; Japanese.
 XX Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)
 CC inhibits protein kinase C (PKC) and is useful in the treatment of
 CC malignant tumours caused by abnormal activation of PKC. CPB-I is
 CC extracted from human or animal organs and may be applied
 CC intravenously, orally, intramuscularly, percutaneously or rectally.
 XX Sequence 319 AA;
 SQ

Query Match 96.7%; Score 1585; DB 14; Length 319;
 Best Local Similarity 99.7%; Pred. No. 8.5e-138;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AQLVGRVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 68
 DB 1 AQLVGRVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 60
 QY 69 GRLLDDLKSELTKGFEKLIVALKMPSRLDYAYELKHALKGAGTNEKVLTEIIASRTPEE 128
 DB 61 GRLLDDLKSELTKGFEKLIVALKMPSRLDYAYELKHALKGAGTNEKVLTEIIASRTPEE 120
 QY 129 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALFQ 180
 QY 189 AGELKMGTDDEKFTITFGTRSVSHLRKVFQKYMVTISGFQIEETIDRETSGNLEQLLAVV 248
 DB 181 AGELKMGTDDEKFTITFGTRSVSHLRKVFQKYMVTISGFQIEETIDRETSGNLEQLLAVV 240
 QY 249 KSIRSIPIYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKRKNFATSLYSMIK 308
 DB 241 KSIRSIPIYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKRKNFATSLYSMIK 300
 QY 309 GDTSGDYKKALLLSGEDD 327
 DB 301 GDTSGDYKKALLLSGEDD 319

RESULT 15

ABG32550
 ID ABG32550 standard; protein; 319 AA.

XX AC ABG32550;

XX 29-NOV-2002 (first entry)

XX Human CPB-1 protein.

XX Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
 XX calcium/phospholipid binding protein; polyhydric alcohol.

XX Homo sapiens.

XX W0200267977-A1.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-JP01563.

XX

PR 26-FEB-2001; 2001JP-0050297.

XX (KOWA) KOWA CO LTD.
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX Naruse H, Sano M, Shinoda Y, Inagi T;

XX WPI; 2002-674988/72.

XX Eye drops for treating e.g. corneal diseases, contain CPB-I and
 PT polyhydric alcohol with specific carbonyl value, without unpleasant
 PT irritation upon dropping but with satisfactory long-term storability -

XX Disclosure; Page 13-14; 16pp; Japanese.

XX The invention relates to eye drops contain CPB-I (anexin V) and a
 CC polyhydric alcohol having a carbonyl value of not more than
 CC 5micro Mol./g. The eye drops are for treating e.g. corneal diseases.
 CC Such eye drops are without unpleasant irritation upon dropping but with
 CC satisfactory long-term storage stability. The present sequence is
 CC the human CPB-I (calcium/phospholipid binding) protein.

XX Sequence 319 AA;

Query Match 96.7%; Score 1585; DB 23; Length 319;
 Best Local Similarity 99.7%; Pred. No. 8.5e-138;

Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AQLVGRVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 68

DB 1 AQLVGRVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 60

QY 69 GRLLDDLKSELTKGFEKLIVALKMPSRLDYAYELKHALKGAGTNEKVLTEIIASRTPEE 128

DB 61 GRLLDDLKSELTKGFEKLIVALKMPSRLDYAYELKHALKGAGTNEKVLTEIIASRTPEE 120

QY 129 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALFQ 188

DB 121 LRAIKQVYEEYSSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALFQ 180

QY 189 AGELKMGTDDEKFTITFGTRSVSHLRKVFQKYMVTISGFQIEETIDRETSGNLEQLLAVV 248

DB 181 AGELKMGTDDEKFTITFGTRSVSHLRKVFQKYMVTISGFQIEETIDRETSGNLEQLLAVV 240

QY 249 KSIRSIPIYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKRKNFATSLYSMIK 308

DB 241 KSIRSIPIYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKRKNFATSLYSMIK 300

QY 309 GDTSGDYKKALLLSGEDD 327

DB 301 GDTSGDYKKALLLSGEDD 319

Search completed: August 22, 2003, 21:33:06

Job time : 39 secs

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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:30:17 ; Search time 15 Seconds
(without alignments)
2096.477 Million cell updates/sec

Title: US-09-970-969-4

Perfect score: 1639

Sequence: 1 MAGCGGHMAQVLRGTVDFF.....KGDTSQYKALLILSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues.

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	DB	ID	Description
1	1590	97.0	320	1	AQHUP		annexin V [validat
2	1536.5	93.7	320	1	S27214		annexin V - bovine
3	1455.5	88.8	319	1	LURT5		annexin V - rat
4	1279	78.0	321	1	LUCH5		annexin V - chick
5	932	56.9	673	1	AQHUP68		annexin VI [valida
6	932	56.9	673	1	S01786		annexin VI - mouse
7	923	56.3	321	1	A42077		annexin IV - human
8	921	56.2	318	1	LUPG4		annexin IV - pig
9	921	56.2	673	1	S52844		annexin VI - rat
10	914	55.8	319	1	LUBO4		annexin IV - bovin
11	896.5	54.7	671	2	JC2029		annexin - chicken
12	865	52.8	503	1	LUBO11		annexin XI form A
13	865	52.8	505	1	S23447		annexin XI form B
14	863	52.7	503	1	LURB11		annexin XI - rabbi
15	855	52.2	505	2	A53152		annexin XI - human
16	831.5	50.7	327	1	LHU8		annexin VIII - hum
17	802.5	49.0	323	1	LHU3		annexin III - huma
18	779	47.5	488	1	LHU7		annexin VII, long
19	775	47.3	324	1	LURT3		annexin III - rat
20	773	47.2	463	2	S29170		annexin VII - mous
21	718	43.8	316	1	LUFF12		annexin XII - Hydr
22	711	43.4	512	2	S70644		annexin VII - Afri
23	709	43.3	676	2	S41022		hypothetical prote
24	698.5	42.6	339	1	LHU36		annexin II - human
25	694.5	42.4	339	1	LUBO36		annexin II - bovin
26	693.5	42.3	339	2	S33700		annexin II - rat
27	691.5	42.2	339	1	LUMS36		annexin II - mouse
28	682.5	41.6	341	2	S55277		annexin II - rat
29	682	41.6	296	1	LUFF9		annexin IX - fruit

ALIGNMENTS

RESULT 1

AQHUP

annexin V [validated] - human

N:Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; place

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000

C:Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S06646;

R:Peppinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Brownin

J. Biol. Chem. 263, 10799-10811, 1988

A:Title: Five distinct calcium and phospholipid binding proteins share homology with

A:Reference number: A32659; MUID:88273202; PMID:2968983

A:Accession: D29250

A:Molecule type: mRNA

A:Residues: 1-320 <PE>

A:Cross-references: GB:M1731; MID:9186969; PIDN:AAA36166.1; PID:g307116

R:Grundmann, U.; Abel, K.J.; Bohn, H.; Loebmann, H.; Lottspeich, F.; Kuepper, H.

Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988

A:Title: Characterization of cDNA encoding human placental anticoagulant protein (pP4

A:Reference number: A30206; MUID:88234495; PMID:2967495

A:Accession: A30206

A:Molecule type: mRNA

A:Residues: 1-320 <GR>

A:Cross-references: GB:M19384; MID:918614; PIDN:AA59545.1; PID:g189615

R:Kaplan, R.; Jaye, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.

J. Biol. Chem. 263, 8037-8043, 1988

A:Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phosphol

A:Reference number: A28076; MUID:88228020; PMID:2967291

A:Accession: A28076

A:Molecule type: mRNA

A:Residues: 1-320 <KAP>

R:Maurer-Fogy, I.; Reutelingersperger, C.P.M.; Pieters, J.; Bodo, G.; Stratowa, C.; Hau

Eur. J. Biochem. 174, 585-592, 1988

A:Title: Cloning and expression of cDNA for human vascular anticoagulant, a Ca-depend

A:Reference number: S01016; MUID:88271329; PMID:2455636

A:Accession: S01016

A:Molecule type: mRNA

A:Residues: 1-320 <MAU>

A:Cross-references: EMBL:X12454; NID:g37636; PIDN:CAA30985.1; PID:g37637

A:Note: part of this sequence was confirmed by protein sequencing

R:Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.

Biochemistry 26, 8087-8092, 1987

A:Title: Primary structure of human placental anticoagulant protein.

A:Reference number: A29417; MUID:88163463; PMID:2964863

A:Accession: A29417

A:Molecule type: mRNA

A:Residues: 1-320 <FUN>

A:Cross-references: EMBL:M18366; NID:gl79131; PIDN:AAA35570.1; PID:gl79132

R:Uwasaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saino, Y.; Araki, K.; Mizoguchi, T.;

J. Biochem. 102, 1261-1273, 1987

A:Title: Structure and expression of cDNA for an inhibitor of blood coagulation isola

A:Reference number: A41514; MUID:88139278; PMID:2963810
 A:Accession: A41514
 A:Molecule type: mRNA
 A:Residues: 1-320 <TAA>
 A:Cross-references: GB:D00172; NID:g219480; PIDN:BAA00122.1; PID:g219481
 A:Note: Part of this sequence was confirmed by protein sequencing
 R:Schlaepfer, D.B.; Mehlmann, T.; Burgess, W.H.; Haigler, H.T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987
 A:Title: Structural and functional characterization of endonexin II, a calcium- and phospholipid-binding site
 A:Reference number: A28038; MUID:87317598; PMID:2957692
 A:Accession: A28038
 A:Molecule type: protein
 A:Residues: 86-131,'W',260-272,274-297,300-315,'X',317-320 <SCH>
 R:Ahm, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
 J. Biol. Chem. 263, 18657-18663, 1988
 A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2 isoforms
 A:Reference number: A92696; MUID:89066652; PMID:2974032
 A:Accession: C31953
 A:Molecule type: protein
 A:Residues: 85-93 <AHN>
 R:Rothhut, B.; Comer, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; Coudane, J.
 Biochem. J. 263, 929-935, 1989
 A:Title: A 32 kDa lipocortin from human mononuclear cells appears to be identical with lipocortin IV
 A:Reference number: S06646; MUID:90088443; PMID:2532007
 A:Accession: S06646
 A:Molecule type: protein
 A:Residues: 7-25;27-42;51-74,'X',76-151,181-198;202-207;209-226;228-238;246-271,277-282;
 R:Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Faques, E.P.
 FEBS Lett. 275, 15-21, 1990
 A:Title: The calcium binding sites in human annexin V by crystal structure analysis at 2.0 angstroms
 A:Reference number: A37250; MUID:91085549; PMID:2148156
 A:Contents: annotation: X-ray crystallography, 2.0 angstroms
 A:Note: three calcium ions are strongly bound at sites in the first, second, and fourth
 R:Funkoshi, T.; Heilmann, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
 Biochemistry 26, 5572-5578, 1987
 A:Title: Human placental anticoagulant protein: isolation and characterization
 A:Reference number: A29670; MUID:88050845; PMID:2960376
 A:Accession: A29670
 A:Molecule type: protein
 A:Residues: 29-73;274-297;300-320 <F02>
 R:Fernandez, M.P.; Morgan, R.O.; Fernandez, M.R.; Carcedo, M.T.
 Gene 149, 253-260, 1994
 A:Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C content
 A:Reference number: I37172; MUID:95047484; PMID:7958998
 A:Accession: I37172
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-320 <RES>
 A:Cross-references: EMBL:U01691; NID:g430964; PIDN:AA840047.1; PID:g430966
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipids; binding rather than proteolytic inactivation. It does not affect thrombin-dependent blood coagulation.
 C:Genetics:
 A:Gene: G08:ANX5
 A:Cross-references: GDB:120555; OMIM:131230
 A:Map position: 4q26-q28
 A:Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
 C:Superfamily: annexin I; annexin repeat homology
 F:2-320/Product: annexin V #status experimental <MAT>
 F:18-89/Domain: annexin repeat homology <AX1>
 F:90-161/Domain: annexin repeat homology <AX2>
 F:101-117/Region: endonexin fold #status predicted
 F:173-245/Domain: annexin repeat homology <AX3>
 F:185-201/Region: endonexin fold #status predicted
 F:249-320/Domain: annexin repeat homology <AX4>
 F:260-276/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:23/Binding site: phosphate (Thr) (covalent) #status predicted
 F:28,30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experimental

F:33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental
 F:73,78/Binding site: calcium, low affinity (Leu, Glu) #status experimental
 F:100,102,104,144/Binding site: calcium, high affinity (Leu, Gly, Asp) #status experimental
 F:259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status experimental

Query Match 97.0%; Score 1590; DB 1; Length 320;
 Best Local Similarity 99.7%; Pred. No. 4.2e-95;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	8	MAQVLRGTVTFDFGDFERADAETLRKAMKGLGTDDEESILTLTSSRSNAQREISAAFKTL	67
DB	1	MAQVLRGTVTFDFGDFERADAETLRKAMKGLGTDDEESILTLTSSRSNAQREISAAFKTL	60
QY	68	FGRLDLDLKLSELTGTFKELIVALKPSRLYDAYELKHALKAGTNEKVLTEIIASRTPE	127
DB	61	FGRLDLDLKLSELTGTFKELIVALKPSRLYDAYELKHALKAGTNEKVLTEIIASRTPE	120
QY	128	ELRAIKQVYEEYSSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVQDAQALF	187
DB	121	ELRAIKQVYEEYSSLEDDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVQDAQALF	180
QY	188	QAGELKNGTDEERFIIFGTRSVSHLRKVPDKVTWTISGFOIETIDRETSNGNLEQLLAV	247
DB	181	QAGELKNGTDEERFIIFGTRSVSHLRKVPDKVTWTISGFOIETIDRETSNGNLEQLLAV	240
QY	248	VKSIRSIPIAYLAETLYYANKGAGTDHDTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI	307
DB	241	VKSIRSIPIAYLAETLYYANKGAGTDHDTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI	300
QY	308	KGDTSGDYRKALLLGGEDD 327	
DB	301	KGDTSGDYRKALLLGGEDD 320	

RESULT 2

S27214
 N:Annexin V - bovine
 N:Alternate names: CaBP33; CaBP37
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
 C:Accession: S27214; S27215
 R:Leamonch, M.P.; Howells, S.A.; Harris, A.C.M.; Ames, B.; Patel, Y.; Giambanco, I.; Biochim. Biophys. Acta 1160, 76-83, 1992
 A:Title: Novel isoforms of CaBP 33/37 (Annexin V) from mammalian brain: structural analysis
 A:Reference number: S27214; MUID:93041974; PMID:1420335
 A:Accession: S27214
 A:Molecule type: protein
 A:Residues: 1-320 <LEA>
 A:Accession: S27215
 A:Molecule type: protein
 A:Residues: 1-35,'T',37-124,'E',126-320 <LE2>
 A:Note: It is uncertain whether the sequence differences are due to allelic variation or to a different protein.
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipids; binding rather than proteolytic inactivation. It does not affect thrombin-dependent blood coagulation.
 C:Genetics:
 A:Gene: G08:ANX5
 A:Cross-references: GDB:120555; OMIM:131230
 A:Map position: 4q26-q28
 A:Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
 C:Superfamily: annexin I; annexin repeat homology
 F:2-320/Product: annexin V #status experimental <MAT>
 F:18-89/Domain: annexin repeat homology <AX1>
 F:90-161/Domain: annexin repeat homology <AX2>
 F:101-117/Region: endonexin fold #status predicted
 F:173-245/Domain: annexin repeat homology <AX3>
 F:185-201/Region: endonexin fold #status predicted
 F:249-320/Domain: annexin repeat homology <AX4>
 F:260-276/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:23/Binding site: phosphate (Thr) (covalent) #status predicted
 F:28,30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experimental

Query Match 93.7%; Score 1536.5; DB 1; Length 320; Mismatches 5; Indels 1; Gaps 1;
Best Local Similarity 96.6%; Pred. No. 1.1e-91;
Matches 309; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 9 AQLRGTVDFPGFDRADAETLRKAMKGLGTDDEESILLLTSRSNAQROEISAARFTLF 68
DB 1 AQLRGTVDFPGFDRADAETLRKAMKGLGTDDEESILLLTSRSNAQROEISAARFTLF 60
QY 69 GRDLLDLKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
DB 61 GRDLLDLKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120
QY 129 LRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLVLOANRDPDAGIDEAQVEQDAQALFQ 188
DB 121 LRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLVLOANRDPDARIDEAQVEQDAQALFQ 180
QY 189 AGEKKGWTDDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAVV 248
DB 181 AGEKKGWTDDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAVV 240
QY 249 KSIRSPAYLAETLYYAMKAGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSNIK 308
DB 241 KSIRSPAYLAETLYYAMKAGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSNIK 300
QY 309 GDTSGDYKKALLLL-SGEDD 327
DB 301 GDTSGDYKKALLLLCGGEDD 320
RESULT 3
LURTS
N;Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; placenta
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: C29250; S66680
R;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning,
J. Biol. Chem. 263, 10799-10811, 1988
A;Title: Five distinct calcium and phospholipid binding proteins share homology with lip
A;Reference number: A92659; MUID:88273202; PMID:2968993
A;Accession: C29250
A;Molecule type: mRNA
A;Residues: 1-319 <PEP>
A;Cross-references: GB:M21730; NID:g205138; PIDN:AAA41512.1; PID:g205139
R;Imai, Y.; Kohsaka, S.
Eur. J. Biochem. 232, 327-334, 1995
A;Title: Structure of rat annexin V gene and molecular diversity of its transcripts.
A;Reference number: S66680; MUID:96035863; PMID:7356178
A;Accession: S66680
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-319 <IMA>
A;Cross-references: EMBL:D42136
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
derstood.
C;Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula
olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende
C;Genetics:
A;Introns: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/3; 299/3
C;Superfamily: annexin I; annexin repeat homology
F;2-319/Product: annexin V #status predicted <MAT>
F;16-87/Domain: annexin repeat homology <AX1>
F;78-159/Domain: annexin repeat homology <AX2>
F;99-115/Region: endonexin fold #status predicted <AX2>
F;171-243/Domain: annexin repeat homology <AX3>
F;183-199/Region: endonexin fold #status predicted <AX3>
F;247-318/Domain: annexin repeat homology <AX4>
F;258-274/Region: endonexin fold #status predicted
F;26,28,30,70/Binding site: calcium, high affinity (Met, Gly, Glu) #status predicted
F;31,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status predicted

F;71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F;98,100,102,142/Binding site: calcium, high affinity (Leu, Gly, Asp)
F;257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Glu, Asp)
Query Match 88.8%; Score 1455.5; DB 1; Length 319;
Best Local Similarity 91.8%; Pred. No. 1.8e-86;
Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
QY 12 LRGTVTDFPGFDRADAETLRKAMKGLGTDDEESILLLTSRSNAQROEISAARFTLFGRD 71
DB 3 LRGTVTDFPGFDRADAETLRKAMKGLGTDDEESILLLTSRSNAQROEISAARFTLFGRD 62
QY 72 LLDLSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELA 131
DB 63 LVNDKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELA 122
QY 132 IKQVYEEYSSLEDDVVGDTSGYQRMVLLVLOANRDPDAGIDEAQVEQDAQALFOAGE 191
DB 123 IKQVYEEYSSLEDDVVGDTSGYQRMVLLVLOANRDPDAGIDEAQVEQDAQALFOAGE 182
QY 192 LKNGTDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAVVKS 251
DB 183 LKNGTDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAVVKS 242
QY 252 RSIPAYLAETLYYAMKAGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSNIK 311
DB 243 RSIPAYLAETLYYAMKAGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSNIK 302
QY 312 SGDYKKALLLL-SGEDD 327
DB 303 SGDYKKALLLLCGGEDD 319
RESULT 4
LURTS
N;Alternate names: annexin CII; endonexin II; lipocortin V; placental anticoagulant
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000
C;Accession: A35381; A28623; B40404; S32523; S08771
R;Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaffie, M.; Deutzmann, R.;
J. Biol. Chem. 265, 8344, 1990
A;Reference number: A35381; MUID:90243721; PMID:2159478
A;Contents: erratum
A;Accession: A35381
A;Molecule type: mRNA
A;Residues: 1-321 <FER>
A;Cross-references: GB:M30971; GB:J03194; NID:g211138; PIDN:AAA48591.1; PID:g211139
R;Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaffie, M.; Deutzmann, R.;
J. Biol. Chem. 263, 5921-5925, 1988
A;Title: The structure of an anchorin CII, a collagen binding protein isolated from cho
A;Reference number: A28623; MUID:88166917; PMID:2833522
A;Accession: A28623
A;Molecule type: mRNA
A;Residues: 1-118; LKCRILNFRNMQYEANLGRNKTIGRRHQAIIFRCQWSSCCRQIEF'.163-167, 'E', 169-32
A;Cross-references: GB:M30971; GB:J03194; NID:g211138
R;Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.
J. Biol. Chem. 266, 10678-10685, 1991
A;Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective parti
A;Reference number: A40404; MUID:91244852; PMID:2037607
A;Accession: B40404
A;Molecule type: protein
A;Residues: 188-199 <GEN>
A;Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched mic
R;Boustead, C.M.; Brown, R.; Walker, J.H.
Biochem. J. 291, 601-608, 1993
A;Title: Isolation, characterization and localization of annexin V from chicken liver
A;Reference number: S32523; MUID:93249384; PMID:8484740
A;Accession: S32523
A;Status: preliminary
A;Molecule type: protein
A;Residues: 6-20;85, 'X', 87-88, 'X', 90-93, 'X', 95-96, 'XX', 99-100, 'X', 102-103, 'XX', 106-10
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

derstood.

C;Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation by binding to phospholipids. It binds to membrane-associated phospholipids and inhibits platelet aggregation and thrombin-induced lipid-binding rather than proteolytic inactivation. It does not affect thrombin-dependent activation of factor X or prothrombin to thrombin.
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding; collagen binding; duplication; endonexin fold; membrane-associated protein; phospholipid binding; phospholipase A2; phospholipase C; phospholipase D; phospholipase E; phospholipase F; 2-321/Product: annexin V #status predicted <M>

F;18-89/Domain: annexin repeat homology <AX1>
F;29-45/Region: endonexin fold #status predicted
F;90-161/Domain: annexin repeat homology <AX2>
F;101-117/Region: endonexin fold #status predicted

```

F;182-217/Region: endonexin fold status predicted
F;173-245/Domain: annexin repeat homology <AX3>
F;185-201/Region: endonexin fold #status predicted

```

F; 249-320/Domain: annexin repeat homology <AX4>
F; 260-276/Region: endonexin fold #status predicted

F;28,30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) #status predicted
F;33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F;72,72/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted

F/F ₀ , %	Binding site: calcium, low affinity ^a (Leu, Glu)	#status predicted
F:100, 102, 104, 144/Binding site: calcium, high affinity ^a (Ile, Gly, Gly, Glu) <td>calcium, high affinity</td> <td>#status predicted</td>	calcium, high affinity	#status predicted
F:359, 261, 263, 303/Binding site: calcium, high affinity ^a (Met, Gly, Gly, Asp) <td>calcium, high affinity</td> <td>#status predicted</td>	calcium, high affinity	#status predicted
F:100, 102, 104, 144/Binding site: calcium, low affinity ^a (Leu, Glu) <td>calcium, low affinity</td> <td>#status predicted</td>	calcium, low affinity	#status predicted

```

r, r235, r201, r203, r303, r305, r307, r309, r311, r313, r315, r317, r319, r321, r323, r325, r327, r329, r331, r333, r335, r337, r339, r341, r343, r345, r347, r349, r351, r353, r355, r357, r359, r361, r363, r365, r367, r369, r371, r373, r375, r377, r379, r381, r383, r385, r387, r389, r391, r393, r395, r397, r399, r401, r403, r405, r407, r409, r411, r413, r415, r417, r419, r421, r423, r425, r427, r429, r431, r433, r435, r437, r439, r441, r443, r445, r447, r449, r451, r453, r455, r457, r459, r461, r463, r465, r467, r469, r471, r473, r475, r477, r479, r481, r483, r485, r487, r489, r491, r493, r495, r497, r499, r501, r503, r505, r507, r509, r511, r513, r515, r517, r519, r521, r523, r525, r527, r529, r531, r533, r535, r537, r539, r541, r543, r545, r547, r549, r551, r553, r555, r557, r559, r561, r563, r565, r567, r569, r571, r573, r575, r577, r579, r581, r583, r585, r587, r589, r591, r593, r595, r597, r599, r601, r603, r605, r607, r609, r611, r613, r615, r617, r619, r621, r623, r625, r627, r629, r631, r633, r635, r637, r639, r641, r643, r645, r647, r649, r651, r653, r655, r657, r659, r661, r663, r665, r667, r669, r671, r673, r675, r677, r679, r681, r683, r685, r687, r689, r691, r693, r695, r697, r699, r701, r703, r705, r707, r709, r711, r713, r715, r717, r719, r721, r723, r725, r727, r729, r731, r733, r735, r737, r739, r741, r743, r745, r747, r749, r751, r753, r755, r757, r759, r761, r763, r765, r767, r769, r771, r773, r775, r777, r779, r781, r783, r785, r787, r789, r791, r793, r795, r797, r799, r801, r803, r805, r807, r809, r811, r813, r815, r817, r819, r821, r823, r825, r827, r829, r831, r833, r835, r837, r839, r841, r843, r845, r847, r849, r851, r853, r855, r857, r859, r861, r863, r865, r867, r869, r871, r873, r875, r877, r879, r881, r883, r885, r887, r889, r891, r893, r895, r897, r899, r901, r903, r905, r907, r909, r911, r913, r915, r917, r919, r921, r923, r925, r927, r929, r931, r933, r935, r937, r939, r941, r943, r945, r947, r949, r951, r953, r955, r957, r959, r961, r963, r965, r967, r969, r971, r973, r975, r977, r979, r981, r983, r985, r987, r989, r991, r993, r995, r997, r999, r1001, r1003, r1005, r1007, r1009, r1011, r1013, r1015, r1017, r1019, r1021, r1023, r1025, r1027, r1029, r1031, r1033, r1035, r1037, r1039, r1041, r1043, r1045, r1047, r1049, r1051, r1053, r1055, r1057, r1059, r1061, r1063, r1065, r1067, r1069, r1071, r1073, r1075, r1077, r1079, r1081, r1083, r1085, r1087, r1089, r1091, r1093, r1095, r1097, r1099, r1101, r1103, r1105, r1107, r1109, r1111, r1113, r1115, r1117, r1119, r1121, r1123, r1125, r1127, r1129, r1131, r1133, r1135, r1137, r1139, r1141, r1143, r1145, r1147, r1149, r1151, r1153, r1155, r1157, r1159, r1161, r1163, r1165, r1167, r1169, r1171, r1173, r1175, r1177, r1179, r1181, r1183, r1185, r1187, r1189, r1191, r1193, r1195, r1197, r1199, r1201, r1203, r1205, r1207, r1209, r1211, r1213, r1215, r1217, r1219, r1221, r1223, r1225, r1227, r1229, r1231, r1233, r1235, r1237, r1239, r1241, r1243, r1245, r1247, r1249, r1251, r1253, r1255, r1257, r1259, r1261, r1263, r1265, r1267, r1269, r1271, r1273, r1275, r1277, r1279, r1281, r1283, r1285, r1287, r1289, r1291, r1293, r1295, r1297, r1299, r1301, r1303, r1305, r1307, r1309, r1311, r1313, r1315, r1317, r1319, r1321, r1323, r1325, r1327, r1329, r1331, r1333, r1335, r1337, r1339, r1341, r1343, r1345, r1347, r1349, r1351, r1353, r1355, r1357, r1359, r1361, r1363, r1365, r1367, r1369, r1371, r1373, r1375, r1377, r1379, r1381, r1383, r1385, r1387, r1389, r1391, r1393, r1395, r1397, r1399, r1401, r1403, r1405, r1407, r1409, r1411, r1413, r1415, r1417, r1419, r1421, r1423, r1425, r1427, r1429, r1431, r1433, r1435, r1437, r1439, r1441, r1443, r1445, r1447, r1449, r1451, r1453, r1455, r1457, r1459, r1461, r1463, r1465, r1467, r1469, r1471, r1473, r1475, r1477, r1479, r1481, r1483, r1485, r1487, r1489, r1491, r1493, r1495, r1497, r1499, r1501, r1503, r1505, r1507, r1509, r1511, r1513, r1515, r1517, r1519, r1521, r1523, r1525, r1527, r1529, r1531, r1533, r1535, r1537, r1539, r1541, r1543, r1545, r1547, r1549, r1551, r1553, r1555, r1557, r1559, r1561, r1563, r1565, r1567, r1569, r1571, r1573, r1575, r1577, r1579, r1581, r1583, r1585, r1587, r1589, r1591, r1593, r1595, r1597, r1599, r1601, r1603, r1605, r1607, r1609, r1611, r1613, r1615, r1617, r1619, r1621, r1623, r1625, r1627, r1629, r1631, r1633, r1635, r1637, r1639, r1641, r1643, r1645, r1647, r1649, r1651, r1653, r1655, r1657, r1659, r1661, r1663, r1665, r1667, r1669, r1671, r1673, r1675, r1677, r1679, r1681, r1683, r1685, r1687, r1689, r1691, r1693, r1695, r1697, r1699, r1701, r1703, r1705, r1707, r1709, r1711, r1713, r1715, r1717, r1719, r1721, r1723, r1725, r1727, r1729, r1731, r1733, r1735, r1737, r1739, r1741, r1743, r1745, r1747, r1749, r1751, r1753, r1755, r1757, r1759, r1761, r1763, r1765, r1767, r1769, r1771, r1773, r1775, r17
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Best Local Similarity 78.1%; Pred. No. 4.1e-75;
Matches 250; Conservative 38; Mismatches 32; Indels 0; Gaps 0;

QY 8 MAQVLRGVTYDFPGFDERADAETLRKAMKGLGTDEESILTILTSRSNAQRQISAAFKTL 67

Db
1 MAKYTRGVTFASFPPDARADAEALRKAMKMGTDDEETILKILTSRNNARQEIASAFKTL 60

68 FGRDLLDDDKSELTKCFEKLIVALKMPSPLYDAYEYELKHALKGAGTNEKVLTEIASRTP 127

db 61 FGRLVDDUKSELGTGKETLVSLMRPARIFDAHALKHAIKGAGTNEKVLTELASRTPA 120

Qy 128 ELRAIKWEEYEGSSLEDDVVGDTSYYQRMWLQANRPDAGIDEAQVEDQALF 187

db EVQNIKQVIMQEYEAULEDKITGETSGHFQRLLVLLQANRDPGRVDEALVEKDAQVLF 180

[illegible]

DB	181	RAGELRWGTDDETFITILZTSVSHLRVRVEDRYMTISGQIETEMIDRETSGOLEKLLIIV	240
QY	248	VKSIRSPAYLAETILYYANKGAGTDGHTLIRVWVSRSSEIDLENIRKEFRKNFATSLYSMI	307

WJ	VASINSFPALEMLIATNRGIDUHLKRVMSSELDUTNKKERANNEAISLSMI	307
246		
Db	VKCISVPAYFASTLYYSMGAGTDDDTLIRVWVSREIDLDIRHEFRKNFAKSQYMI	300
241		

QY	308 KQDTSQDYKKALLLSGEDD 327	300
----	-----------------------------	-----

db 301 QKOTSGDYRKALLILCGDD 320

DEPT. 5

RESULT 5
AQUH68
annexin VI [va] [idated] - human

annexin VI [various] - human
 C;Alternate names: calcium-binding protein, 68K; calelectrin; calphobindin II
 C;Species: Homo sapiens (man)

C:Accession: JU0032; S00263; S19519; A31079; JX0091; B34459; B31953; A33507

R.; Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; Sh. J. Biochem. 106, 43-49, 1989

A; title: Structure and expression of cDNA for calphobindin II, a human placental coagulation factor XIII inhibitor. *Submitted*.
A; Reference number: J00032; MUID:89380132; PMID:2528541

A; Accession: J00032
A; Molecule type: mRNA
A; Residues: 1-673 (76A)

A;cross-references: ENEL:D00510; NID:g219550; PIDN:BA00400.1; PID:g219551
A;residues: 1-6/3 <IWA>
R;Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crumpton, M.J.

OWENS, R.D.; TOLLEY, N.F.; TOWSS, S.E.; WATERFIELD, M.D.; CRUMPTON, M.J.; EMBO J. 7, 21-27, 1988

A,Reference number: S00263; PMID:88196081; PMID:3258820
 A,Accession: S00263

A: Molecule type: mRNA
A: Residues: 1-618, 'D', 620-673 <CR1>

A:Cross-references: EMBL:Y00097; NID:g35217; PIDN:CA68286.1; PID:g35218
A:Accession: S18519

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Db 11 RGSIHDPGPDNODAEALYAMKGFSGDKEALDITTSRSNQRQVCSYKSLYKGL 70
Qy 73 LDDLKSLTCKFKFKLIVALKMPSRLYDAYELKHALKAGTNEKVLTEIIASRTPEELRAI 132
Db 71 IADLKVELTCKFKFERLIVGLMRPPAYCDAREIKDAISIGTDEKCLIEILASRTNEOHQL 130
Qy 133 KQVTEEGSSLEDVVDGTSYGYQRMVLVLLQANRPDAGIDEAQVQDQALFQAGEL 192
Db 131 VAAYKDAYERDLEADIIIGDTSGHFQKMLVLLQGTREDDVSDLVQDDVQDLYEAGEL 190
Qy 193 KWTDEKFKTITGTRSVSHLRKVDFKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252
Db 191 KWTDEAQFTYILGNRSKQHLRVDFEYLTGTGPIEASIRGELSGDFEKLMLAVVKCIR 250
Qy 253 SIPAYLAETLYAMKAGGTDDHTLIRVMVSRSETDLFNIRKFRKNFATSLYSMIKGDTS 312
Db 251 STPEYFAERLFKAMKGLGTGTRDNTLIRVMVSRSELMDLDIRFRTKYEKSLYSMIKNDTS 310
Qy 313 GDYKALLLLSGDD 327
Db 311 GEYKALLLLSGDD 325

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RESULT 6

S01786

annexin VI - mouse

N:Alternate names: calcium-binding protein p68; calelectrin; calphobindin II
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S01786
 R:Moss, S.E.; Crompton, M.R.; Crumpton, M.J.
 Eur. J. Biochem. 177, 21-27, 1988
 A:Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family.
 A:Reference number: S01786; MUID:89030687; PMID:2972541
 A:Accession: S01786
 A:Molecule type: mRNA
 A:Residues: 1-673 <MOS>
 A:Cross-references: EMBL:X13460; NID:g53580; PIDN:CAA31808.1; PID:g53581
 A:Note: the authors translated the codon GCC for residue 329 as Gly
 C:Comment: This abundant cytosolic protein binds to the inner surface of the cell membrane
 C:Superfamily: annexin VI; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phospholipid binding; annexin VI #status predicted <AX1>
 F:2-673/Product: annexin VI #status predicted <AX1>
 F:23-94/Domain: endonexin repeat homology <AX1>
 F:34-50/Region: endonexin fold #status predicted
 F:95-166/Domain: annexin repeat homology <AX2>
 F:106-122/Region: endonexin fold #status predicted
 F:178-250/Domain: annexin repeat homology <AX3>
 F:190-206/Region: endonexin fold #status predicted
 F:254-325/Domain: annexin repeat homology <AX4>
 F:366-437/Domain: annexin repeat homology <AX5>
 F:377-393/Region: endonexin fold #status predicted
 F:438-509/Domain: annexin repeat homology <AX6>
 F:449-465/Region: endonexin fold #status predicted
 F:527-598/Domain: annexin repeat homology <AX7>
 F:538-554/Region: endonexin fold #status predicted
 F:602-673/Domain: annexin repeat homology <AX8>
 F:613-629/Region: endonexin fold #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

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Query Match 56.98; Score 932; DB 1; Length 673;
Best Local Similarity 59.08; Pred. No. 2,1e-52;
Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

Qy 13 RGVTDPPGPDERADATLIRKAMKGLGTDEESILTLTTSRNRQRBISAFKTLFGDL 72
Db 11 RGSVHDPPEPDANODAEALYAMKGFSGDKEALDITTSRSNQRQVCSYKSLYKGL 70
Qy 73 LDDLKSLTCKFKFKLIVALKMPSRLYDAYELKHALKAGTNEKVLTEIIASRTPEELRAI 132
Db 71 IEDLKVELTCKFKFERLIVGLMRPPAYCDAREIKDAISIGTDEKCLIEILASRTNEOHQL 130

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Qy 133 KQVTEEGSSLEDVVDGTSYGYQRMVLVLLQANRPDAGIDEAQVQDQALFQAGEL 192
Db 131 VAAYKDAYERDLEADIIIGDTSGHFQKMLVLLQGTREDDVSDLVQDDVQDLYEAGEL 190
Qy 193 KWTDEKFKTITGTRSVSHLRKVDFKYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252
Db 191 KWTDEAQFTYILGNRSKQHLRVDFEYLTGTGPIEASIRGELSGDFEKLMLAVVKCIR 250
Qy 253 SIPAYLAETLYAMKAGGTDDHTLIRVMVSRSETDLFNIRKFRKNFATSLYSMIKGDTS 312
Db 251 STPEYFAERLFKAMKGLGTGTRDNTLIRVMVSRSELMDLDIRFRTKYEKSLYSMIKNDTS 310
Qy 313 GDYKALLLLSGDD 327
Db 311 GEYKALLLLSGDD 325

RESULT 7
A42077
annexin IV - human
N:Alternate names: endonexin I; placental anticoagulant protein II; PP4-X protein
C:Species: Homo sapiens (man)
C>Date: 30-Jan-1993 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: A42077; S07434; A31953; A31046
R:Tait, J.F.; Smith, C.; Frankenberg, D.A.; Miao, C.H.; Adler, D.A.; Distche, C.M.
Genomics 12, 313-318, 1992
A:Title: Chromosomal mapping of the human annexin IV (ANX4) gene.
A:Reference number: A42077; MUID:92155721; PMID:1346776
A:Accession: A42077
A:Molecule type: mRNA
A:Residues: 1-321 <TAI>
A:Cross-references: GB:M82809; NID:g178698; PIDN:AAA51740.1; PID:g178699
A:Accession: B42077
A:Molecule type: DNA
A:Residues: 87-129 <TA2>
R:Grundmann, U.; Amann, E.; Abel, K.J.; Kuepper, H.A.
Behring Inst. Mitt. 82, 59-67, 1988
A:Title: Isolation and expression of cDNA coding for a new member of the phospholipase
A:Reference number: S07434; MUID:88309022; PMID:2970257
A:Accession: S07434
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97, 'Q', '99-321 <GRU>
A:Cross-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
R:Abn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C
J. Biol. Chem. 263, 18657-18663, 1988
A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
inhibitor.
A:Reference number: A92696; MUID:89066652; PMID:2974032
A:Accession: A31953
A:Molecule type: protein
A:Residues: 29-58,101-126;282-310 <AHNS>
R:Tait, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E
Biochemistry 27, 6268-6276, 1988
A:Title: Placental anticoagulant proteins: Isolation and comparative characterization
A:Reference number: A90534; MUID:89118212; PMID:2975506
A:Accession: A31046
A:Molecule type: protein
A:Residues: 4-17;30-74;102-146;283-321 <TA3>
C:Genetics:
A:Gene: GDB:ANX4
A:Cross-references: GDB:I31395; OMIM:106491
A:Map position: 2p13-2p13
A:Introns: 102/3
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; glyco
P:2-321/Product: annexin IV #status predicted <MAT>
F:19-90/Domain: annexin repeat homology <AX1>
F:30-46/Region: endonexin fold #status predicted
F:91-162/Domain: annexin repeat homology <AX2>
F:102-118/Region: endonexin fold #status predicted
F:174-246/Domain: annexin repeat homology <AX3>

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F:186-202/Region: endonexin fold #status predicted
F:250-321/Domain: annexin repeat homology <AX4>
F:261-277/Region: endonexin fold #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F:9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:247/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.3%; Score 923; DB 1; Length 321;
Best Local Similarity 58.3%; Pred. No. 3.1e-52;
Matches 183; Conservative 53; Mismatches 78; Indels 0; Gaps 0;

QY 14 GTVTDFPQDERADATLTKAMKGLTDEESILTLTSRNSAQRQISAAFKTLFGDRL 73
DB 8 GTVKAASGNAEDADATLTKAMKGLTDEDAIISVLAYRNTAQOIRTAQYKSTIGRDLL 67
QY 74 DDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
DB 68 DDLKSELGNEFEQIVGMWPTVLYDVQELRRANKGAGTDEGCLIEILASRTPEEIRRI 127
QY 134 QVYEEYGSLEDDVVDGTSYGYQYRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGELK 193
DB 128 QTYQOYGRSLEDIRSDTSFMFQYVLSVLSAGGRDEGNYLDDALVRQDAQDLYEAGEKK 187
QY 194 WGTDEKFTITFTRSVSHLRKVFQKYMVTISGQIEETIDRTSGNLEQLLLAVVKSIRS 253
DB 188 WGTDEKFTITFTRSVSHLRKVFQKYMVTISGQIEETIDRTSGNLEQLLLAVVKSIRS 247
QY 254 IPAYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKEPKNEATSLYSIKMGDTSG 313
DB 248 KSAYFAERLYKSMKGLGTDNTLIRVWVSRAEIDMDIRANFRKLYGKSLYSIKMGDTSG 307
QY 314 DYKALLLSGGDD 327
DB 308 DYRKVLLVLCGGDD 321

RESULT 8
LUP64
annexin IV - pig
N:Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocortin IV; protein I
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24-Nov-1999
C:Accession: A27107
R:Reber, K.; Johnson, N.; Plessmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; Vandekerckh
EMBO J. 6, 1599-1604, 1987
A:Title: The amino acid sequence of protein II and its phosphorylation site for protein
A:Reference number: A27107; MUID:87275850; PMID:2956093
A:Accession: A27107
A:Molecule type: protein
A:Residues: 1-318 <WEB>
A:Experimental source: intestinal epithelium
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
derstood.
C:Superfamily: annexin I; annexin repeat homology
F:Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprotein
F:16-87/Domain: annexin repeat homology <AX1>
F:27-43/Region: endonexin fold #status predicted
F:88-159/Domain: annexin repeat homology <AX2>
F:99-115/Region: endonexin fold #status predicted
F:171-243/Domain: annexin repeat homology <AX3>
F:183-199/Region: endonexin fold #status predicted
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: endonexin fold #status predicted
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F:5/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:124,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.2%; Score 921; DB 1; Length 318;
Best Local Similarity 58.6%; Pred. No. 4.1e-52;
Matches 184; Conservative 51; Mismatches 79; Indels 0; Gaps 0;

QY 14 GTVTDFPQDERADATLTKAMKGLTDEESILTLTSRNSAQRQISAAFKTLFGDRL 73
DB 8 GTVKAASGNAEDADATLTKAMKGLTDEDAIISVLAYRNTAQOIRTAQYKSTIGRDLL 67

DB 5 GTVKAASGNAEDADATLTKAMKGLTDEDAIISVLAYRNTAQOIRTAQYKSTIGRDLL 64
QY 74 DDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
DB 65 DDLKSELGNEFEQIVGMWPTVLYDVQELRRANKGAGTDEGCLIEILASRTPEEIRRI 124
QY 134 QVYEEYGSLEDDVVDGTSYGYQYRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGELK 193
DB 125 QTYQOYGRSLEDIRSDTSFMFQYVLSVLSAGGRDEGNYLDDALVRQDAQDLYEAGEKK 184
QY 194 WGTDEKFTITFTRSVSHLRKVFQKYMVTISGQIEETIDRTSGNLEQLLLAVVKSIRS 253
DB 185 WGTDEKFTITFTRSVSHLRKVFQKYMVTISGQIEETIDRTSGNLEQLLLAVVKSIRS 244
QY 254 IPAYLAETLYAMKAGTDDHTLIRVWVSSEIDLFNIRKEPKNEATSLYSIKMGDTSG 313
DB 245 KSAYFAERLYKSMKGLGTDNTLIRVWVSRAEIDMDIRANFRKLYGKSLYSIKMGDTSG 304
QY 314 DYKALLLSGGDD 327
DB 305 DYRKVLLVLCGGDD 318

RESULT 9
S52844
annexin VI - rat
N:Alternate names: calcium-binding protein 65/67
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S65683; S52844
R:Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W.
Eur. J. Biochem. 230, 741-751, 1995
A:Title: cDNA cloning and tissue-specific regulation of expression of rat calcium-bin
A:Reference number: S65683; MUID:95331313; PMID:7607247
A:Accession: S65683
A:Molecule type: mRNA
A:Residues: 1-673 <FAN>
A:Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181
A:Experimental source: liver
C:Superfamily: annexin VI; annexin repeat homology
F:Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associate
F:2-673/Product: annexin VI #status predicted <NA>
F:23-94/Domain: annexin repeat homology <AX1>
F:34-50/Region: endonexin fold #status predicted
F:95-166/Domain: annexin repeat homology <AX2>
F:106-122/Region: endonexin fold #status predicted
F:178-250/Domain: annexin repeat homology <AX3>
F:190-206/Region: endonexin fold #status predicted
F:254-325/Domain: annexin repeat homology <AX4>
F:265-281/Region: endonexin fold #status predicted
F:366-437/Domain: annexin repeat homology <AX5>
F:377-393/Region: endonexin fold #status predicted
F:438-509/Domain: annexin repeat homology <AX6>
F:449-465/Region: endonexin fold #status predicted
F:527-598/Domain: annexin repeat homology <AX7>
F:538-554/Region: endonexin fold #status predicted
F:602-673/Domain: annexin repeat homology <AX8>
F:613-629/Region: endonexin fold #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 56.2%; Score 921; DB 1; Length 673;
Best Local Similarity 58.7%; Pred. No. 1e-51;
Matches 195; Conservative 48; Mismatches 82; Indels 0; Gaps 0;

QY 13 RGTVDTPQDERADATLTKAMKGLTDEESILTLTSRNSAQRQISAAFKTLFGDRL 72
DB 11 RGSVHDFADFDANQDAEALYTKMGFGSKESILELTSRNSKQROEIQCSYKSLYKGLD 70
QY 73 LDDLKSELGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
DB 71 IADLYELGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 130
QY 133 KQVYEEYGSLEDDVVDGTSYGYQYRMVLVLLQANRPDAGIDEAQVEQDAQALFOAGEL 192

Db 306 DTSGEYKALLKLCGGDD 324

RESULT 12
LUB011
annexin XI form A - bovine
N;Alternate names: calyculin-associated protein peptide, CAP-50
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C:Accession: A42113; A42909; B42909; C42909; D42909
R:Towle, C.A.; Treadwell, B.V., 1992
J. Biol. Chem. 267, 5416-5423, 1992
A:Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis, and characterization of the protein.
A:Reference number: A42113; MUID:92184796; PMID:1372001
A:Accession: A42113
A:Molecule type: mRNA
A:Residues: 1-503 <TOW>
A:Cross-references: GB:M82802; NID:gl62673; PIDN:AAA30379.1; PID:gl62674
A:Note: the authors did not translate the codon GAC for residue 503
R:Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka, J. Biol. Chem. 267, 13498-13504, 1992
A:Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblast
A:Reference number: A42909; MUID:92317074; PMID:1618851
A:Accession: A42909
A:Molecule type: protein
A:Residues: 213-223, 'X', 225-226; 319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-339; 441-450, 'X',
A:Experimental source: lung
A:Note: sequence modified after extraction from NCBI backbone
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid
derstood.
C:Genetics:
A:Introns: 19/1; 56/2
A:Note: the list of introns is incomplete
C:Superfamily: annexin VII; annexin repeat homology
C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid binding
F:201-272/Domain: annexin repeat homology <AX1>
F:212-228/Region: endonexin fold #status predicted
F:273-344/Domain: annexin repeat homology <AX2>
F:284-300/Region: endonexin fold #status predicted
F:356-428/Domain: annexin repeat homology <AX3>
F:368-384/Region: endonexin fold #status predicted
F:432-503/Domain: annexin repeat homology <AX4>
F:443-459/Region: endonexin fold #status predicted
F:59,111/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 52.8%; Score 865; DB 1: Length 503;
Best Local Similarity 54.9%; Pred. No. 2.9e-48;
Matches 173; Conservative 58; Mismatches 84; Indels 0; Gaps 0;

QY 13 RGTVTDFPGFDERADAEIIRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGRLD 72
Db 189 RGTITDASGDFPLRDAEVLKAMKGFCTDEQATIDCLGSRNKRQOILLSPKATYKGLD 248
QY 73 LDDKSELGCKPEKLIVALKMPSRLYDAYELKHALGAGTNEKVLTEILASRTPEELRAI 132
Db 249 IKDLKSELGNFEKTLALMKTPVDFDAYEIKAGAGTDEACLEILASRSNEHIREL 308
QY 133 KOVYEEYGSLLDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAOVEQDAQALFOAGEL 192
Db 309 NRKYTEFKTLEEARSDTSQGHFORLLISLSCGNRDESTNVDMTLVQRDVQELYAAGEN 368
QY 193 KWTDEEKFITIFGTRSVSHLRKVFQKMTISGFQIEETIDRTSGNLEQLLAVVKSIR 252
Db 369 RLGTDESKFNAILCSRAHLVAVFNEYQRTGRTDEKISCREMSGDLEQGLAVVVKCLK 428
QY 253 SIPAYLAETLYAMKAGAGTDDHTLIRVMVSRSDIDLFNIRKPKFNATSLYSNMGKDTIS 312
Db 429 NTPAFFAERLNKAMRGAGTKDRTLIRIMVSRSDIDLDIRAEYKRLYKSLYHDITGDTIS 488
QY 313 GYKALLLSGDD 327
Db 489 GYRKILLKICGND 503

RESULT 13

S23447

annexin XI form B - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 22-Nov-1993 #sequence_revision 10-Feb-1995 #text_change 22-Jun-1999

C:Accession: S23447; S36136

R:Towle, C.

submitted to the EMBL Data Library, February 1992

A:Reference number: S23447

A:Accession: S23447

A:Molecule type: mRNA

A:Residues: 1-505 <TOW>

A:Cross-references: EMBL:Z11742; NID:g77; PIDN:CAA77801.1; PID:g78

R:Towle, C.A.; Weissbach, L.; Treadwell, B.V.

Biochim. Biophys. Acta 1131, 223-226, 1992

A:Title: Alternatively spliced annexin XI transcripts encode proteins that differ near

A:Reference number: S36136; MUID:92305067; PMID:1535225

A:Accession: S36136

A:Molecule type: mRNA

A:Residues: 1-77 <TOW>

A:Cross-references: EMBL:Z11742

C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid
derstood.
C:Genetics:
A:Introns: 19/1; 58/2
A:Note: the list of introns is incomplete
C:Superfamily: annexin VII; annexin repeat homology
C:Keywords: alternative splicing; calcium binding; duplication; endonexin fold; glyco

F:203-274/Domain: annexin repeat homology <AX1>

F:214-230/Region: endonexin fold #status predicted

F:275-346/Domain: annexin repeat homology <AX2>

F:286-302/Region: endonexin fold #status predicted

F:358-430/Domain: annexin repeat homology <AX3>

F:370-386/Region: endonexin fold #status predicted

F:434-505/Domain: annexin repeat homology <AX4>

F:445-461/Region: endonexin fold #status predicted

F:61,113/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 52.8%; Score 865; DB 1: Length 505;
Best Local Similarity 54.9%; Pred. No. 2.9e-48;
Matches 173; Conservative 58; Mismatches 84; Indels 0; Gaps 0;

QY 13 RGTVTDFPGFDERADAEIIRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGRLD 72

Db 191 RGTITDASGDFPLRDAEVLKAMKGFCTDEQATIDCLGSRNKRQOILLSPKATYKGLD 250

QY 73 LDDKSELGCKPEKLIVALKMPSRLYDAYELKHALGAGTNEKVLTEILASRTPEELRAI 132

Db 251 IKDLKSELGNFEKTLALMKTPVDFDAYEIKAGAGTDEACLEILASRSNEHIREL 310

QY 133 KOVYEEYGSLLDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAOVEQDAQALFOAGEL 192

Db 311 NRKYTEFKTLEEARSDTSQGHFORLLISLSCGNRDESTNVDMTLVQRDVQELYAAGEN 370

QY 193 KWTDEEKFITIFGTRSVSHLRKVFQKMTISGFQIEETIDRTSGNLEQLLAVVKSIR 252

Db 371 RLGTDESKFNAILCSRAHLVAVFNEYQRTGRTDEKISCREMSGDLEQGLAVVVKCLK 430

QY 253 SIPAYLAETLYAMKAGAGTDDHTLIRVMVSRSDIDLFNIRKPKFNATSLYSNMGKDTIS 312

Db 431 NTPAFFAERLNKAMRGAGTKDRTLIRIMVSRSDIDLDIRAEYKRLYKSLYHDITGDTIS 490

QY 313 GYKALLLSGDD 327

Db 491 GYRKILLKICGND 505

RESULT 14

LUB011

annexin XI - rabbit

N;Alternate names: calyculin-associated annexin protein CAP-50

C:Species: Oryctolagus cuniculus (domestic rabbit)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:28:42 ; Search time 8.66667 Seconds
(without alignments)
1774.354 Million cell updates/sec

Title: US-09-970-969-4

Perfect score: 1639

Sequence: 1 MAGCGGHNAQVLGTVTFPP.....KGDTSQDYKKALLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1585	96.7	319	1 ANX5_HUMAN	P08758 homo sapien
2	1536.5	93.7	320	1 ANX5_BOVIN	P81287 bos taurus
3	1479.5	90.3	319	1 ANX5_MOUSE	P48036 mus musculus
4	1455.5	88.8	318	1 ANX5_RAT	P14668 rattus norv
5	1279	78.0	321	1 ANX5_CHICK	P17153 gallus gall
6	1086	66.3	323	1 ANX5_CYNPY	P70075 cynops pyrr
7	932	56.9	672	1 ANX6_HUMAN	P08133 homo sapien
8	932	56.9	672	1 ANX6_MOUSE	P14824 mus musculus
9	923	56.3	318	1 ANX4_HUMAN	P09525 homo sapien
10	921	56.2	318	1 ANX4_PIG	P08132 sus scrofa
11	921	56.2	672	1 ANX6_RAT	P48037 rattus norv
12	916	55.9	318	1 ANX4_MOUSE	P97429 mus musculus
13	914	55.8	318	1 ANX4_BOVIN	P13214 bos taurus
14	901	55.0	318	1 ANX4_CANFA	P50994 canis famil
15	896.5	54.7	671	1 ANX6_CHICK	P51901 gallus gall
16	891	54.4	318	1 ANX4_RAT	P55260 rattus norv
17	865	52.8	503	1 ANXB_BOVIN	P72124 bos taurus
18	863	52.7	503	1 ANXB_RABIT	P33477 oryctolagus
19	855	52.2	505	1 ANXB_HUMAN	P50995 homo sapien
20	847	51.7	503	1 ANXB_MOUSE	P97384 mus musculus
21	841.5	51.3	327	1 ANXB_MOUSE	O35640 mus musculus
22	831.5	50.7	327	1 ANX8_HUMAN	P13928 homo sapien
23	802.5	49.0	323	1 ANX3_HUMAN	P12429 homo sapien
24	799	48.7	323	1 ANX3_MOUSE	O35639 mus musculus
25	779	47.5	466	1 ANX7_HUMAN	P20073 homo sapien
26	777	47.4	463	1 ANX7_MOUSE	Q07076 mus musculus
27	771	47.0	324	1 ANX3_RAT	P14669 rattus norv
28	761	46.4	618	1 ANX6_BOVIN	P79134 bos taurus
29	718	43.8	316	1 ANXC_HYDAT	P26256 hydra atten
30	711	43.4	512	1 ANX7_XENLA	Q92125 xenopus lae
31	701	42.8	324	1 ANX9_DROME	P22464 drosophila
32	698.5	42.6	338	1 ANX2_HUMAN	P07355 homo sapien
33	694.5	42.4	338	1 ANX2_BOVIN	P04272 bos taurus

RESULT 1

ID	ANX5_HUMAN	STANDARD;	PRT;	319 AA.
AC	P08758;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchorin CII).			
DE	ANCHORIN CII.			
GN	ANXA5 OR ANX5 OR ENX2 OR PP4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88234495; PubMed=2967495;			
RA	Grundmann U., Abel K.-J., Bohn H., Loebermann H., Lottspeich F., Kuepper H.;			
RT	"Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=88271329; PubMed=2455636;			
RA	Maurer-Fogy I., Reutellingsperger C.P.M., Pieters J., Bodo G., Stratowa C., Hauptmann R.;			
RT	"Cloning and expression of cDNA for human vascular anticoagulant, a Ca2+-dependent phospholipid-binding protein.";			
RL	Eur. J. Biochem. 174:585-592(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88273202; PubMed=2968983;			
RA	Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;			
RT	"Five distinct calcium and phospholipid binding proteins share homology with lipocortin I.";			
RL	J. Biol. Chem. 263:10799-10811(1988).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88163463; PubMed=2964863;			
RA	Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;			
RT	"Primary structure of human placental anticoagulant protein.";			
RL	Biochemistry 26:8087-8092(1987).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND SEQUENCE.			
RX	MEDLINE=88139278; PubMed=2963810;			
RA	Iwasaki A., Suda M., Nakao H., Nagoya T., Saino Y., Arai K., Mizoguchi T., Sato F., Yoshizaki H., Hirata M., Miyata T., Shidara Y., Murata M., Maki M.;			
RT	"Structure and expression of cDNA for an inhibitor of blood coagulation isolated from human placenta: a new lipocortin-like protein.";			

Q07936 rattus norv
P07356 mus musculu
P22465 drosophila
P27216 homo sapien
P27006 xenopus lae
Q29471 canis famil
P17785 gallus gall
P24801 xenopus lae
P15652 oryctolagus
P14087 cavia cutle
P04083 homo sapien
P46193 bos taurus

ALIGNMENTS

RL J. Biochem. 102:1261-1273(1987).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88228020; PubMed=2967291;
 RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
 RT "Cloning and expression of cDNA for human endonexin II, a Ca²⁺ and
 RL phospholipid binding protein.";
 RN J. Biol. Chem. 263:8037-8043(1988).
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RA MEDLINE=95047484; PubMed=7958998;
 RT Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
 RL "The gene encoding human annexin V has a TATA-less promoter with a
 RT high G+C content.";
 RN Gene 149:253-260(1994).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94307733; PubMed=8034319;
 RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
 RT Tait J.F.;
 RL "Organization of the human annexin V (ANX5) gene.";
 RN Genomics 20:463-467(1994).
 RP SEQUENCE FROM N.A.
 RX TISSUE=Muscle, Ovary, and Skin;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Halek J.A., Guarnatone P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Mueny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP PARTIAL SEQUENCE.
 RX MEDLINE=90088443; PubMed=2532007;
 RA Rothhut R., Comera C., Cortial S., Haumont P.-Y., Diep Le K.H.,
 RA Cavadore J.-C., Conrad J., Russo-Marie F., Lederer P.;
 RT "A 32 kDa lipocortin from human mononuclear cells appears to be
 RL identical with the placental inhibitor of blood coagulation.";
 RN Biochem. J. 263:929-935(1989).
 RP SEQUENCE OF 85-130; 258-296 AND 299-319.
 RX MEDLINE=87317598; PubMed=2957692;
 RA Schlaepfer D.D., Mehman T., Burgess W.H., Haigler H.T.;
 RT "Structural and functional characterization of endonexin II, a
 RL calcium- and phospholipid-binding protein.";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
 RP SEQUENCE OF 84-92.
 RX MEDLINE=89066652; PubMed=2974032;
 RA Ahn N.G., Teller D.C., Blenkowski M.J., McMullen B.A., Lipkin E.W.,
 RA de Haen C.;
 RT "Sedimentation equilibrium analysis of five lipocortin-related
 RT phospholipase A2 inhibitors from human placenta. Evidence against a
 RT mechanistically relevant association between enzyme and inhibitor.";
 RN J. Biol. Chem. 263:18657-18663(1988).
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=91065314; PubMed=2147412;
 RA Huber R., Roemisch J., Paques E.-P.;
 RT "The crystal and molecular structure of human annexin V, an
 RT anticoagulant protein that binds to calcium and membranes.";
 RN EMBO J. 9:3867-3874(1990).
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=91085549; PubMed=2148156;
 RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
 RT "The calcium binding sites in human annexin V by crystal structure
 RT analysis at 2.0-A resolution. Implications for membrane binding and
 RL calcium channel activity.";
 RN FEBS Lett. 275:15-21(1990).
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=92177413; PubMed=1311770;
 RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
 RA Luecke H., Roemisch J., Paques E.-P.;
 RT "Crystal and molecular structure of human annexin V after refinement.
 RT Implications for structure, membrane binding and ion channel
 RL formation of the annexin family of proteins.";
 RN J. Mol. Biol. 223:683-704(1992).
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=98062349; PubMed=9398511;
 RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
 RT "Crystal structure of annexin V with its ligand K-201 as a calcium
 RL channel activity inhibitor.";
 RN J. Mol. Biol. 274:16-20(1997).
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=98118533; PubMed=9435213;
 RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
 RT "Residue-specific bioincorporation of non-natural, biologically
 RT active amino acids into proteins as possible drug carriers: structure
 RT and stability of the per-thiaproline mutant of annexin V.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
 CC -I- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 CC -I- SUBUNIT: MONOMER. BINDS ATR (BY SIMILARITY).
 CC -I- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -I- SIMILARITY: Contains 4 annexin repeats.
 CC -I- CAUTION: THIS PROTEIN HAS BEEN INDEPENDENTLY SEQUENCED BY AT LEAST
 CC SEVEN GROUPS UNDER DIFFERENT NAMES!
 CC -I- DATABASE: NAME-RED Systems' cytokine source book: Annexin 5;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=185".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X12454; CAA30985.1;
 DR EMBL: M19384; AAB59545.1;
 DR EMBL: M18366; AAB35570.1;
 DR EMBL: M21731; AAB36166.1;
 DR EMBL: D00172; BAA00122.1;
 DR EMBL: J03745; AAB52386.1;
 DR EMBL: U01691; AAB40047.1;
 DR EMBL: U01681; AAB40047.1; JOINED.
 DR EMBL: U01682; AAB40047.1; JOINED.
 DR EMBL: U01683; AAB40047.1; JOINED.
 DR EMBL: U01685; AAB40047.1; JOINED.
 DR EMBL: U01686; AAB40047.1; JOINED.
 DR EMBL: U01687; AAB40047.1; JOINED.
 DR EMBL: U01689; AAB40047.1; JOINED.
 DR EMBL: U01690; AAB40047.1; JOINED.

Query Match 96.7%; Score 1585; DB 1; Length 319;
 Best Local Similarity 99.7%; Pred. No. 3.2e-95;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AQLRGVTPFPFGRADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFKTLF 68
 DB 1 AQLRGVTPFPFGRADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFKTLF 60

QY 69 GROLDDKSELGKFEKFLVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
 DB 61 GROLDDKSELGKFEKFLVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120

QY 129 LRAIKOVYEEYSSLEDDVVGDTSGYYQRMVLLQANRPDPAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKOVYEEYSSLEDDVVGDTSGYYQRMVLLQANRPDPAGIDEAQVEQDAQALFQ 180

QY 189 AGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFOETEIDRTSGNLEQLLAVV 248
 DB 181 AGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFOETEIDRTSGNLEQLLAVV 240

QY 249 KSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFKFNKFNATSLYSMIK 308
 DB 241 KSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFKFNKFNATSLYSMIK 300

QY 309 GDTSGDYKALLLGGEDD 327
 DB 301 GDTSGDYKALLLGGEDD 319

RESULT 2
 ANX5_BOVIN
 ID ANX5_BOVIN STANDARD; PRT; 320 AA.
 AC P81287;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchorin CII).
 GN ANX5 OR ANX5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=33041974; PubMed=1420335;
 RA Learmonth M.P., Howell S.A., Harris A.C.M., Amess B., Patel Y.,
 RA Giambanco I., Bianchi R., Pula G., Ceccarelli P., Donato R.,
 RA Green B.N., Aitken A.;
 RT "Novel isoforms of CBP 33/37 (annexin V) from mammalian brain:
 RT structural and phosphorylation differences that suggest distinct
 RT biological roles.";
 RL Biochim. Biophys. Acta 1160:76-83(1992).
 CC -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 CC -1- SUBUNIT: MONOMER. BINDS ATRX (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 DR PIN; S27214; S27214.
 DR HSSP; P08758; IANW.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Acetylation.
 FT INIT_MET 0 0
 FT REPEAT 23 83 ANNEXIN 1.
 FT REPEAT 95 155 ANNEXIN 2.
 FT REPEAT 179 239 ANNEXIN 3.
 FT REPEAT 254 314 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT VARIANT 36 36 S -> T.
 FT VARIANT 125 125 K -> E.
 SQ SEQUENCE 320 AA; 35942 MW; 50FCEI8E95F19CB0 CRC64;

Query Match 93.7%; Score 1536.5; DB 1; Length 320;
 Best Local Similarity 96.6%; Pred. No. 4.2e-92;
 Matches 309; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 9 AQLRGVTPFPFGRADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFKTLF 68
 DB 1 AQLRGVTPFPFGRADAEATLRKAMKGLGTDEESILTLTTSRNSAQROEISAAFKTLF 60

QY 69 GROLDDKSELGKFEKFLVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 128
 DB 61 GROLDDKSELGKFEKFLVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEE 120

QY 129 LRAIKOVYEEYSSLEDDVVGDTSGYYQRMVLLQANRPDPAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKOVYEEYSSLEDDVVGDTSGYYQRMVLLQANRPDPAGIDEAQVEQDAQALFQ 180

QY 189 AGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFOETEIDRTSGNLEQLLAVV 248
 DB 181 AGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFOETEIDRTSGNLEQLLAVV 240

QY 249 KSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFKFNKFNATSLYSMIK 308
 DB 241 KSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFKFNKFNATSLYSMIK 300

QY 309 GDTSGDYKALLLGGEDD 327.
 DB 301 GDTSGDYKALLLGGEDD 320

RESULT 3
 ANX5_MOUSE
 ID ANX5_MOUSE STANDARD; PRT; 319 AA.
 AC P48036;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchorin CII).
 GN ANX5 OR ANX5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal cavity;
 RX MEDLINE=96422179; PubMed=8824796;
 RA Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
 RT "Mouse annexin V chromosomal localization, cDNA sequence
 RT conservation, and molecular evolution.";
 RL Genomics 31:151-157(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adachi T., Kojima K., Fukuoaka S.-I., Ogawa H., Matsumoto I.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;

RX MEDLINE-99072820; PubMed-9854034;
 RA Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,
 RA Fernandez M.P.;
 RT "Mouse annexin V genomic organization includes an endogenous
 RT retrovirus".
 RL J. Biochem. 337:125-131(1999).
 CC -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 CC -1- SUBUNIT: MONOMER. BINDS ATRX (BY similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL: U29396; AAC52530.1; -;
 DR EMBL: D63423; BAA09728.1; -;
 DR EMBL: AJ230108; CAA13092.1; -;
 DR EMBL: AJ230110; CAA13092.1; JOINED.
 DR EMBL: AJ230111; CAA13092.1; JOINED.
 DR EMBL: AJ230114; CAA13092.1; JOINED.
 DR EMBL: AJ230116; CAA13092.1; JOINED.
 DR EMBL: AJ230118; CAA13092.1; JOINED.
 DR EMBL: AJ230119; CAA13092.1; JOINED.
 DR EMBL: AJ230120; CAA13092.1; JOINED.
 DR EMBL: AJ230121; CAA13092.1; JOINED.
 DR EMBL: AJ230122; CAA13092.1; JOINED.
 DR EMBL: AJ230123; CAA13092.1; JOINED.
 DR EMBL: AJ230124; CAA13092.1; JOINED.
 DR HSSP: P14668; 1A8B.
 DR SWISS-2DPAGE: P48036; MOUSE.
 DR MGD: MGI:106008; Anx5.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Placenta.
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 SQ SEQUENCE 319 AA; 35752 MW; 55055BAF2E1C3687 CRC64;

Query Match 90.3%; Score 1479.5; DB 1; Length 319;
 Best Local Similarity 93.7%; Pred. No. 1.9e-88;
 Matches 296; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 13 RGVTVDFPGFDRADATLRKAMKGLGTDBESILLTSRSNAQOEISAAPKTLFGRLD 72
 DB 4 RGVTVDFPGFDRADAEVLRKAMKGLGTDBESILLTSRSNAQOEISAAPKTLFGRLD 63
 QY 73 LDDLSKELTGKPEKLVAMKPSRLYDAYELKHALKGAGTNGKVLFEIIASRTPELRAI 132
 DB 64 VDDLKSELTGKPEKLVAMKPSRLYDAYELKHALKGAGTNGKVLFEIIASRTPELSAI 123
 QY 133 KQVYEEYSSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVDAQALFQAGEL 192
 DB 124 KQVYEEYGSNLEDDVVGDTSGYYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAGEL 183
 QY 193 KNGTDEEKFTITFCRTSVSHLRKVKFDKMTYISGFOIEETIDRETSGNLEQLLVAVVKSIR 252
 DB 184 KNGTDEEKFTITFCRTSVSHLRKVKFDKMTYISGFOIEETIDRETSGNLEQLLVAVVKSIR 243

QY 253 SIPAYLAETLYYAMKAGAGTDDHTLRVMSRSSEIDLFNIRKFRKFNKFAISLYSMIKGDT 312
 DB 244 SIPAYLAETLYYAMKAGAGTDDHTLRVMSRSSEIDLFNIRKFRKFNKFAISLYSMIKGDT 303
 QY 313 GDYKKALLLL-SGEDD 327
 DB 304 GDYKKALLLLCGEDD 319
 RESULT 4
 ANX5_RAT
 ID ANX5_RAT STANDARD; PRT; 318 AA.
 AC P14668;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88273202; PubMed-2968983;
 RA Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K.,
 RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
 RA Pratt D., Wichter L., Hession C., Frey A.Z., Wallner B.P.;
 RT "Five distinct calcium and phospholipid binding proteins share
 RT homology with lipocortin I".
 RL J. Biol. Chem. 263:10799-10811(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Wistar;
 RC MEDLINE-96035863; PubMed-7556178;
 RA Imai Y., Kohsaka S.;
 RT "Structure of rat annexin V gene and molecular diversity of its
 RT transcripts".
 RL Eur. J. Biochem. 232:327-334(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-93369587; PubMed-8362244;
 RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Rat annexin V crystal structure: Ca(2+)-induced conformational
 RT changes".
 RL Science 261:1321-1324(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC TISSUE-Kidney;
 RX MEDLINE-96069783; PubMed-7583670;
 RA Swairjo M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Ca(2+)-bridging mechanism and phospholipid head group recognition in
 RT the membrane-binding protein annexin V".
 RL Nat. Struct. Biol. 2:968-974(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
 RX MEDLINE-98272673; PubMed-9609693;
 RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swairjo M.A., Balch C.,
 RA Head J.F., Reizinger G., Dedman J.R., Seaton B.A.;
 RT "Mutational and crystallographic analyses of interfacial residues in
 RT annexin V suggest direct interactions with phospholipid membrane
 RT components".
 RL Biochemistry 37:8004-8010(1998).
 RN [6]
 RP INTERACTION WITH DNMT1.
 RC STRAIN-Wistar; TISSUE-Brain;
 RX MEDLINE-96301899; PubMed-8667030;
 RA Ohnawa K., Imai Y., Ito D., Kohsaka S.;
 RT "Molecular cloning and characterization of annexin V-binding proteins

with highly hydrophilic peptide structure.*;
 J. Neurochem. 67:89-97(1996).
 -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 -1- SUBUNIT: MONOMER. Binds ATRX and DNMT1.
 -1- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.
 -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 -1- SIMILARITY: Contains 4 annexin repeats.

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 EMBL; M21730; AAA41512.1; -
 EMBL; D42137; BAA07708.1; -
 EMBL; D42129; BAA07708.1; JOINED.
 EMBL; D42130; BAA07708.1; JOINED.
 EMBL; D63337; BAA07708.1; JOINED.
 EMBL; D42131; BAA07708.1; JOINED.
 EMBL; D42132; BAA07708.1; JOINED.
 EMBL; D42133; BAA07708.1; JOINED.
 EMBL; D42134; BAA07708.1; JOINED.
 EMBL; D42135; BAA07708.1; JOINED.
 EMBL; D42136; BAA07708.1; JOINED.
 EMBL; C29250; LURT5.
 PIR; 2RAN; 30-NOV-94.
 DR PDB; 1A8A; 17-JUN-98.
 DR PDB; 1A8B; 17-JUN-98.
 DR PDB; 1BC0; 13-JAN-99.
 DR PDB; 1BC1; 13-JAN-99.
 DR PDB; 1BC3; 13-JAN-99.
 DR PDB; 1BCW; 13-JAN-99.
 DR PDB; 1BCY; 13-JAN-99.
 DR PDB; 1G5N; 13-MAR-02.
 DR PDB; 1N41; 04-FEB-03.
 DR PDB; 1N42; 04-FEB-03.
 DR PDB; 1N44; 04-FEB-03.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 FW Placenta; Acetylation; 3D-structure.
 FT INIT_MET 0
 FT REPEAT 20 80 ANNEXIN 1.
 FT REPEAT 92 152 ANNEXIN 2.
 FT REPEAT 176 236 ANNEXIN 3.
 FT REPEAT 251 311 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION.
 FT TURN 10 11
 FT HELIX 14 25
 FT TURN 32 39
 FT HELIX 40 41
 FT TURN 44 58
 FT HELIX 62 69
 FT HELIX 72 82
 FT HELIX 85 97
 FT HELIX 104 113
 FT HELIX 116 130
 FT HELIX 134 141
 FT HELIX 144 154
 FT TURN 155 156
 FT TURN 166 179
 FT TURN 180 182

FT HELIX 188 197
 FT HELIX 200 214
 FT HELIX 218 225
 FT HELIX 228 242
 FT HELIX 244 256
 FT HELIX 263 273
 FT TURN 274 277
 FT HELIX 278 289
 FT HELIX 293 300
 FT HELIX 303 313
 SQ SEQUENCE 318 AA; 35613 MW; 1A755A7C11FALICE CRC64;
 Query Match 88.8%; Score 1455.5; DB 1; Length 318;
 Best Local Similarity 91.8%; Pred. No. 6.7e-87;
 Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
 QY 12 LRGIVTDFPFDEERADAEFLRKAMKGLGTDEESILTLTSSNAQRQEIISAAFKTLFGDRD 71
 DB 2 LRGVTDFSGFDGRADAEVLKAMKGLGTDEDSILNLLTARSNAQRQIEEFKTLFGDRD 61
 QY 72 LLDLKSSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 131
 DB 62 LVNDKSELTKGFEKLIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRA 121
 QY 132 IKQVVEEYSGSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQAGE 191
 DB 122 IKQAYEEYSGNSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEDQAALFQAGE 181
 QY 192 LKWTDEEKFTITFGTRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLELLAVYKSI 251
 DB 182 LKWTDEEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLELLAVYKSI 241
 QY 252 RSIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSNIKGD 311
 DB 242 RSIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSNIKGD 301
 QY 312 SGDYKALLLL-SGEDD 327
 DB 302 SGDYKALLLLCGGEDD 318
 RESULT 5
 ANX5_CHICK STANDARD; PRT; 321 AA.
 AC P17153;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-1) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Ancholin CII).
 GN ANXA5 OR ANX5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88186917; PubMed=2833522;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
 RA Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of ancholin CII, a collagen binding protein isolated
 from chondrocyte membrane".
 RL J. Biol. Chem. 263:5921-5925(1988).
 RN [2]
 RP SUGGEST SEQUENCING ERROR.
 RX MEDLINE=90020458; PubMed=2552626;
 RA Moss S.E., Crumpton M.J.;
 RT "Alternative splicing or cloning artefact?";
 RN Trends Biochem. Sci. 14:325-325(1989).
 RN [3]

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5]
SEQUENCE OF 26-55; 98-123 AND 279-307.
MEDLINE=8906652; PubMed=2974032;
Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
de Haen C.;
"Sedimentation equilibrium analysis of five lipocortin-related
phospholipase A2 inhibitors from human placenta. Evidence against a
mechanistically relevant association between enzyme and inhibitor.";
J. Biol. Chem. 263:18657-18663(1988).
[6]
SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
MEDLINE=69118212; PubMed=2975506;
Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
Hendrickson L.E., Fujikawa K.;
"Placental anticoagulant proteins: isolation and comparative
characterization four members of the lipocortin family.";
Biochemistry 27:6268-6276(1988).
[7]
X-RAY CRYSTALLOGRAPHY.
MEDLINE=91073383; PubMed=2254922;
Reemont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;
"Crystallization and preliminary X-ray crystallographic studies of
human placental annexin IV.";
J. Mol. Biol. 216:219-221(1990).
CC -I- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
CC -I- DOMAIN: A pair of annexin repeats may form one binding site for
calcium and phospholipid.
CC -I- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
CC -I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -I- SIMILARITY: Contains 4 annexin repeats.

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or send an email to license@isb-sib.ch).

DR EMBL; M19383; AAC41689.1; ALT_INIT.
DR EMBL; M82809; AAA51740.1; -
DR EMBL; D78152; BAA11227.1; ALT_INIT.
DR EMBL; BC000182; AAH0182.1; ALT_INIT.
DR EMBL; BC011659; AAH11659.1; ALT_INIT.
DR HSP; P13214; IANN
DR SWISS-2DPAGE; P09525; HUMAN.
DR PMMA-2DPAGE; P09525; -
DR Genew; HGNC:542; ANXA4.
DR MIM; 106491; -
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin.4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin. 4.
DR SMART; SM00335; ANX. 4.
DR PROSITE; PS00223; ANNEXIN. 4.
DR Annexin; Calcium/phospholipid-binding; Repeat.
KW INIT_MET 0
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
FT CONFLICT 95 95 R -> Q (IN REF. 1).
SQ SEQUENCE 318 AA; 35751 MW; 16B19E01500350F7 CRC64;

Query Match 56.3%; Score 923; DB 1; Length 318;
Best Local Similarity 58.3%; Pred. No. 1.2e-52;
Matches 183; Conservative 53; Mismatches 78; Indels 0; Gaps 0;

Qy 14 GTVDFPGFDERADAEETLRKAMKGLGDEESIIITLTSRNAQRQETSAFKTLFGDLL 73
III III: ||| ||||| |||||::: ||| ||||| |||: |||:
Db 5 GTKAAQSGFNAMDEAOTLRKAMKGLGDEDAIISVLAVRNTAQRQETRTAKSTIGRDLI 64

CC CA(2+) FROM INTRACELLULAR STORES.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -!- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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 CC -----
 CC EMBL; X86086; CAA60040.1; -
 CC PIR; S65683; S52844.
 CC HSSP; P79134; IAVC.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 8.
 CC PRINTS; PR00196; ANNEXIN.
 CC ProDom; PD000143; Annexin; 8.
 CC SMART; SM00335; ANX; 8.
 CC PROSITE; PS00223; ANNEXIN; 7.
 CC Annexin; Calcium/phospholipid-binding; Repeat.
 CC INIT_MET 0 BY SIMILARITY.
 CC REPEAT 28 88
 CC ANNEXIN 1.
 CC REPEAT 100 160
 CC ANNEXIN 2.
 CC REPEAT 184 244
 CC ANNEXIN 3.
 CC REPEAT 259 319
 CC ANNEXIN 4.
 CC REPEAT 371 431
 CC ANNEXIN 5.
 CC REPEAT 443 503
 CC ANNEXIN 6.
 CC REPEAT 532 592
 CC ANNEXIN 7.
 CC REPEAT 607 667
 CC ANNEXIN 8.
 CC REPEAT 672 732
 CC ANNEXIN 9.
 CC SEQUENCE 672 AA; 75622 MW; BBE798A9CAB1511 CRC64;
 Query Match 56.2%; Score 921; DB 1; Length 672;
 Best Local Similarity 58.7%; Pred. No. 4e-52;
 Matches 185; Conservative 48; Mismatches 82; Indels 0; Gaps 0;
 QY 13 RGVTFDPGDFERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAPKTLFGEDL 72
 DB 10 RGSVHDFADFDANQDAALYAMKGFSGDKRESILTLTSRSNAQROEISAKYSLYKDL 69
 QY 73 LDDLKSELTKRFEKLIIVALKPRLYDAYELKHALKGAGTNEKVLTEIATSRTPPEELRAI 132
 DB 70 IADLKVELTKRFEKLIIVNLRLAYCDKAEIKDAISGIGTDEKCLIELILASRTNEIQHL 129
 QY 133 KQVTEEGYSGSLEDVVDGTSYGYORMLVLLQANRPDAGIDEAQVEQDAQALFQAGEL 192
 DB 130 VAAKDAYERDLESIIIGDTSGHFQKMLVLLQGTRENDVVDVSEDVQDDVQDLYEAGEL 189
 QY 193 KWGDEKFTIFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSGNLEQLLAVVKSIR 252
 DB 190 KWGDEAQFVILGNRSKQHLRVDFEYLTGTGPIEASIRGELSGDFEKLMLAVVKCIR 249
 QY 253 SIPAYLAETIYAMKAGTDHDTLIRVMVSRSEIDLFNIRKFRKFNATSLYMKIGDTS 312
 DB 250 STPEYFAERFLPKAMKGLGTRDNTLIRVMVSRSEIDLFNIRKFRKFNATSLYMKIGDTS 309
 QY 313 GDYKALLLLSGEDD 327
 DB 310 GEYKALLLLCGGDD 324

RESULT 12

ANX4_MOUSE
 ID ANX4_MOUSE STANDARD; PRT; 318 AA.
 AC P97429;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV).

GN ANXA4 OR ANXA4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HeJ;
 RL Sable C.L., Shannon J., Riches D.W.H.;
 RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -!- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U72941; AAB40697.1; -
 CC HSSP; P13214; IANN.
 CC MGD; MGI:88030; Anxa4.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 4.
 CC PRINTS; PR00196; ANNEXIN.
 CC ProDom; PD000143; Annexin; 4.
 CC SMART; SM00335; ANX; 4.
 CC PROSITE; PS00223; ANNEXIN; 4.
 CC Annexin; Calcium/phospholipid-binding; Repeat.
 CC INIT_MET 0 BY SIMILARITY.
 CC REPEAT 22 82
 CC ANNEXIN 1.
 CC REPEAT 94 154
 CC ANNEXIN 2.
 CC REPEAT 178 238
 CC ANNEXIN 3.
 CC REPEAT 253 313
 CC ANNEXIN 4.
 CC SEQUENCE 318 AA; 35858 MW; 53FAC7AD8006BC0D CRC64;
 Query Match 55.9%; Score 916; DB 1; Length 318;
 Best Local Similarity 57.3%; Pred. No. 3.4e-52;
 Matches 180; Conservative 58; Mismatches 76; Indels 0; Gaps 0;
 QY 14 GTVTDFPGDFERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAPKTLFGEDL 73
 DB 5 GTVKAASGFNATEDAQTLRKAMKGLGTDEDAIIGILAVNTAQROEISAYKSTIGRDLI 64
 QY 74 DDLKSELTKRFEKLIIVALKPRLYDAYELKHALKGAGTNEKVLTEIATSRTPPEELRAI 133
 DB 65 EDLKEYSNFEQVILGLMTPTLYDQVELSRAMKAGTDEGCLTEILASRTPEIRIN 124
 QY 134 QVYEEYSGSLEDVVDGTSYGYORMLVLLQANRPDAGIDEAQVEQDAQALFQAGEL 193
 DB 125 QTYQQQVGRSLEEDICSDTSEFMFORVFLVLSAAGDEGNLYDDALMKQDAQELVGEGR 184
 QY 194 WGTDEKFTIFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSGNLEQLLAVVKSIR 253
 DB 185 WGTDEKFTIFGTRSVSHLRKVFQDKYMTISGFQIETIDRETSGNLEQLLAVVKSIR 244
 QY 254 IPAYLAETIYAMKAGTDHDTLIRVMVSRSEIDLFNIRKFRKFNATSLYMKIGDTS 313
 DB 245 KPSYFAERFLYKSMKGLGTRDNTLIRVMVSRSEIDLFNIRKFRKFNATSLYMKIGDTS 304
 QY 314 DYKALLLLSGEDD 327
 DB 305 DYKALLLLCGGDD 318

RESULT 13
 ANX4_BOVIN STANDARD; PRT; 318 AA.
 AC PI3214;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
 DE (PP4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41)
 DE (P33/41).
 GN ANX4 OR ANX4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=89050088; PubMed=2847715;
 RA Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
 RT "Cloning and characterization of a cDNA encoding bovine endonexin
 (chromobindin 4).";
 RL Biochem. Biophys. Res. Commun. 156:660-667(1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96205957; PubMed=8631806;
 RA Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;
 RT "Characterization of carbohydrate-binding protein p33/41: relation
 with annexin IV, molecular basis of the doublet forms (p33 and p41),
 RT and modulation of the carbohydrate binding activity by
 RT phospholipids.";
 RL J. Biol. Chem. 271:7679-7685(1996).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA Sutton R.B., Sprang S.R.;
 RL Submitted (SEP-1995) to the PDB data bank.
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RX MEDLINE=98070213; PubMed=9405281;
 RA Zanotti G., Malpell G., Glibich F., Polli C., Stoppini M., Olivi L.,
 RA Savola A., Berni R.;
 RT "Structure of the trigonal crystal form of bovine annexin IV.";
 RL Biochem. J. 329:101-106(1998).
 CC [-] SUBUNIT: Monomer.
 CC [-] DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC [-] MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC [-] SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC [-] SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; M22248; AAA30507.1; -;
 DR EMBL; X13627; CAA31954.1; -;
 DR EMBL; D78178; BAA11243.1; -;
 DR PIR; A31578; LUBO4
 DR PDB; 1ANN; 29-JAN-96.
 DR PDB; 1AOW; 14-JAN-98.
 DR PDB; 1I4A; 25-APR-01.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR PRODOM; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.

Annexin: Calcium/phospholipid-binding; Repeat; 3D-structure.
 KW INIT_MET 0 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 94 94 L -> V (IN REF. 2).
 FT CONFLICT 210 210 E -> K (IN REF. 2).
 FT HELIX 15 26
 FT HELIX 33 40
 FT TURN 41 42
 FT HELIX 45 59
 FT HELIX 63 70
 FT HELIX 73 83
 FT HELIX 86 98
 FT HELIX 105 114
 FT HELIX 117 131
 FT HELIX 135 142
 FT HELIX 145 155
 FT TURN 156 156
 FT HELIX 167 182
 FT TURN 183 185
 FT HELIX 189 198
 FT HELIX 201 215
 FT HELIX 219 226
 FT HELIX 229 257
 FT HELIX 264 274
 FT TURN 275 278
 FT HELIX 279 290
 FT HELIX 294 301
 FT HELIX 304 314
 SQ SEQUENCE 318 AA; 35757 MW; 86BDBDF349D774FD CRC64;
 Query Match 55.8%; Score 914; DB 1; Length 318;
 Best Local Similarity 58.0%; Pred. No. 4.5e-52;
 Matches 182; Conservative 51; Mismatches 81; Indels 0; Gaps 0;
 QY 14 GTVDPGPFDERADAEETLRKAMKGLGTDEESILTLTSRNAQRQISAAFKTLFGROLL 73
 DB 5 GTVKAASGFNAEDACTLRKAMKGLGTDEDAINVLAYSTAQORQIRIAYKTTIGRDL 64
 QY 74 DLKSELTKFKELIVALKMPSRLYDAYELKHALKAGTNEKVLTVETIIASRTPEELRAK 133
 DB 65 DDLKSELGNFEQVILGMMTPVLYDVQBELRKAMKAGTDEGLIBILASRTPEETIRIN 124
 QY 134 QVTEEEYSGSLEDDVVGDTSGVYVRLVLLQANRPDAGIDEAQVEQDAQALFOAGELK 193
 DB 125 QTYQOYGRSLEDDEIRSDTSFMPQVRLVLSAGGRDESNYLDALMRQDAQDLYAGEKK 184
 QY 194 WGTDEEKFTITFGRSVSHLRKRVFKYMTISGFQIETIDRETSGHLEQLLAVVKSIRS 253
 DB 185 WGTDEVKFTLVLCSSRNHLLHVFDEYKRIAKQKDIQSIKSETSGSFEDALLAIVKMRN 244
 QY 254 IPAYLAETIYAMKAGTODDHTLIRVMVSRSEIDFNIRKFRKNFATSLYSMIKGDTS 313
 DB 245 KSAVFAERLYKSMKGLGTDDTLIRVMVSRSEIDFNIRKFRKNFATSLYSMIKGDTS 304
 QY 314 DYKKAALLLSGEDD 327
 DB 305 DYRKVLLILCGGDD 318
 RESULT 14
 ANX4_CANFA
 ID ANX4_CANFA STANDARD; PRT; 318 AA.
 AC P50994;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule
 DE membrane associated protein) (ZAP36).
 GN ANX4 OR ANX4.
 OS Canis familiaris (Dog).

Search completed: August 22, 2003, 21:33:38
Job time : 9.66667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:29:22 ; Search time 31.6667 seconds
(without alignments)
2664.733 Million cell updates/sec

Title: us-09-970-969-4

Perfect score: 1639

Sequence: 1 MAGCGHMAQVLRGTVDFF.....KGTSGDYKALLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 256052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:**

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1585	96.7	320	4	Q8WV69	Q8WV69 homo sapien
2	1475.5	90.0	319	11	Q99LA1	Q99LA1 mus musculus
3	1390	84.8	302	11	O70371	O70371 rattus norv
4	1042	63.6	317	13	O93445	O93445 oryzias lat
5	932	56.9	476	11	O8CEX0	O8CEX0 mus musculus
6	932	56.9	667	11	O99JX6	O99JX6 mus musculus
7	930	56.7	673	11	O8BS54	O8BS54 mus musculus
8	866	52.8	320	13	O93444	O93444 oryzias lat
9	856	52.2	508	13	O93447	O93447 oryzias lat
10	849	51.8	321	13	O90X16	O90X16 xenopus lae
11	847	51.7	503	11	O921F1	O921F1 mus musculus
12	840.5	51.3	327	11	O8K2N9	O8K2N9 mus musculus
13	836.5	51.0	327	6	Q95L54	Q95L54 bos taurus
14	822.5	50.2	327	6	O97529	O97529 oryctolagus
15	799	48.7	323	11	O8C1X9	O8C1X9 mus musculus
16	773	47.2	463	11	Q922A2	Q922A2 mus musculus

17	770	47.0	463	11	Q8VIN2	Q8VIN2 rattus norv
18	769	46.9	463	11	Q8BP75	Q8BP75 mus musculus
19	752	45.9	324	5	Q9NL61	Q9NL61 bombyx mori
20	752	45.9	324	5	Q8IGJ8	Q8IGJ8 drosophila
21	743.5	45.4	301	11	Q921D0	Q921D0 mus musculus
22	729	44.5	323	5	Q9NL59	Q9NL59 bombyx mori
23	720	43.9	324	5	Q9NG55	Q9NG55 drosophila
24	715	43.6	321	5	O8WPG9	O8WPG9 bombyx mori
25	714	43.6	486	5	O8WPH0	O8WPH0 bombyx mori
26	709	43.3	497	5	O27512	O27512 caenorhabdi
27	705	43.0	323	5	Q9NG66	Q9NG66 bombyx mori
28	701	42.8	323	5	Q9NL60	Q9NL60 bombyx mori
29	701	42.8	324	5	Q969D3	Q969D3 drosophila
30	694.5	42.4	339	4	O8TBV2	O8TBV2 homo sapien
31	686.5	41.9	339	11	Q9C3I7	Q9C3I7 mus musculus
32	685	41.8	315	5	Q95V57	Q95V57 artemia san
33	680	41.5	317	11	Q99JG3	Q99JG3 mus musculus
34	673	41.1	357	6	Q8MJ85	Q8MJ85 oryctolagus
35	660	40.3	511	5	Q9VXG3	Q9VXG3 drosophila
36	657	40.1	337	13	O93446	O93446 oryzias lat
37	655	40.0	322	5	Q9VXG4	Q9VXG4 drosophila
38	646.5	39.4	316	13	Q98SH7	Q98SH7 brachydanio
39	644.5	39.3	345	6	O8HZM6	O8HZM6 equus cabal
40	629	38.4	314	13	Q92128	Q92128 xenopus lae
41	582	35.5	322	5	Q27884	Q27884 caenorhabdi
42	573.5	35.0	415	11	O8CCV9	O8CCV9 mus musculus
43	572	34.9	209	11	O8BSL2	O8BSL2 mus musculus
44	540	32.9	317	5	Q27473	Q27473 caenorhabdi
45	528	32.2	365	5	Q9XY89	Q9XY89 schistosoma

ALIGNMENTS

RESULT 1

Q8WV69 ID Q8WV69 PRELIMINARY; PRT; 320 AA.
AC Q8WV69;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Annexin A5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skin;
RA Strausberg R.;
RL Submitted (DDB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC -!- CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC018671; AAH18671.1; -
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 320 AA; 35924 MW; 45FAC411DDBA4D1A CRC64;

Query Match 96.7%; Score 1585; DB 4; Length 320;
Best Local Similarity 99.4%; Pred. No. 1.4e-103;
Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 MAQVLRTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 67
|||||
Db 1 MAQVLRTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 60

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QY 68 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
Db 61 FGRDLLDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQVEQDAQALF 187
Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQVEQDAQALF 180
QY 188 QAGELKWCQDEKFTIFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLLAY 247
Db 181 QAGELKWCQDEKFTIFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLLAY 240
QY 248 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKFNATSLYSMI 307
Db 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKFNATSLYSMI 300
QY 308 KGDTSGDYKALLLLSGEDD 327
Db 301 KGDTSGDYKALLLLSGEDD 320

RESULT 2
Q99LAI PRELIMINARY; PRT; 319 AA.
ID Q99LAI
AC Q99LAI;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Annexin A5.
GN ANXA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC003716; AA03716.1; -.
DR HSSP; PI4668; IA8B.
DR MGD; MGI:106008; Anxa5.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 319 AA; 35738 MW; 52E2C7CCEA386917 CRC64;

Query Match 90.0%; Score 1475.5; DB 11; Length 319;
Best Local Similarity 93.4%; Pred. No. 7.1e-96;
Matches 295; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNRQREISAAFKTLFGRDL 72
Db 4 RGTVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNRQREISAAFKTLFGRDL 63
QY 73 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEELRAI 132
Db 64 VDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIASRTPEELSAI 123
QY 133 KQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQVEQDAQALFOAGEL 192
Db 124 KQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPDTAIDDAQVELDAQALFOAGEL 183
QY 193 KWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLLAVVKSIR 252

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Db 184 KWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLLAVVKSIR 243
QY 253 SIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKFNATSLYSMIKGDTS 312
Db 244 SIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKFNATSLYSMIKGDTS 303
QY 313 GDYKALLLL-SGEDD 327
Db 304 GDYKALLLLSGEDD 319

RESULT 3
Q70371 PRELIMINARY; PRT; 302 AA.
ID Q70371
AC Q70371;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lipocortin V (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE-99362163; PubMed-10329451;
RA Wen Y., Edelman J.L., Kang T., Sachs G.;
RT "Lipocortin V may function as a signaling protein for vascular
RL endothelial growth factor receptor-2/Fik-1."
RL Biochem. Biophys. Res. Commun. 258:713-721(1999).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF051895; AAC06290.1; -.
DR HSSP; PI4668; IA8B.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 3.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
FT NON_TER 302 302
SQ SEQUENCE 302 AA; 33965 MW; AB9FB40934A3D007 CRC64;

Query Match 84.8%; Score 1390; DB 11; Length 302;
Best Local Similarity 92.0%; Pred. No. 6.7e-90;
Matches 276; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 12 LRGTVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNRQREISAAFKTLFGRD 71
Db 3 LRGTVTDFPGFDERADAETLRKAMKGLGTDEESTLTLTSSRNRQREISAAFKTLFGRD 62
QY 72 LDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEELRA 131
Db 63 LVNDKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIASRTPEELRA 122
QY 132 IKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQVEQDAQALFOAGE 191
Db 123 IKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPDTAIDDAQVELDAQALFOAGE 182
QY 192 LKWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLLAVVKS 251
Db 183 LKWTGDEKFTIFGTRSVSHLRKVFYDKYMTISGFOIETIDRETSGNLEQLLLAVVKS 242
QY 252 RSIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKFNATSLYSMIKGD 311
Db 243 RSIPAYLAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKFRKFNATSLYSMIKGD 302

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DR PRINTS; PRO0196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 8.
DR SMART; SM00335; ANK; 8.
DR PROSITE; PS00223; ANNEXIN; 8.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 667 AA; 75260 MW; 363088A2A5CFF34 CRC64;

Query Match
Best Local Similarity 56.9%; Score 932; DB 11; Length 667;
Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGVTFDPGDERADAEETLRKAMKGLGTDEESILTLTSSRNAQROEISAAFKTLFGRDL 72
DB 11 RGSVHDFPEFDANADAEALYATKMGFGSKESILELTSRNKQROEIQYKSLYKGLD 70
QY 73 LDDLSKELGKPEKFLVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 132
DB 71 IEDLKELGKPEKFLVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 130
QY 133 KOVYEEYSSLEDDVVGDTSGYYQRLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 192
DB 131 VAAYKDAYERDLESIIIGTSGHFQKMLVLLQGTRENDVYSEDLVQDQVQDLYEAGEL 190
QY 193 KNGTDEEKITITFTGTSVSHLRKVPDKYMTISGFIQEEETIDRTSNLQALLAVVKSIR 252
DB 191 KNGTDEAQPIYILGNRSKQHLRVFDEYLTGTPKPIEASIRGELSGDFEKLMLAVVKIR 250
QY 253 STPAYLAETLYAMKAGGDDHTLIRVMYSRSDILFNIRKPKKFNATSLYSMIKGDTS 312
DB 251 STPEYFAERLFRAMKGLGTDRNTLIRIMVSRSELDMLDIREIFRTYKESLSYMIKNDTS 310
QY 313 GYKALLLLSGDD 327
DB 311 GEYKALLKLGDD 325

RESULT 8
O93444
ID O93444 PRELIMINARY; PRT; 320 AA.
AC O93444;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Annexin maxl.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99025617; PubMed=9809745;
RA Osterloh D., Wittbrodt J., Gerke V.;
RT "Characterization and developmentally regulated expression of four
annexins in the killifish medaka.";
RL DNA Cell Biol. 17:835-847(1998).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; Y11252; CAA72122.1; -.
DR HSSP; P13214; IANN.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PRO0196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANK; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 320 AA; 35424 MW; D2EED32C8676777D CRC64;

Query Match
Best Local Similarity 52.8%; Score 866; DB 13; Length 320;
Matches 170; Conservative 59; Mismatches 83; Indels 0; Gaps 0;

QY 13 RGVTFDPGDERADAEETLRKAMKGLGTDEESILTLTSSRNAQROEISAAFKTLFGRDL 72
DB 7 RGVTFEASGFNPDDDAQKLRAMKAGTDEAIIKYLHRTIAQRRIILAYKQSVYKGLD 66
QY 73 LDDLSKELGKPEKFLVALMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 132
DB 67 AEDLSSELGHSQSVVGLLMPAPYDAYELKAMKAGTDEACILIDILASRNSNNAL 126
QY 133 KOVYEEYSSLEDDVVGDTSGYYQRLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 192
DB 127 NEVYKEYCKTLEDAVCGDTSGMFGVRLVSLTAGRDESKVDEAQAVKADKIPAGEA 186
QY 193 KNGTDEEKITITFTGTSVSHLRKVPDKYMTISGFIQEEETIDRTSNLQALLAVVKSIR 252
DB 187 RKGTDVVKFLTLVLCVNRNHLRVFDEYKTKISKRIEDSKIKRMGSGSLEDVFLAVKCLR 246

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Qy 313 GDYKALLLLSGEDD 327
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Db 494 GDYKLLLLKCGSSD 508

RESULT 10
Q90X16 PRELIMINARY; PRT; 321 AA.
AC Q90X16;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Anexin 4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Seville R.A., Nijjar S., Barnett M.W., Jones E.A.;
RT "Anexin 4 (Xanx-4) has a role in the development of the pronephric
RT tubules in Xenopus laevis."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DE EMBL: AY039235; AAK83461.1;
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 321 AA; 35801 MW; 5C28CAFAAC17687D CRC64;

Query Match 51.8%; Score 849; DB 13; Length 321;
Best Local Similarity 54.0%; Pred. No. 8e-52;
Matches 170; Conservative 55; Mismatches 90; Indels 0; Gaps 0;

Qy 13 RGVTDPPGFERADAEITLKKAMKGLGTDEESILTLLTSSNAQROEISAAFKTLFGRDL 72
      . ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 7 KGTIKPPNPAADQVQLRNAMKGAGTDEDAVIDIANRTLSORGEIKTAYKTTVGKDL 66

Qy 73 LDDLKSELTKGFEKLIVALKMPSRLDYAEELKALKAGATNEKVLTEITASRTPPELRAI 132
      ||||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 67 DDLKSELTKGNFKVILGITSYLDVVELKAMKGAGTDEGLTEILASRSAEIKNI 126

Qy 133 KQVVEEYGSGLDDVVGDTSYGYORMVLVLLQANRDPDAGIDAEQVEDDAALFOAGEL 192
      | : : ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 127 NITYKIKYKSLDEDDTCSDFSPFQVRLVSLAAGGRDQSSVTVEDLAKDANDLYPAGEK 186

Qy 193 KWTDEEKFTITGTRSVHLRKVFQKYMISGQIEETIDRETSGNLEQLLVVKSIR 252
      ||||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 187 KWGTFDEKFTILCSRNRNLLKVFEEYKKAIAKDLKLEASIKSEMSGHLESLAIVKCIK 246

Qy 253 SIPAYAEITLYAMKAGTDHDLIRVWVSRSEIDLNFNIRKEPRKFNATSLYSIMIKGDTIS 312
      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 247 SRPAYAEIRLYKMKGLGTDKTLIRVWVSRCEIDMLTEIRCEPKMYKGLSHSFIKGDCS 306

Qy 313 GDYKALLLLSGEDD 327
      |||| ||| | |
Db 307 GDYKVVLLKCGGED 321

RESULT 11
Q921F1 PRELIMINARY; PRT; 503 AA.
ID Q921F1
AC Q921F1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)

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DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to annexin A11.
GN ANXA11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC012875; AAI12875.1; -.
DR MGD; MGI:108481; Anxa11.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 503 AA; 54079 MW; 33F3471EE21A0D32 CRC64;

Query Match 51.7%; Score 847; DB 11; Length 503;
Best Local Similarity 53.7%; Pred. No. 2.1e-51;
Matches 169; Conservative 59; Mismatches 87; Indels 0; Gaps 0;

QY 13 RGVTFPPGDERADAETLRKAMKGLGTDEESTLTLTSSRAQROEISAAFTLFGRLD 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 189 RGTITRAGSDPDLDAEVLRLKAMKGGTDEQALIDCLGSNSRQROQILLFPTATGKDL 248

QY 73 LDKLSLTKFKFKLVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIRTPPEELRAI 132
   : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 249 IKOLKSELNGFKETILALMKTPVLFVDFVYEIKAIKAGTDEACLEIPASRNEHLRL 308

QY 133 KOVTEEYSGSLEDDVGTSGYQYRMVLLQANRPDAGIDEAQVEQDAQALFOAGEL 192
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
DB 309 SRAYTEFQKLEARSSTSGHFORLLISLSOGNDESTNVDMSLVQRVDQVLYAAGEN 368

QY 193 KWGTDEKFTIFGTRSVSHLRKVFQKYMITSFGQIEETIDRETSGNLEQLLAVVKSIR 252
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 369 RLGTDESKFNAILCSRAHLVAVFNEYQRMTCGRDIEKSCREMSGDLEQGLAVVVKLK 428

QY 253 SIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMTKGTSGDYKALL 312
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 429 NTPAFPAERLNKAMRGATKDRTLIRIMVSRSELDLLDIRAEYKRYGKSLYHDITGDS 488

QY 313 GDYKALLLLSGEDD 327
   ||| ||| ||| : |||
DB 489 GDYRKILLKICGND 503

RESULT 12
QBK2N9 PRELIMINARY; PRT; 327 AA.
AC QBK2N9;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to annexin A8.
GN ANXA8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;

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RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030407; AAH30407.1; -.
DR MGD; MGI:1201374; Anxa8.
DR InterPro: IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
SQ SEQUENCE 327 AA; 36724 MW; 56DB9CFAFAC2B21 CRC64;

Query Match 51.3%; Score 840.5; DB 11; Length 327;
Best Local Similarity 57.8%; Pred. No. 3.3e-51;
Matches 177; Conservative 49; Mismatches 79; Indels 1; Gaps 1;

QY 22 FDERADAETLRKAMKGLGTDEESTLTLTSSRAQROEISAAFTLFGRLDLDLKLSELT 81
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 21 FNPDPDAETLYKAMKGGTNEQAIIDVLTKRNSVQRQOIAKSFKAQFGKDLTETLKSELS 80

QY 82 GKPEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIRTPPEELRAIKOVYBEYEG 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 81 GKFERLIVALKMPSPYSYEAKELHDMKGLGTKEGVIEILLASRTKNQLRIMKAYEDYG 140

QY 142 SSLEDDVGTSGYQYRMVLLQANRPDAG-IDEAQVEQDAQALFOAGELKWTGDEEK 200
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 STLEEDIQGTSGYLERILVCLLQGSRDDVSGFVDPGLVLDQAALHEAGEKIMGTDENK 200

QY 201 FITIFGTRSVSHLRKVFQKYMITSFGQIEETIDRETSGNLEQLLAVVKSIRTPAYLAE 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 FITILCTRSTATHLMRVFEYERKANKCIEDSIKSETHGSLSEEAFLTIVVKTRNVHSYFAE 260

QY 261 TLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKPKNFATSLYSMTKGTSGDYKALL 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 261 RLYAMKAGTDRGTLLRNVSRSEIDLNLKQFKMYKCTLSSMIMADTSGYKWTALL 320

QY 321 LLSGED 326
   |||
DB 321 NLVGTGTD 326

RESULT 13
Q95L54 PRELIMINARY; PRT; 327 AA.
AC Q95L54;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Annexin VIII.
OC Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA White A.H., Wallis G.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF417637; AAL13308.1; -.
DR InterPro: IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 327 AA; 36787 MW; 2EB178E13738CF22 CRC64;

Query Match 51.0%; Score 836.5; DB 6; Length 327;

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Db 309 GDYRTVLLKICGEDD 323

Search completed: August 22, 2003, 21:35:25
Job time : 32.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:27:21 ; Search time 37.6667 Seconds
(without alignments)
1377.971 Million cell updates/sec

Title: US-09-970-969-6

Perfect score: 1642

Sequence: 1 MACGCGHMAQLRGRTVTDFP.....KGTSGDYKALLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1642	100.0	327	22	AA050865 Modified human ann
2	1630	99.3	327	22	AA050863 Modified human ann
3	1630	99.3	327	22	AA050864 Modified human ann
4	1590	96.8	320	9	AA080511 Placental coagulat
5	1590	96.8	320	10	AA091953 Vascular anti-coag
6	1590	96.8	320	12	AA013082 PAP-I. Homo sapie
7	1590	96.8	320	20	AA013923 S65T GFP variant/h
8	1590	96.8	320	21	AA084788 Amino acid sequenc
9	1590	96.8	320	23	AA031220 Human annexin V, c

10	1587	96.7	320	10	AA090053 anticoagulant pp4
11	1587	96.7	600	21	AA092930 Annexin V/urokinas
12	1586	96.6	320	9	AA082317 PAP-I isolated fro
13	1585	96.5	319	13	AA026276 CPB-I. Homo sapie
14	1585	96.5	319	14	AA041021 Calphobindin I (CP
15	1585	96.5	319	23	AA032550 Human CPB-I protei
16	1584	96.5	320	9	AA080242 Sequence vascular
17	1584	96.5	320	9	AA080714 Sequence vascular
18	1584	96.5	320	12	AA011910 Vascular anticoagu
19	1580	96.2	319	13	AA026180 CPB-I. Homo sapie
20	1577	96.0	320	10	AA091383 Human lipocortin-V
21	1553	94.6	319	13	AA025718 CPB-I. Homo sapie
22	1479.5	90.1	319	20	AA013924 S65T GFP variant/h
23	1479.5	90.1	319	23	AA057067 Mouse ischaemic co
24	1455.5	88.6	318	20	AA013925 S65T GFP variant/h
25	1448.5	88.2	319	16	AA075695 Rat annexin-V. Ra
26	1442.5	87.9	319	24	AA056248 Human annexin V pr
27	1442.5	87.9	669	24	AA056249 Modified annexin p
28	1012	61.6	208	21	AA058393 Lung cancer associ
29	932	56.8	672	11	AA030725 Human placenta-der
30	932	56.8	675	24	AA054621 Human NOVX polyep
31	931	56.7	786	11	AA030726 Human placenta-der
32	923	56.2	321	20	AA013926 S65T GFP variant/h
33	923	56.2	321	23	AA096279 Human ovarian canc
34	923	56.2	324	21	AA043617 Human cancer assoc
35	922	56.2	321	10	AA091913 Anticoagulative pp
36	906.5	55.2	320	21	AA084790 Amino acid sequenc
37	879.5	53.6	736	22	AA019948 Novel human diagno
38	865	52.7	503	14	AA034127 Annexin XI type I
39	857	52.2	505	14	AA034128 Annexin XI type I
40	855	52.1	505	20	AA070117 Lung cancer associ
41	844	51.4	299	23	AA069394 Human polypeptide
42	831.5	50.6	327	9	AA080715 Sequence vascular
43	831.5	50.6	327	10	AA091954 Vascular anti-coag
44	831.5	50.6	327	14	AA035754 VAC-beta. Synthet
45	831.5	50.6	327	22	AA078665 Human protein SEQ

ALIGNMENTS

RESULT 1	
AA050865	
ID	AA050865 standard; Protein; 327 AA.
XX	
AC	AA050865;
XX	
DT	16-MAR-2001 (first entry)
XX	
DE	Modified human annexin, SEQ ID NO: 6.
XX	
KW	Human; annexin; chelation site; nuclear imaging; apoptosis;
KW	transplant rejection.
XX	
OS	Homo sapiens.
XX	
PN	WO200073332-A1.
XX	
PD	07-DEC-2000.
XX	
PF	25-MAY-2000; 2000WO-US14324.
XX	
PR	01-JUN-1999; 99US-0324096.
XX	
PA	(UNIW) UNIV WASHINGTON.
XX	
PI	Tait JF, Brown DS;
XX	
DR	WPI; 2001-080465/09.
DR	N-PSDB; AAC91370.
XX	
PT	Novel modified annexin useful for imaging vascular thrombi
PT	apoptosis, has N-terminal chelation site comprising amino a

XX 01-JUN-1999; 99US-0324096.
 XX (UNIW) UNIV WASHINGTON.
 XX Tait JF, Brown DS;
 XX WPI; 2001-080465/09.
 XX N-PSDB; AAC91369.
 XX Novel modified annexin useful for imaging vascular thrombi and
 XX apoptosis, has N-terminal chelation site comprising amino acid
 XX extension which comprises a glycine and a cysteine residue -
 XX
 XX Claim 15; Page 33-35; 39pp; English.
 XX
 XX The present sequence is a modified annexin having an N-terminal
 XX chelation site, which comprises an amino acid extension including a
 XX glycine and a cysteine residue. The modified annexin is useful for
 XX imaging vascular thrombi or apoptosis which is associated with response
 XX to a chemotherapeutic agent or with rejection as a result of
 XX transplantation. The modified annexin can effectively chelate a
 XX radionuclide and retain annexin bioactivity. It can be readily prepared
 XX in high radiochemical yield and with high radiochemical purity. In
 XX contrast to conventional conjugation chemistries that provide a
 XX distribution of conjugation products, the modified annexin has a single
 XX chelation site remote from the site of biological activity.
 XX
 XX Sequence 327 AA;
 XX
 XX Query Match 99.3%; Score 1630; DB 22; Length 327;
 XX Best Local Similarity 99.7%; Pred. No. 1.9e-142;
 XX Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MACCGHMAQVLRGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEI 60
 Db 1 MACCGHMAQVLRGTVDTPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEI 60
 QY 61 SAAFTLFGRLDDDLKSELTKFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
 Db 61 SAAFTLFGRLDDDLKSELTKFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEI 120
 QY 121 IASRTPPELRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVE 180
 Db 121 IASRTPPELRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVE 180
 QY 181 ODAQALFOAGELKNGTDEEKFTITFGTRSVSHLRKVFQKYMFTISGFQIEETIDRETSGNL 240
 Db 181 ODAQALFOAGELKNGTDEEKFTITFGTRSVSHLRKVFQKYMFTISGFQIEETIDRETSGNL 240
 QY 241 EQLLLAVVKSIRSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKNFA 300
 Db 241 EQLLLAVVKSIRSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKNFA 300
 QY 301 TSLYSWKMGDTSGDYKKALLLSGEDD 327
 Db 301 TSLYSWKMGDTSGDYKKALLLSGEDD 327
 RESULT 4
 AAP80511
 ID AAP80511 standard; protein; 320 AA.
 AC AAP80511;
 XX
 XX 25-MAR-2003 (updated)
 XX 10-MAR-2003 (updated)
 XX 12-NOV-1990 (first entry)
 XX
 XX Placental coagulation inhibitor.
 XX
 XX Placental coagulation inhibitor; disseminated vascular coagulation;
 XX thrombosis.

XX Homo sapiens.
 XX EP279459-A.
 XX JP03219875-A.
 XX 24-AUG-1988.
 XX 19-FEB-1988; 88EP-0102468.
 XX 20-FEB-1987; 87JP-0037227.
 XX 23-JUL-1987; 87JP-0184428.
 XX (KOWA) KOWA CO LTD.
 XX Saino Y, Iwasaki A, Suda M;
 XX WPI; 1988-236733/34.
 XX WPI; 1991-329110/45.
 XX N-PSDB; AAN81113.
 XX Recombinant placental coagulation inhibitor - useful for the prevention
 XX and treatment of thromboses or disseminated intra-vascular coagulation.
 XX Disclosure; Page ?; ?pp; English.
 XX
 XX This polypeptide exhibits strong anticoagulant activities and is useful
 XX for the treatment and prevention of e.g. thrombosis or disseminated
 XX intravascular coagulation in the brain, heart and peripheral blood
 XX vessels, such as cerebral and myocardial infarction. It has no
 XX antigenicity against man and can be produced in large ams. using
 XX recombinant methods.
 XX (Updated on 10-MAR-2003 to add missing OS field.)
 XX (Updated on 25-MAR-2003 to correct PF field.)
 XX (Updated on 25-MAR-2003 to correct PR field.)
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 320 AA;
 XX
 XX Query Match 96.8%; Score 1590; DB 9; Length 320;
 XX Best Local Similarity 99.7%; Pred. No. 9.3e-139;
 XX Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGVTVDPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 67
 Db 1 MAQVLRGVTVDPGDFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 60
 QY 68 FGRDLLDLKSELTKFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTP 127
 Db 61 FGRDLLDLKSELTKFKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTP 120
 QY 128 ELRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEQDAQALF 187
 Db 121 ELRAIKQVYEEYSSLEDDVVGDTSGYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 188 QAGELKNGTDEEKFTITFGTRSVSHLRKVFQKYMFTISGFQIEETIDRETSGNLQALLAV 247
 Db 181 QAGELKNGTDEEKFTITFGTRSVSHLRKVFQKYMFTISGFQIEETIDRETSGNLQALLAV 240
 QY 248 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI 307
 Db 241 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMI 300
 QY 308 KGTSGDYKKALLLSGEDD 327
 Db 301 KGTSGDYKKALLLSGEDD 320
 RESULT 5
 AAP91953
 ID AAP91953 standard; protein; 320 AA.
 XX
 XX AAP91953;

XX 25-MAR-2003 (updated)
 DT 10-MAR-2003 (updated)
 DT 30-JUL-1989 (first entry)
 XX
 DE Vascular anti-coagulating protein-alpha.
 XX
 KW Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..320
 FT /product=VAC-alpha protein
 XX
 XX DE3810331-A.
 XX
 XX 05-OCT-1989.
 XX
 XX 25-MAR-1988; 88DE-3810331.
 XX
 XX 26-MAR-1988; 88DE-3810331.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM.
 XX
 XX Gunther A;
 XX
 XX WPI: 1989-293724/41.
 XX N-PSDB; AAN91353.
 XX
 XX Monoclonal antibodies to vascular anti-coagulating proteins - and
 XX hybridomas producing such antibodies.
 XX
 XX Disclosure; fig 1; 11pp; German.
 XX
 XX This vascular anti-coagulating protein (VAC)-alpha is used in the
 XX preparation of monoclonal antibodies (Mabs). The VAC-alpha is injected
 XX into a host animal, in conjugation with eg keyhole limpet haemocyanin,
 XX and the B-cells from immunised hosts are then fused with myeloma cells.
 XX The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-
 XX alpha. Abs can be used as immunoassay reagents to detect VAC proteins,
 XX as affinity ligands for protein purification, and as medicaments for binding
 XX and/or neutralising VAC proteins in vivo. See also AAN91354 and
 XX EP-181465.
 XX (Updated on 10-MAR-2003 to add missing OS field.)
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 320 AA;
 XX
 XX Query Match 96.8%; Score 1590; DB 10; Length 320;
 XX Best Local Similarity 99.7%; Pred. No. 9.3e-139;
 XX Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVTDFFGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAPKTL 67
 DB 1 MAQVLRGTVTDFFGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAPKTL 60
 QY 68 FGRDLLDLKSELGTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRDLLDLKSELGTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 128 ELRAIKQVVEEYEGSSLEDDVGDTSYGYQRMVLVLLQANRPDAGIDEAQVEDQAALF 187
 DB 121 ELRAIKQVVEEYEGSSLEDDVGDTSYGYQRMVLVLLQANRPDAGIDEAQVEDQAALF 180
 QY 188 QAGELKNGTDEEKFITIFGTRSVSHLRKVPDKYMTISGGFOIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKNGTDEEKFITIFGTRSVSHLRKVPDKYMTISGGFOIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRSPAYLAETLYAMKAGCTDDHTLLRVMSRSEIDLFNIRKEFRKNFATSLYSMI 307
 DB 241 VKSIRSPAYLAETLYAMKAGCTDDHTLLRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300

QY 308 KGDTSGDYKKALLLLSGEDD 327
 DB 301 KGDTSGDYKKALLLLSGEDD 320
 XX
 XX RESULT 6
 XX AAR13082
 XX ID AAR13082 standard; Protein; 320 AA.
 XX AC AAR13082;
 XX DT 25-MAR-2003 (updated)
 XX DT 30-SEP-1991 (first entry)
 XX DE PAP-I.
 XX KW Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;
 XX KW gla-domain; VKDP.
 XX OS Homo sapiens.
 XX PN WO9109953-A.
 XX PD 11-JUL-1991.
 XX PF 13-DEC-1990; 90WO-US07335.
 XX PR 29-DEC-1989; 89US-0459082.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Foster DC;
 XX WPI: 1991-222905/30.
 XX N-PSDB; AAQ12679.
 XX Recombinant prodn. of hybrid phospholipid-binding proteins -
 XX comprising lipocortin phospholipid-binding domain and
 XX vitamin K-dependent protein
 XX Disclosure; Fig 7; 57pp; English.
 XX This sequence, or a fragment of it, is used in the construction of
 XX hybrid phospholipid-binding proteins (PBP) comprising at least one
 XX lipocortin phospholipid binding domain (PBD), e.g. of PAP-I, joined
 XX to a gla-domainless vitamin K-dependent protein, e.g. protein C or
 XX activated protein C. See AAQ12680-81 for such examples.
 XX See also AAQ12679-81.
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 320 AA;
 XX
 XX Query Match 96.8%; Score 1590; DB 12; Length 320;
 XX Best Local Similarity 99.7%; Pred. No. 9.3e-139;
 XX Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVTDFFGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAPKTL 67
 DB 1 MAQVLRGTVTDFFGFDERADAETLRKAMKGLGTDDEESILTLTSSRNAQREISAAPKTL 60
 QY 68 FGRDLLDLKSELGTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRDLLDLKSELGTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 128 ELRAIKQVVEEYEGSSLEDDVGDTSYGYQRMVLVLLQANRPDAGIDEAQVEDQAALF 187
 DB 121 ELRAIKQVVEEYEGSSLEDDVGDTSYGYQRMVLVLLQANRPDAGIDEAQVEDQAALF 180
 QY 188 QAGELKNGTDEEKFITIFGTRSVSHLRKVPDKYMTISGGFOIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKNGTDEEKFITIFGTRSVSHLRKVPDKYMTISGGFOIETIDRETSGNLEQLLAV 240

QY 248 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKFKRKNFATSLYSMI 307
DB 241 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKFKRKNFATSLYSMI 300
QY 308 KGDTSYGYKKALLLLSGEDD 327
DB 301 KGDTSYGYKKALLLLCGEDD 320

RESULT 7
AA13923
ID AAY13923 standard; protein; 320 AA.
XX
AC AAY13923;
XX
DT 13-JUL-1999 (first entry)
XX
XX S65T GFP variant/hAnnexin V protein.
XX
XX GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
XX fluorescent intensity; anionic phospholipid binding affinity;
XX asymmetric distribution; plasma membrane phospholipid;
XX apoptotic cell detection.
XX
OS Aequorea victoria.
OS Homo sapiens.
OS Synthetic.
XX
PN W09919470-A2.
XX
XX 22-APR-1999.
XX
XX 09-OCT-1998; 98WO-US21444.
XX
XX 09-OCT-1997; 97US-0948276.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Ernst JD;
XX
XX WPI; 1999-277634/23.
XX
XX Bifunctional fusion protein useful for the detection of apoptotic
XX cells
XX
XX Claim 2; Page 14-15; 23pp; English.
XX
XX This sequence represents an example of a protein of the invention.
XX The proteins are bifunctional Aequorea victoria green fluorescent protein
XX (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
XX greater or equal fluorescent intensity and anionic phospholipid binding
XX affinity, respectively, than do the corresponding unfused GFP and annexin
XX proteins. An early manifestation of apoptosis is the loss of the
XX asymmetric distribution of plasma membrane phospholipids, which results
XX in exposure of anionic phospholipids on the extracellular leaflet of the
XX plasma membrane. The GFP-annexin V fusion proteins are used for the
XX detection of apoptotic cells by flow cytometry or fluorescent microscopy.
XX The fusion proteins provide for homogeneously labelled annexin, with
XX fluorescence properties that do not change upon binding membrane
XX phospholipids, unlike prior art FITC-labelled annexins, where quenching
XX of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
XX membranes.
XX
XX Sequence 320 AA;
XX
XX Query Match 96.8%; Score 1590; DB 20; Length 320;
XX Best Local Similarity 99.7%; Pred. No. 9.3e-139;
XX Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 8 MAQVLRGVTVDFPGFDERADATLIRKAMKGLGTDEESILTLTTSRINAQROEISAAFKTL 67
DB 1 MAQVLRGVTVDFPGFDERADATLIRKAMKGLGTDEESILTLTTSRINAQROEISAAFKTL 60

QY 68 FGRLLDDLKSELTKFKFKLIVALKMKPSRLYDAYELKHALKGAGTNEKVLFEITIASRTPE 127
DB 61 FGRLLDDLKSELTKFKFKLIVALKMKPSRLYDAYELKHALKGAGTNEKVLFEITIASRTPE 120
QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYVYRMVLLQANRDPDAGIDEAQVEQDAQALF 187
DB 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYVYRMVLLQANRDPDAGIDEAQVEQDAQALF 180
QY 188 QAGELKWTGDEKFTITFGRSVSHLRKRVFKYMTISGFQIEETIDRETSGNLEQLLAV 247
DB 181 QAGELKWTGDEKFTITFGRSVSHLRKRVFKYMTISGFQIEETIDRETSGNLEQLLAV 240
QY 248 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKFKRKNFATSLYSMI 307
DB 241 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKFKRKNFATSLYSMI 300
QY 308 KGDTSYGYKKALLLLSGEDD 327
DB 301 KGDTSYGYKKALLLLCGEDD 320

RESULT 8
AAY84788
ID AAY84788 standard; peptide; 320 AA.
XX
XX AAY84788;
XX
DT 08-AUG-2000 (first entry)
XX
XX Amino acid sequence of annexin V.
XX
XX Annexin; phospholipid; antithrombotic; antitumor; antinflammatory;
XX coating; thrombogenic biomaterial; labelling compound; negative charge.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Domain 16..91
XX FT /note= "domain 1"
XX
XX FR2784106-A1.
XX
XX 07-APR-2000.
XX
XX 02-OCT-1998; 98FR-0012366.
XX
XX 02-OCT-1998; 98FR-0012366.
XX
XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerols R;
XX WPI; 2000-320664/28.
XX
XX Chemical structure having affinity for phospholipid comprises chemical
XX platform comprising six residues supporting set of chemical functions
XX that are capable of binding to phospholipid
XX
XX Claim 13; Fig 6b; 63pp; French.
XX
XX The present sequence represents an annexin polypeptide. The domain of
XX annexin, which may be modified, is used to construct the chemical
XX compounds of the invention. The specification describes chemical
XX compounds which have an affinity for a phospholipid. The chemical
XX compounds comprise at least one chemical platform comprising six
XX residues supporting a set of chemical functions that are capable of
XX binding to the phospholipid and at least partly define the affinity
XX of the structure for the phospholipid. The compounds act as
XX phospholipid sequestrers. The compounds are useful for preparing
XX antithrombotic, antitumor and antinflammatory medicaments, for
XX making coatings for thrombogenic biomaterials, and for preparing
XX labelling compounds useful for analysing and detecting negative

CC charges on cell surfaces and microvesicles in blood.
 XX
 SQ Sequence 320 AA;
 Query Match 96.8%; Score 1590; DB 21; Length 320;
 Best Local Similarity 99.7%; Pred. No. 9.3e-139;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 67
 DB 1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 60
 QY 68 FGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
 DB 61 FGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
 QY 128 ELRAIKQVYEEYSSLEDDVGDTSYQYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 187
 DB 121 ELRAIKQVYEEYSSLEDDVGDTSYQYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 180
 QY 188 QAGELKWTGDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKWTGDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFINRKEFRKNFATSLYSMI 307
 DB 241 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFINRKEFRKNFATSLYSMI 300
 QY 308 KGDTSGDYKKALLLGGEDD 327
 DB 301 KGDTSGDYKKALLLGGEDD 320
 RESULT 9
 ID ABG31220 standard; Protein; 320 AA.
 XX
 AC ABG31220;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human annexin V, containing a delta RACK binding site.
 XX
 KW Human; annexin V; delta RACK; delta protein kinase C; deltaPKC;
 KW V1 domain; vasotropic; cerebroprotective; deltaV1-1; deltaV1-2; RACK;
 KW pseudo-delta RACK; pseudo-delta receptor for activated C-kinase;
 KW deltaV1-5; PKC; protein kinase C; signal transduction; cell growth;
 KW gene expression; ion channel activity; translocation; hypoxia; stroke;
 KW ischemic damage; creatine kinase.
 XX
 OS Homo sapiens.
 XX
 PN WO200257413-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 09-NOV-2001; 2001NO-US47556.
 XX
 PR 18-JAN-2001; 2001US-262060P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Mochly-Rosen D;
 XX
 DR WPI; 2002-599715/64.
 XX
 PT New delta protein kinase C peptide for reducing or enhancing damage to
 PT cells or tissues exposed to ischemic or hypoxic event caused by stroke,
 PT or for protecting tissue from damage due to ischemia -
 XX
 PS Claim 45; Page 64-65; 65pp; English.
 XX
 CC The invention discloses peptides comprising deltaV1-1, deltaV1-2,

CC pseudo-delta receptors for activated C-kinase (RACK), deltaV1-5 or their
 CC derivatives or fragments. Protein kinase C (PKC) is a key enzyme in
 CC signal transduction involved in a variety of cellular functions including
 CC cell growth, regulation of gene expression and ion channel activity. The
 CC localisation of different PKC isozymes to different areas of the cell in
 CC turn appears due to binding of the activated isozymes to the specific
 CC anchoring molecules (RACKs). Peptides that mimic either the PKC-binding
 CC site on RACKs or the RACK-binding site on PKC are isozyme specific
 CC translocation inhibitors of PKC. The disclosed peptides are useful in
 CC activating or inhibiting translocation or function of deltaPKC. The
 CC deltaPKC agonists or antagonists are useful in reducing, enhancing or
 CC protecting against damage to cells or tissues due to ischemic or hypoxic
 CC event caused by stroke. Acute administration of the peptides, conjugated
 CC to a carrier peptide or a Tat-derived peptide, protected hearts against
 CC ischemic damage as shown by decreased release of creatine kinase. The
 CC data indicate that in an intact heart, inhibition of deltaPKC conferred
 CC greater than 50% protection against ischemic damage. The sequence
 CC presented is human annexin V, which contains a delta RACK binding site.
 XX
 SQ Sequence 320 AA;
 Query Match 96.8%; Score 1590; DB 23; Length 320;
 Best Local Similarity 99.7%; Pred. No. 9.3e-139;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 67
 DB 1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 60
 QY 68 FGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
 DB 61 FGRDLDDLKSELGTGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
 QY 128 ELRAIKQVYEEYSSLEDDVGDTSYQYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 187
 DB 121 ELRAIKQVYEEYSSLEDDVGDTSYQYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 180
 QY 188 QAGELKWTGDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGIETIDRETSGNLEQLLAV 247
 DB 181 QAGELKWTGDEEKFTIFGTRSVSHLRKVFYDKYMTISGFGIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFINRKEFRKNFATSLYSMI 307
 DB 241 VKSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFINRKEFRKNFATSLYSMI 300
 QY 308 KGDTSGDYKKALLLGGEDD 327
 DB 301 KGDTSGDYKKALLLGGEDD 320
 RESULT 10
 AAP90053
 ID AAP90053 standard; protein; 320 AA.
 XX
 AC AAP90053;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE antioagulant PP4 protein.
 XX
 KW Anticoagulant; PP4 protein; thromboplastin.
 XX
 OS Homo sapiens (human).
 XX
 PN EP318703-A.
 XX
 PD 07-JUN-1989.
 XX
 PF 29-OCT-1988; 88EP-0118039.
 XX
 PR 03-NOV-1987; 87DE-3737239.
 XX

PA (BEHW) BEHRINGERWERKE AG.
XX
PI Grundmann U, Abel KJ, Kupper H;
XX
DR WPI; 1989-166767/23.
XX
XX New DNA sequence encoding anticoagulant PP4 protein
PT - and new recombinant protein, vectors, antibodies, etc.,
PT useful therapeutically and diagnostically.
XX
XX Claim 1; page 11 and Table 1; 12pp; German.
XX
CC Amino acid sequence of anticoagulant PP4 protein. This
CC inhibits blood coagulation at the thromboplastin stage.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 320 AA;
Query Match 96.7%; Score 1587; DB 10; Length 320;
Best Local Similarity 99.4%; Pred. No. 1.8e-138;
Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 67
Db 1 MAQVLRGTVTFPGFDERADAOTLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 60
QY 68 FGRDLLDLKSELGTGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
Db 61 FGRDLLDLKSELGTGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 120
QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 187
Db 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 180
QY 188 QAGELKWGTDEEKFTIFGTRSVSHLRKVFVKYMTISGFOIETIDRETSGNLEQLLAV 247
Db 181 QAGELKWGTDEEKFTIFGTRSVSHLRKVFVKYMTISGFOIETIDRETSGNLEQLLAV 240
QY 248 VKSIRSIPIAYLAETLYAMKAGCTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
Db 241 VKSIRSIPIAYLAETLYAMKAGCTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
QY 308 KGDTSGDYKKALLLLSGEDD 327
Db 301 KGDTSGDYKKALLLLCGEDD 320
RESULT 11
AAV92930
ID AAV92930 standard; Protein; 600 AA.
XX
AC AAV92930;
XX
DT 25-OCT-2000 (first entry)
XX
DE Annexin V/urokinase fusion protein.
XX
KW Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;
KW urokinase; insect cell; fibrinolysis.
XX
OS Unidentified.
XX
XX CN1247195-A.
XX
XX 15-MAR-2000.
XX
XX 12-MAR-1999; 99CN-0113524.
XX
XX 12-MAR-1999; 99CN-0113524.
XX
XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.

XX
PI Wu X, Sun J, Yang G;
XX
DR WPI; 2000-413098/36.
DR N-PSDB; AAA11241.
XX
XX New thrombolytic fusion protein for targeting thrombus - comprises
PT fusion of Annexin V and urokinase
XX
XX Claim 2; Page 2-4; 20pp; Chinese.
XX
CC Annexin V, which has high affinity for active thrombocytes, is used
CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion
CC protein. The protein (this sequence) is the result of expression of a
CC fusion gene comprising the annexin V gene and a low-molecular urokinase
CC gene, in insect cells. The annexin V-scu-PA-32 fusion protein, expressed
CC in insect cell strain Tn-5B1-4, has high affinity for active thrombocytes
CC and has the fibrinolytic activity of urokinase.
XX
SQ Sequence 600 AA;
Query Match 96.7%; Score 1587; DB 21; Length 600;
Best Local Similarity 99.4%; Pred. No. 4.3e-138;
Matches 318; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 67
Db 281 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAPKTL 340
QY 68 FGRDLLDLKSELGTGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 127
Db 341 FGRDLLDLKSELGTGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIASRTPE 400
QY 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 187
Db 401 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVQDAQALF 460
QY 188 QAGELKWGTDEEKFTIFGTRSVSHLRKVFVKYMTISGFOIETIDRETSGNLEQLLAV 247
Db 461 QAGELKWGTDEEKFTIFGTRSVSHLRKVFVKYMTISGFOIETIDRETSGNLEQLLAV 520
QY 248 VKSIRSIPIAYLAETLYAMKAGCTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
Db 521 VKSIRSIPIAYLAETLYAMKAGCTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 580
QY 308 KGDTSGDYKKALLLLSGEDD 327
Db 581 KGDTSGDYKKALLLLCGEDD 600
RESULT 12
AAP82317
ID AAP82317 standard; protein; 320 AA.
XX
AC AAP82317;
XX
DT 25-MAR-2003 (updated)
DT 13-NOV-1990 (first entry)
XX
XX PAP-I isolated from biological fluid, used as anticoagulant.
DE PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;
XX phospholipase A2; disseminated intravascular coagulation;
KW deep vein thrombosis.
XX
OS Homo sapiens.
XX
XX WO805659-A.
XX
XX 11-AUG-1988.
XX
XX 05-FEB-1988; 88WO-US00340.
XX

PR 06-FEB-1987; 87US-0011782.
 PR 05-JUN-1987; 87US-0059355.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Fujikawa K, Irani MH, Carter BLA;
 XX
 DR WPI; 1988-235049/33.
 DR N-PSDB; AAN82107.
 XX
 PT Human proteins having anticoagulant and antiinflammatory activity -
 PT isolated from biological fluid by anion-exchange chromatographoc media.
 XX
 PS Disclosure: Page ?; 7pp; English.
 XX
 CC The protein does not contain a leader peptide sequence,
 CC indicating that PAP-I is probably not constitutively secreted.
 CC The Met residue is removed at in a post-translational event and the
 CC newly formed NH2-terminal Ala residue is blocked by acetylation.
 CC It binds to phospholipid and inhibits phospholipase A2.
 CC The protein can substitute heparin or other anticoagulants in
 CC the treatment of disseminated intravascular coagulation, deep vein
 CC thrombosis, or other disorders. It also has antiinflammatory
 CC properties.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 320 AA;
 Query Match 96.6%; Score 1586; DB 9; Length 320;
 Best Local Similarity 99.4%; Pred. No. 2.2e-138;
 Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 MAQVLRGVTDFPGFDERADAEALRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 67
 DB 1 MAQVLRGVTDFPGFDERADAEALRKAMKGLGTDEESILTLTSSNAQROEISAAFKTL 60
 QY 68 FGRLDLLDKSELTKGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
 DB 61 FGRLDLLDKSELTKGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 128 ELRAIKQVVEEYSGSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALF 187
 DB 121 ELRAIKQVVEEYSGSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALF 180
 QY 188 QAGELKMGTDDEKFTITFGTRSVSHLRKVDFKYMVTISGFQIEETIDRETSGNLEQLLAV 247
 DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVDFKYMVTISGFQIEETIDRETSGNLEQLLAV 240
 QY 248 VKSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
 DB 241 VKSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
 QY 308 KGDTSGDYKKALLLLSGEDD 327
 DB 301 KGDTSGDYKKALLLLCGEDD 320
 RESULT 13
 AAR26276
 ID AAR26276 standard; protein; 319 AA.
 XX
 AC AAR26276;
 XX
 DT 10-MAR-2003 (updated)
 DT 04-FEB-1993 (first entry)
 XX
 DE CPB-I.
 XX
 KW CPB-I; stabilisation; frozen; molten; processed; activity.
 XX
 OS Homo sapiens.
 XX

PN -JP04198195-A.
 XX
 PD 17-JUL-1992.
 XX
 PF 28-NOV-1990; 90JP-0328286.
 XX
 PR 28-NOV-1990; 90JP-0328286.
 XX
 PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
 PA (KOWA) KOWA CO LTD.
 XX
 DR WPI; 1992-288937/35.
 XX
 PT Stabilisation of CPB-I for drug compan. - by adding basic
 PT aminoacid selected from lysine, arginine and/or ornithine
 XX
 PS Disclosure: Page 2; 4pp; Japanese.
 XX
 CC The sequence given is the amino acid sequence of CPB-I. CPB-I was
 CC used within a method which involved adding basic amino acids to it
 CC which resulted in its stabilisation. This lead to the production of
 CC CPB-I which keeps its activity when it is frozen, molten or has been
 CC processed by several procedures.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 319 AA;
 Query Match 96.5%; Score 1585; DB 13; Length 319;
 Best Local Similarity 99.7%; Pred. No. 2.7e-138;
 Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 AQVLRGVTDFPGFDERADAEALRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 68
 DB 1 AQVLRGVTDFPGFDERADAEALRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLF 60
 QY 69 GRDLLDDKSELTKGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
 DB 61 GRDLLDDKSELTKGKFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 120
 QY 129 LRAIKQVVEEYSGSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALFQ 188
 DB 121 LRAIKQVVEEYSGSLEDDVVGDTSGYYORMLVLLQANRPDAGIDEAQVEQDAQALFQ 180
 QY 189 AGEKMGTDDEKFTITFGTRSVSHLRKVDFKYMVTISGFQIEETIDRETSGNLEQLLAV 248
 DB 181 AGEKMGTDDEKFTITFGTRSVSHLRKVDFKYMVTISGFQIEETIDRETSGNLEQLLAV 240
 QY 249 KSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 308
 DB 241 KSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 300
 QY 309 GDTSGDYKKALLLLSGEDD 327
 DB 301 GDTSGDYKKALLLLCGEDD 319
 RESULT 14
 AAR41021
 ID AAR41021 standard; protein; 319 AA.
 XX
 AC AAR41021;
 XX
 DT 29-MAR-1994 (first entry)
 DE Calphobindin I (CPB-I).
 XX
 KW Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
 XX
 OS Homo sapiens.
 XX
 PN JP05213769-A.
 XX
 PD 24-AUG-1993.

```
XX 04-FEB-1992; 92JP-0019032.
XX (KOWA ) KOWA CO LTD.
XX (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO.
XX WPI; 1993-299558/38.
XX Protein kinase C inhibitor effective against malignant tumours -
XX contg. (opt. recombinant) calphobindin I
XX Claim 1; Page 2-3; 6pp; Japanese.
XX Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)
XX inhibits protein kinase C (PKC) and is useful in the treatment of
XX malignant tumours caused by abnormal activation of PKC. CPB-I is
XX extracted from human or animal organs and may be applied
XX intravenously, orally, intramuscularly, percutaneously or rectally.
XX SQ Sequence 319 AA;
XX Query Match 96.5%; Score 1585; DB 14; Length 319;
XX Best Local Similarity 99.7%; Pred. No. 2.7e-138;
XX Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAPKTLF 68
DB 1 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAPKTLF 60
QY 69 GRLLDDLKSELTKGKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
DB 61 GRLLDDLKSELTKGKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 120
QY 129 LRAIKQVYEEYSGSLEDDVVGDTSGYYQRMVLLVLLQANRDPDAGIDEAQVEQDAALFQ 188
DB 121 LRAIKQVYEEYSGSLEDDVVGDTSGYYQRMVLLVLLQANRDPDAGIDEAQVEQDAALFQ 180
QY 189 AGELKWTDEEKFTIFGTRSVSHLRKVFDMYMTISGFIETIDRETSGNLEQLLAVV 248
DB 181 AGELKWTDEEKFTIFGTRSVSHLRKVFDMYMTISGFIETIDRETSGNLEQLLAVV 240
QY 249 KSRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFNIRKEFRKNFATSLYSNIK 308
DB 241 KSRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFNIRKEFRKNFATSLYSNIK 300
QY 309 GDTSGDYKKALLLLSGEDD 327
DB 301 GDTSGDYKKALLLLCGEDD 319
RESULT 15
ABG32550
ID ABG32550 standard; protein; 319 AA.
XX AC ABG32550;
XX 29-NOV-2002 (first entry)
XX Human CPB-1 protein.
XX Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
XX calcium/phospholipid binding protein; polyhydric alcohol.
XX Homo sapiens.
XX WO200267977-A1.
XX 06-SEP-2002.
XX 21-FEB-2002; 2002WO-JP01563.
XX
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```
PR 26-FEB-2001; 2001JP-0050297.
XX (KOWA ) KOWA CO LTD.
XX (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX Naruse H, Sano M, Shinoda Y, Inagi T;
XX WPI; 2002-674988/72.
XX Eye drops for treating e.g. corneal diseases, contain CPB-I and
XX polyhydric alcohol with specific carbonyl value, without unpleasant
XX irritation upon dropping but with satisfactory long-term storability
XX Disclosure; Page 13-14; 16pp; Japanese.
XX The invention relates to eye drops contain CPB-I (anexin V) and a
XX polyhydric alcohol having a carbonyl value of not more than
XX 5micro Mol./g. The eye drops are for treating e.g. corneal diseases.
XX Such eye drops are without unpleasant irritation upon dropping but with
XX satisfactory long-term storage stability. The present sequence is
XX the human CPB-I (calcium/phospholipid binding) protein.
XX SQ Sequence 319 AA;
XX Query Match 96.5%; Score 1585; DB 23; Length 319;
XX Best Local Similarity 99.7%; Pred. No. 2.7e-138;
XX Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAPKTLF 68
DB 1 AQLRGVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSSNAQROEISAAPKTLF 60
QY 69 GRLLDDLKSELTKGKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
DB 61 GRLLDDLKSELTKGKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 120
QY 129 LRAIKQVYEEYSGSLEDDVVGDTSGYYQRMVLLVLLQANRDPDAGIDEAQVEQDAALFQ 188
DB 121 LRAIKQVYEEYSGSLEDDVVGDTSGYYQRMVLLVLLQANRDPDAGIDEAQVEQDAALFQ 180
QY 189 AGELKWTDEEKFTIFGTRSVSHLRKVFDMYMTISGFIETIDRETSGNLEQLLAVV 248
DB 181 AGELKWTDEEKFTIFGTRSVSHLRKVFDMYMTISGFIETIDRETSGNLEQLLAVV 240
QY 249 KSRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFNIRKEFRKNFATSLYSNIK 308
DB 241 KSRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLNFNIRKEFRKNFATSLYSNIK 300
QY 309 GDTSGDYKKALLLLSGEDD 327
DB 301 GDTSGDYKKALLLLCGEDD 319
Search completed: August 22, 2003, 21:33:07
Job time : 39 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:28:42 ; Search time 8.66667 Seconds
(without alignments)
1774.354 Million cell updates/sec

Title: US-09-970-969-6
Perfect score: 1642
Sequence: 1 MACCGHMAQVLRGTVDFP.....KGDTSGDYKKALLLSGEDD 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1585	96.5	319	1 ANX5_HUMAN	P08758 homo sapien
2	1536.5	93.6	320	1 ANX5_BOVIN	P81287 bos taurus
3	1479.5	90.1	319	1 ANX5_MOUSE	P48036 mus musculus
4	1455.5	88.6	318	1 ANX5_RAT	P14668 rattus norv
5	1279	77.9	321	1 ANX5_CHICK	P17153 gallus gall
6	1089.5	66.4	323	1 ANX5_CYNPY	P70075 cynops pyrr
7	932	56.8	672	1 ANX6_HUMAN	P08133 homo sapien
8	932	56.8	672	1 ANX6_MOUSE	P14824 mus musculus
9	923	56.2	318	1 ANX4_HUMAN	P09525 homo sapien
10	921	56.1	318	1 ANX4_PIG	P08132 sus scrofa
11	921	56.1	672	1 ANX6_RAT	P48037 rattus norv
12	916	55.8	318	1 ANX4_MOUSE	P97429 mus musculus
13	914	55.7	318	1 ANX4_BOVIN	P13214 bos taurus
14	901	54.9	318	1 ANX4_CANFA	P50994 canis famli
15	896.5	54.6	671	1 ANX6_CHICK	P51901 gallus gall
16	891	54.3	318	1 ANX4_RAT	P55260 rattus norv
17	865	52.7	503	1 ANX8_BOVIN	P27214 bos taurus
18	863	52.6	503	1 ANXB_RABIT	P33477 oryctolagus
19	855	52.1	505	1 ANXB_HUMAN	P50995 homo sapien
20	847	51.6	503	1 ANXB_MOUSE	P97384 mus musculus
21	841.5	51.2	327	1 ANXB_MOUSE	O35640 mus musculus
22	831.5	50.6	327	1 ANX8_HUMAN	P13928 homo sapien
23	802.5	48.9	323	1 ANX3_HUMAN	P13429 homo sapien
24	799	48.7	323	1 ANX3_MOUSE	O35639 mus musculus
25	779	47.4	466	1 ANX7_HUMAN	P20073 homo sapien
26	777	47.3	463	1 ANX7_MOUSE	O07076 mus musculus
27	771	47.0	324	1 ANX3_RAT	P14669 rattus norv
28	761	46.3	618	1 ANX6_BOVIN	P79134 bos taurus
29	718	43.7	316	1 ANXC_HYDAT	P26256 hydra atten
30	711	43.3	512	1 ANX7_XENLA	O92125 xenopus lae
31	701	42.7	324	1 ANX9_DROME	P22464 drosophila
32	698.5	42.5	338	1 ANX2_HUMAN	P07355 homo sapien
33	694.5	42.3	338	1 ANX2_BOVIN	P04272 bos taurus

ALIGNMENTS

RESULT 1

ID	ANX5_HUMAN	STANDARD;	PRT;	319 AA.
AC	P08758;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)			
DE	(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)			
DE	(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)			
DE	(Anchoring CII).			
GN	ANXA5 OR ANX5 OR ENX2 OR PP4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88234495; PubMed=2967495;			
RA	Grundmann U., Abel K.-J., Bohn H., Loebermann H., Lottspeich F.,			
RA	Kuepper H.;			
RT	"Characterization of cDNA encoding human placental anticoagulant			
RT	protein (pp4): homology with the lipocortin family.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).			
RL	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=88271329; PubMed=2455636;			
RA	Maurer-Fogy I., Reutlingsperger C.P.M., Pieters J., Bodo G.,			
RA	Stratowa C., Hauptmann R.;			
RT	"Cloning and expression of cDNA for human vascular anticoagulant, a			
RT	Ca2+-dependent phospholipid-binding protein.";			
RL	Eur. J. Biochem. 174:585-592(1988).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88273202; PubMed=2968983;			
RA	Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., Miller G.T.,			
RA	Browning J.L., Chow B.P., Burne C., Huang K.-S., Pratt D., Wachter L.,			
RA	Hession C., Frey A.Z., Wallner B.P.;			
RT	"Five distinct calcium and phospholipid binding proteins share			
RT	homology with lipocortin I.";			
RL	J. Biol. Chem. 263:10799-10811(1988).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88163463; PubMed=2964863;			
RA	Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;			
RT	"Primary structure of human placental anticoagulant protein.";			
RL	Biochemistry 26:8087-8092(1987).			
RL	[5]			
RP	SEQUENCE FROM N.A., AND SEQUENCE.			
RX	MEDLINE=88139278; PubMed=2963810;			
RA	Iwasaki K., Suda M., Nakao H., Nagoya T., Saino Y., Arai K.,			
RA	Mizoguchi T., Sato F., Yoshizaki H., Hirata M., Miyata T.,			
RA	Shidara Y., Murata M., Maki M.;			
RT	"Structure and expression of cDNA for an inhibitor of blood			
RT	coagulation isolated from human placenta: a new lipocortin-like			
RT	protein.";			

34	693.5	42.2	338	1	ANX2_RAT	Q07936 rattus norv
35	691.5	42.1	338	1	ANX2_MOUSE	P07356 mus musculus
36	685.5	41.7	320	1	ANXX_DROME	P22465 drosophila
37	679	41.4	315	1	ANXD_HUMAN	P27216 homo sapien
38	675.5	41.1	339	1	ANXB_XENLA	P27006 xenopus lae
39	671	40.9	315	1	ANXD_CANFA	Q29471 canis famli
40	666.5	40.6	338	1	ANX2_CHICK	P17785 gallus gall
41	662.5	40.3	339	1	ANX2_XENLA	P24801 xenopus lae
42	649	39.5	346	1	ANX1_RABIT	P51662 oryctolagus
43	648	39.5	346	1	ANX1_CAVCU	P14087 cavia cutie
44	643	39.2	345	1	ANX1_HUMAN	P04083 homo sapien
45	643	39.2	346	1	ANX1_BOVIN	P46193 bos taurus

RL J. Biochem. 102:1261-1273(1987).
RP [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228020; PubMed=2967291;
RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
RT "Cloning and expression of cDNA for human endonexin II, a Ca²⁺ and
phospholipid binding protein.";
RL J. Biol. Chem. 263:8037-8043(1988).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RC MEDLINE=95047484; PubMed=7958998;
RA Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
RT "The gene encoding human annexin V has a TATA-less promoter with a
high G+C content.";
RL Gene 149:253-260(1994).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94307733; PubMed=8034319;
RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
RA Tait J.F.;
RT "Organization of the human annexin V (ANX5) gene.";
RL Genomics 20:463-467(1994).
RN [9]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, Ovary, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=90088443; PubMed=2532007;
RA Rothhut R., Comera C., Cortial S., Haumont P.-Y., Diep Le K.H.,
RA Cavadore J.-C., Conard J., Russo-Marie F., Lederer F.;
RT "A 32 kDa lipocortin from human mononuclear cells appears to be
identical with the placental inhibitor of blood coagulation.";
RL Biochem. J. 263:929-935(1989).
RN [11]
RP SEQUENCE OF 85-130; 258-296 AND 299-319.
RX MEDLINE=87317598; PubMed=2957692;
RA Schlaepfer D.D., Wehlman T., Burgess W.H., Haigler H.T.;
RT "Structural and functional characterization of endonexin II, a
calcium- and phospholipid-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
RN [12]
RP SEQUENCE OF 84-92.
RX MEDLINE=89066652; PubMed=2974032;
RA Ann N.G., Teller D.C., Blenkowski M.J., McMullen B.A., Lipkin E.W.,
RA de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
phospholipase A2 inhibitors from human placenta. Evidence against a
mechanistically relevant association between enzyme and inhibitor.";
RL J. Biol. Chem. 263:18657-18663(1988).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ÅNGSTROMS).
RX MEDLINE=91065314; PubMed=2147412;
RA Huber R., Roemisch J., Paques E.-P.;
RT "The crystal and molecular structure of human annexin V, an
anticoagulant protein that binds to calcium and membranes.";
RL EMBO J. 9:3867-3874(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ÅNGSTROMS).
RX MEDLINE=91085549; PubMed=2148156;
RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
RT "The calcium binding sites in human annexin V by crystal structure
analysis at 2.0-Å resolution. Implications for membrane binding and
calcium channel activity.";
RL FEBS Lett. 275:15-21(1990).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ÅNGSTROMS).
RX MEDLINE=92177413; PubMed=1311770;
RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
RA Luecke H., Roemisch J., Paques E.-P.;
RT "Crystal and molecular structure of human annexin V after refinement.
Implications for structure, membrane binding and ion channel
formation of the annexin family of proteins.";
RL J. Mol. Biol. 223:683-704(1992).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (3.0 ÅNGSTROMS).
RX MEDLINE=98062349; PubMed=9398511;
RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
RT "Crystal structure of annexin V with its ligand K-201 as a calcium
channel activity inhibitor.";
RL J. Mol. Biol. 274:16-20(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ÅNGSTROMS).
RX MEDLINE=98118533; PubMed=9435213;
RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
RT "Residue-specific biolincorporation of non-natural, biologically
active amino acids into proteins as possible drug carriers: structure
and stability of the per-thioproline mutant of annexin V.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
RN [18]
RP FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
CC -1- SUBUNIT: MONOMER. BINDS ATRX (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
calcium and phospholipid.
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -1- CAUTION: THIS PROTEIN HAS BEEN INDEPENDENTLY SEQUENCED BY AT LEAST
SEVEN GROUPS UNDER DIFFERENT NAMES!
CC -1- DATABASE: NAME-R&D Systems' cytokine source book: Annexin 5;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=185".

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CC EMBL; X12454; CAA30985.1; -
DR EMBL; M19384; AAB59545.1; -
DR EMBL; M18366; AAA35570.1; -
DR EMBL; M21731; AAA36166.1; -
DR EMBL; D00172; BAA00122.1; -
DR EMBL; J03745; AAA52386.1; -
DR EMBL; U01691; AAB40047.1; -
DR EMBL; U01681; AAB40047.1; JOINED.
DR EMBL; U01682; AAB40047.1; JOINED.
DR EMBL; U01683; AAB40047.1; JOINED.
DR EMBL; U01685; AAB40047.1; JOINED.
DR EMBL; U01686; AAB40047.1; JOINED.
DR EMBL; U01687; AAB40047.1; JOINED.
DR EMBL; U01688; AAB40047.1; JOINED.
DR EMBL; U01689; AAB40047.1; JOINED.
DR EMBL; U01690; AAB40047.1; JOINED.

Query Match 96.5%; Score 1585; DB 1; Length 319;
Best Local Similarity 99.7%; Pred. No. 1e-95;
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AQLVGTGVTDPGPFDERADAETLRKAMKGLGTDDESILTLTSSNAQROEISAFAKTLF 68
DB 1 AQLVGTGVTDPGPFDERADAETLRKAMKGLGTDDESILTLTSSNAQROEISAFAKTLF 60
QY 69 GRDLDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEE 128
DB 61 GRDLDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEE 120
QY 129 LRAIKQVYEEYGSLEDDVVDGTSYGYQRMVLLVLLQANRDPDAGIDEAQVEDQAALFQ 188
DB 121 LRAIKQVYEEYGSLEDDVVDGTSYGYQRMVLLVLLQANRDPDAGIDEAQVEDQAALFQ 180
QY 189 AGELKMGTDDEKFTIFGTRSVSHLRKVFQKMTISGFQETIDRETSGNLQOLLAVV 248
DB 181 AGELKMGTDDEKFTIFGTRSVSHLRKVFQKMTISGFQETIDRETSGNLQOLLAVV 240
QY 249 KSIRIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEFKNFATSLYSMIK 308
DB 241 KSIRIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEFKNFATSLYSMIK 300
QY 309 GDTSGDYKALLLSGDEDD 327
DB 301 GDTSGDYKALLLSGDEDD 319

RESULT 2
ANX5_BOVIN STANDARD; PRT; 320 AA.

ID ANX5_BOVIN
AC P81287;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchocin CII).
GN ANXA5 OR ANX5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RC TISSUE=Brain;
RX MEDLINE=93041974; PubMed=1420335;
RA Learnmonth M.P., Howell S.A., Harris A.C.M., Amess B., Patel Y.,
RA Giambanco I., Bianchi R., Pula G., Ceccarelli P., Donato R.,
RA Green B.N., Aitken A.;
RA "Novel isoforms of Cabp 33/37 (annexin V) from mammalian brain:
RT structural and phosphorylation differences that suggest distinct
RT biological roles.";
RT Blochm. Biophys. Acta 1160:76-83(1992).
CC -I- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
CC -I- SUBUNIT: MONOMER. BINDS ATRX (By similarity).
CC -I- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -I- SIMILARITY: Contains 4 annexin repeats.
DR PIR; S27214; S27214.
DR HSSP; P08738; IANW.
DR InterPro; IPR001454; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; calcium/phospholipid-binding; Repeat; Blood coagulation;
KW Acetylation.
FT INIT_MET 0 0 ANNEXIN 1.
FT REPEAT 23 83 ANNEXIN 2.
FT REPEAT 95 155 ANNEXIN 3.
FT REPEAT 179 239 ANNEXIN 4.
FT REPEAT 254 314 ANNEXIN 4.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT VARIANT 36 36 S -> T.
FT VARIANT 125 125 K -> E.
SQ SEQUENCE 320 AA; 35942 MW; 50FC8E18E95F19CB0 CRC64;

Query Match 93.6%; Score 1536.5; DB 1; Length 320;
Best Local Similarity 96.6%; Pred. No. 1.4e-92;
Matches 309; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 9 AQLVGTGVTDPGPFDERADAETLRKAMKGLGTDDESILTLTSSNAQROEISAFAKTLF 68
DB 1 AQLVGTGVTDPGPFDERADAETLRKAMKGLGTDDESILTLTSSNAQROEISAFAKTLF 60
QY 69 GRDLDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEE 128
DB 61 GRDLDDLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIASRTPEE 120
QY 129 LRAIKQVYEEYGSLEDDVVDGTSYGYQRMVLLVLLQANRDPDAGIDEAQVEDQAALFQ 188
DB 121 LRAIKQVYEEYGSLEDDVVDGTSYGYQRMVLLVLLQANRDPDAGIDEAQVEDQAALFQ 180
QY 189 AGELKMGTDDEKFTIFGTRSVSHLRKVFQKMTISGFQETIDRETSGNLQOLLAVV 248
DB 181 AGELKMGTDDEKFTIFGTRSVSHLRKVFQKMTISGFQETIDRETSGNLQOLLAVV 240
QY 249 KSIRIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEFKNFATSLYSMIK 308
DB 241 KSIRIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLFNIRKEFKNFATSLYSMIK 300
QY 309 GDTSGDYKALLLSGDEDD 327
DB 301 GDTSGDYKALLLSGDEDD 320

RESULT 3
ANX5_MOUSE STANDARD; PRT; 319 AA.

ID ANX5_MOUSE
AC P48036;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchocin CII).
GN ANXA5 OR ANX5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=Peritoneal cavity;
RX MEDLINE=96422179; PubMed=8824796;
RA Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
RT "Mouse annexin V chromosomal localization, cDNA sequence
RT conservation, and molecular evolution.";
RL Genomics 31:151-157(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneal cavity;
RX MEDLINE=96422179; PubMed=8824796;
RA Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
RT "Mouse annexin V chromosomal localization, cDNA sequence
RT conservation, and molecular evolution.";
RL Genomics 31:151-157(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Adachi T., Kojima K., Fukuoaka S.-I., Ogawa H., Matsumoto I.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN=129/SVJ; TISSUE=Liver;

EX MEDLINE-99072820; PubMed-9854034;
 RA Rodriguez-Garcia M.L., Morgan R.O., Fernandez M.R., Bances P.,
 RA Fernandez M.P.;
 RT "Mouse annexin V genomic organization includes an endogenous
 RT retrovirus";
 RL J. Blocher. 337:125-131(1999).
 CC -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
 CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
 CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
 CC -1- SUBUNIT: MONOMER. BINDS ATRX (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U29396; AAC52530.1; ..
 CC EMBL; D63423; BAA09728.1; ..
 CC EMBL; AJ230108; CAAL3092.1; JOINED.
 CC EMBL; AJ230110; CAAL3092.1; JOINED.
 CC EMBL; AJ230111; CAAL3092.1; JOINED.
 CC EMBL; AJ230114; CAAL3092.1; JOINED.
 CC EMBL; AJ230116; CAAL3092.1; JOINED.
 CC EMBL; AJ230118; CAAL3092.1; JOINED.
 CC EMBL; AJ230119; CAAL3092.1; JOINED.
 CC EMBL; AJ230120; CAAL3092.1; JOINED.
 CC EMBL; AJ230121; CAAL3092.1; JOINED.
 CC EMBL; AJ230122; CAAL3092.1; JOINED.
 CC EMBL; AJ230123; CAAL3092.1; JOINED.
 CC EMBL; AJ230124; CAAL3092.1; JOINED.
 CC HSP; P14666; IAB8.
 CC SWISS-2DPAGE; P48036; MOUSE.
 CC MGD; MGI:106008; Annex5.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 4.
 CC PRINTS; PR00196; ANNEXIN.
 CC ProDom; PD000143; Annexin; 4.
 CC SMART; SM00335; ANX; 4.
 CC PROSITE; PS00223; ANNEXIN; 4.
 CC Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Placenta.
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 SQ SEQUENCE 319 AA; 35752 MW; 55055BAF2E1C36B7 CRC64;
 Query Match 90.18; Score 1479.5; DB 1; Length 319;
 Best Local Similarity 93.78; Pred. No. 6.6e-89;
 Matches 296; Conservative 9; Mismatches 10; Indels 1; Gaps 1;
 QY 13 RGVTFPGFDERADAEELKAMKGLGTDSEITLTLTSRNASQROEISAFTKFGDRL 72
 Db 4 RGVTFPGFDERADAEELKAMKGLGTDSEITLTLTSRNASQROEISAFTKFGDRL 63
 QY 73 LDDLKSELTGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTETIISRTPEELRAI 132
 Db 64 VDDLKSELTGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTETIISRTPEELSAI 123
 QY 133 KQVEEYGSLSDDVVGDTSGYYQRMVLLQANRPDPDAGIDEAQVEQDAQALFQAGEL 192
 Db 124 KQVEEYGSLSDDVVGDTSGYYQRMVLLQANRPDPDAGIDEAQVEQDAQALFQAGEL 183
 QY 193 KWTGDEKFTITGTSVSHLRKVRFDKMTISGFIQETIDRETSGNLEQLLAVVKSIR 252
 Db 184 KWTGDEKFTITGTSVSHLRKVRFDKMTISGFIQETIDRETSGNLEQLLAVVKSIR 243

QY 253 SIPAYLAETLYAMKGAGTDDHTLIRVWVSSEIDLFNIRKEFRNFATSLYSMIKGDTS 312
 Db 244 SIPAYLAETLYAMKGAGTDDHTLIRVWVSSEIDLFNIRKEFRNFATSLYSMIKGDTS 303
 QY 313 GDYKKALLLL-SGEDD 327
 Db 304 GDYKKALLLLCGGEDD 319

RESULT 4 ANX5_RAT

ID ANX5_RAT STANDARD; PRT; 318 AA.
 AC P14668;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Ancholin CII).
 GN ANX5 OR ANX5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP MEDLINE-88273202; PubMed-2968983;
 RA Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K.,
 RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
 RA Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
 RT "Five distinct calcium and phospholipid binding proteins share
 RT homology with lipocortin I".
 RL J. Biol. Chem. 263:10799-10811(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar;
 RX MEDLINE-96035863; PubMed-7556178;
 RA Imai Y., Kohsaka S.;
 RT "Structure of rat annexin V gene and molecular diversity of its
 RT transcripts".
 RL Eur. J. Biochem. 232:327-334(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-93369587; PubMed-8362244;
 RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Rat annexin V crystal structure: Ca(2+)-induced conformational
 RT changes".
 RL Science 261:1321-1324(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC TISSUE-Kidney;
 RX MEDLINE-96069783; PubMed-7583670;
 RA Swairjo M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Ca(2+)-bridging mechanism and phospholipid head group recognition in
 RT the membrane-binding protein annexin V".
 RL Nat. Struct. Biol. 2:968-974(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
 RX MEDLINE-98272673; PubMed-9609693;
 RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swairjo M.A., Balch C.,
 RA Head J.F., Retzinger G., Dedman J.R., Seaton B.A.;
 RT "Mutational and crystallographic analyses of interfacial residues in
 RT annexin V suggest direct interactions with phospholipid membrane
 RT components".
 RL Biochemistry 37:8004-8010(1998).
 RN [6]
 RP INTERACTION WITH DNMT1.
 RC STRAIN-Wistar; TISSUE-Brain;
 RX MEDLINE-96301899; PubMed-8667030;
 RA Ohgawa K., Imai Y., Ito D., Kohsaka S.;
 RT "Molecular cloning and characterization of annexin V-binding proteins

with highly hydrophilic peptide structure.*;

RL J. Neurochem. 67:89-97(1996).

CC -1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS

CC AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,

CC WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.

CC -1- SUBUNIT: MONOMER. Binds ATRX and DNMT1.

CC -1- DOMAIN: A pair of annexin repeats may form one binding site for

CC calcium and phospholipid.

CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M21730; AAA41512.1; -

DR EMBL; D42137; BAA07708.1; -

DR EMBL; D42129; BAA07708.1; JOINED.

DR EMBL; D42130; BAA07708.1; JOINED.

DR EMBL; D63337; BAA07708.1; JOINED.

DR EMBL; D42131; BAA07708.1; JOINED.

DR EMBL; D42132; BAA07708.1; JOINED.

DR EMBL; D42133; BAA07708.1; JOINED.

DR EMBL; D42134; BAA07708.1; JOINED.

DR EMBL; D42135; BAA07708.1; JOINED.

DR EMBL; D42136; BAA07708.1; JOINED.

DR PIR; C29250; L0RT5.

DR PIR; ZRAN; 30-NOV-94.

DR PDB; 1A8A; 17-JUN-98.

DR PDB; 1A8B; 17-JUN-98.

DR PDB; 1BC0; 13-JAN-99.

DR PDB; 1BC1; 13-JAN-99.

DR PDB; 1BC3; 13-JAN-99.

DR PDB; 1BCW; 13-JAN-99.

DR PDB; 1BCY; 13-JAN-99.

DR PDB; 1BCZ; 13-JAN-99.

DR PDB; 1G5N; 13-MAR-02.

DR PDB; 1N41; 04-FEB-03.

DR PDB; 1N42; 04-FEB-03.

DR PDB; 1N44; 04-FEB-03.

DR InterPro; IPR001464; Annexin.

DR Pfam; PF00191; annexin; 4.

DR PRINTS; PR00196; ANNEXIN.

DR PRODOM; PD000143; Annexin; 4.

DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 4.

KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;

KW Placenta; Acetylation; 3D-structure.

FT INIT_MET 0 0

FT REPEAT 20 80 ANNEXIN 1.

FT REPEAT 92 152 ANNEXIN 2.

FT REPEAT 176 236 ANNEXIN 3.

FT REPEAT 251 311 ANNEXIN 4.

FT MOD_RES 1 1

FT TURN 10 11

FT HELIX 14 25

FT HELIX 32 39

FT TURN 40 41

FT HELIX 44 58

FT HELIX 62 69

FT HELIX 72 82

FT HELIX 85 97

FT HELIX 104 113

FT HELIX 116 130

FT HELIX 134 141

FT HELIX 144 154

FT TURN 155 156

FT HELIX 166 179

FT TURN 180 182

FT HELIX 188 197

FT HELIX 200 214

FT HELIX 218 225

FT HELIX 228 242

FT HELIX 244 256

FT HELIX 263 273

FT TURN 274 277

FT HELIX 278 289

FT HELIX 293 300

FT HELIX 303 313

SQ SEQUENCE 318 AA; 35613 MW; 1A755A7C11FA1ICE CRC64;

Query Match 88.6%; Score 1455.5; DB 1; Length 318;

Best Local Similarity 91.8%; Pred. No. 2.3e-87;

Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 12 LRCVTYDFPGFDRADAETLRKAMKGLGDTDEESTLTLLTSRSNAOROEISAAPKTLFGRD 71

DB 2 LRGTVTFDFSGFDRADAETLRKAMKGLGDTDEESTLTLLTSRSNAOROEISAAPKTLFGRD 61

QY 72 LLDLKSLELTGKPEKLTIVALKMPSRLYDAYELHALKAGCTNEKVLTEIISRTPEELRA 131

DB 62 LVNDKSELGTGKPEKLTIVALKMPSRLYDAYELHALKAGCTDEKVLTEIISRTPEELRA 121

QY 132 IKQYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQQVDAQALFOAGE 191

DB 122 IKQAYEEYEGSNLEDDVVGDTSGYYQRMVLVLLQANRDPDTAIDDAQVELDAQALFOAGE 181

QY 192 LKWTDEEKETITFGTSVSHLRKRVFDKYMKTISGFQIEETIDRETSGNLELLAVVKSI 251

DB 182 LKWTDEEKETITILGTSVSHLRKRVFDKYMKTISGFQIEETIDRETSGNLELLAVVKSI 241

QY 252 RSIPAYLAETLYAMKAGAGTDDHTLIRVMVSRSEIDLINIRKEPKKFNATSLYMIKGD 311

DB 242 RSIPAYLAETLYAMKAGAGTDDHTLIRVIVSRSEIDLINIRKEPKKFNATSLYMIKGD 301

QY 312 SGDYKKALLL-SGEDD 327

DB 302 SGDYKKALLLLOGGEDD 318

RESULT 5

ANX5_CHICK STANDARD; PRT; 321 AA.

AC P17153;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)

DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Ancholin CII).

DE ANXA5 OR ANX5.

GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RX SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=88186917; PubMed=2833522;

RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,

RA Deutzmann R., Mollenhauer J., von der Mark K.;

RT "The structure of ancholin CII, a collagen binding protein isolated from chondrocyte membrane.";

RL J. Biol. Chem. 263:5921-5925(1988).

RN [2]

RN SUGGEST SEQUENCING ERROR.

RX MEDLINE=90020458; PubMed=2552626;

RA Moss S.E., Crumpton M.J.;

RT "Alternative splicing or cloning artefact?";

RN Trends Biochem. Sci. 14:325-325(1989).

RN [3]

RP REVISIONS.
 RA MEDLINE-90243721; PubMed-2159478;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaffle M.,
 RA Deutzmann R., Mollenhauer J., von der Mark K.:
 RT "The structure of anchoring CII, a collagen binding protein isolated
 RT from chondrocyte membrane.";
 RL J. Biol. Chem. 265:8344-8344(1990).
 RN [4]
 RP REVISIONS.
 RA Pfaffle M., Ruggiero F., Hofmann H., Fernandez M.P., Selmin O.,
 RA Yamada Y., Garrone R., von der Mark K.:
 RL EMBO J. 9:1336-1336(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-White leghorn; TISSUE=Liver;
 RX MEDLINE-94215900; PubMed-8163186;
 RA Fernandez M.P., Fernandez M.R., Morgan R.O.:
 RT "Structure of the gene encoding anchoring CII (chick annexin V).";
 RL Gene 141:179-186(1994).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE-93249384; PubMed-8484740;
 RA Boustead C.M., Brown R., Walker J.H.:
 RT "Isolation, characterization and localization of annexin V from
 RT chicken liver.";
 RL Biochem. J. 291:601-608(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-93229489; PubMed-8471604;
 RA Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.:
 RT "Structure of chicken annexin V at 2.25-A resolution.";
 RL Biochemistry 32:3923-3929(1993).
 CC -|- FUNCTION: COLLAGEN-BINDING PROTEIN.
 CC -|- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -|- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -|- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M30971; AAA48591.1; ALT_SEQ.
 CC EMBL; U01678; AAB39917.1; JOINED.
 CC EMBL; U01671; AAB39917.1; JOINED.
 CC EMBL; U01672; AAB39917.1; JOINED.
 CC EMBL; U01673; AAB39917.1; JOINED.
 CC EMBL; U01675; AAB39917.1; JOINED.
 CC EMBL; U01676; AAB39917.1; JOINED.
 CC EMBL; U01677; AAB39917.1; JOINED.
 CC EMBL; U01678; AAB39917.1; JOINED.
 CC EMBL; U01679; AAB39917.1; JOINED.
 CC EMBL; A35381; LUCH5.
 CC PDB; 1ALA; 31-OCT-93.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 4.
 CC PRINTS; PR00196; ANNEXIN.
 CC PRODOM; PD000143; Annexin; 4.
 CC SMART; SM00335; ANN; 4.
 CC PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 FT REPEAT 24 84 ANNEXIN 1.
 FT REPEAT 96 156 ANNEXIN 2.
 FT REPEAT 180 240 ANNEXIN 3.
 FT REPEAT 255 315 ANNEXIN 4.
 FT CONFLICT 168 168 D -> E (IN REF. 1).
 FT TURN 13 14
 FT HELIX 17 28

FT HELIX 35 44
 FT HELIX 47 61
 FT HELIX 65 72
 FT HELIX 75 85
 FT TURN 88 90
 FT HELIX 91 100
 FT HELIX 107 116
 FT HELIX 119 133
 FT HELIX 137 144
 FT HELIX 147 157
 FT TURN 158 158
 FT HELIX 169 184
 FT TURN 185 187
 FT HELIX 191 200
 FT HELIX 203 217
 FT HELIX 221 224
 FT HELIX 232 245
 FT HELIX 247 259
 FT TURN 266 275
 FT TURN 276 280
 FT HELIX 281 292
 FT HELIX 296 303
 FT HELIX 306 316
 SQ SEQUENCE 321 AA; 36198 MW; 43E2983F86797025 CRC64;
 Query Match 77.9%; Score 1279; DB 1; Length 321;
 Best Local Similarity 78.1%; Pred. No. 6.1e-76;
 Matches 250; Conservative 38; Mismatches 32; Indels 0; Gaps 0;
 QY 8 MAQLVGLTVDPPGDDERADAETLRKAMKGLGTDESILTLTSRNAQRQISAAFKTL 67
 DB 1 MAKYRTGTVTAFSPFDARADAEALRKAMKMGTDDETLKILTSRNAQRQISAAFKTL 60
 QY 68 FGRLDLDLKLSELTGKFEKLI VALKPSRLYDAYELKHALKGAGTNEKVLTTIASRTPE 127
 DB 61 FGRLDLDLKLSELTGKFEKLI VALKPSRLYDAYELKHALKGAGTNEKVLTTIASRTPE 120
 QY 128 ELRAIKQVVEEYBEGSLEDVVGVDTSGYYQRMVLVLLQANRPDAGIDEAEOQAQLF 187
 DB 121 EVQNIKQVYMQEYEALENDKITGETSGHFQRLVLLQANRPDGRVDEALVEKDAQVLF 180
 QY 188 QAGELKWTDEKFTIFGTRSVSHLRKVDKYMTISGQIETIDRETSGNLEQLLAV 247
 DB 181 RAGELKWTDEFTITLGTSRVSHLRVDFKYMTISGQIETIDRETSGNLEQLLAV 240
 QY 248 VKSIRISAPYLAETLYYAMKAGAGTDHDTLIRVWVSREIDLFNIRKPKNFATSLYSMI 307
 DB 241 VKCIRSVPAFYAETLYYSKMGAGTDDDTLIRVWVSREIDDLIRHFKNFAKSLYQMI 300
 QY 308 KGDTSQDYKKALLLGGEDD 327
 DB 301 QKDTSGDYRKALLLGGEDD 320
 RESULT 6
 ANX5_CYNPY STANDARD; PRT; 323 AA.
 ID ANX5_CYNPY
 AC P70075;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Yamamoto T., Hikono T., Abe S.I.:
 RT "Differential expression of annexin V during spermatogenesis in the
 RT newt Cynops pyrrhogaster.";
 RL Dev. Genes Evol. 206:64-71(1996).

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CC -----
 DR EMBL: D00510; BAA00400.1; -;
 DR EMBL: Y00097; CAA68286.1; -;
 DR EMBL: J03578; AAA35656.1; -;
 DR EMBL: BC017046; AAH17046.1; -;
 DR PIR: J00032; AQU068.
 DR PDB: 1M91; 07-AUG-02.
 DR Genew: HGNC:544; ANXA6.
 DR MIM: 114070; -;
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 8.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 8.
 DR SMART: SM00335; ANX; 8.
 DR Annsite: PS00223; ANNEXIN; 8.
 KW Annexin: Calcium/phospholipid-binding; Repeat; Acetylation;
 KW Phosphorylation; 3D-structure.
 FT INIT_MET 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 FT MOD_RES 1 1 ACETYLATION.
 FT CONFLICT 225 226 IE -> MK (IN REF. 2).
 FT CONFLICT 554 554 S -> T (IN REF. 2).
 FT CONFLICT 618 618 E -> D (IN REF. 1).
 SQ SEQUENCE 672 AA; 75742 MW; 2829237029BD1DCB CRC64;

Query Match 56.8%; Score 932; DB 1; Length 672;
 Best Local Similarity 58.1%; Pred. No. 4e-53;
 Matches 183; Conservative 52; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGVTVDFPGFDERADATLTKAMKGLGTDEESTLTLTSRNSAQRGEISAAFTLFGDRL 72
 DB 10 RGSIHDFPGFDPNQDAEALYTKAMKFGSDKEALDIITSRNRQRCVCSYKSLYKGLD 69
 QY 73 LDKLSELTKGKFKELVALMKPSRLDYDELKALGAGTNEKVLTEIATSRTPPELRAI 132
 DB 70 IADLKYELTKGKFERLVGLMRPYPAYCDAKEIKDAISGIGTDEKCLTEILASRTNEQMHQL 129
 QY 133 KQVTEEGSSLEDDVVGDTSGYVQRMVLLQANRDPDAGIDEAQVEDQAALFOAGEL 192
 DB 130 VAAYKDAYERDLEADIIGTSGHFQKMLVVLQGTREDDVSDLVQDDVQDLYAGEL 189
 QY 193 KNGTDEKFTITFTGTRSVSHLRKRVFDKMTISGFIETETIDRTSGNLEQLLIAYVKISR 252
 DB 190 KNGTDEAQFTIYILGNRSKQHLRVDPDEYELTKTKPIEASIRGLSGDFEKLMLAVVKIR 249
 QY 253 SIPAYLAETLYAMKAGCAGTDDHTLRVMSRSIDLFNTRKEPRKNFATSLYSKIMKGDTS 312
 DB 250 STPEYFAERLFKAMKGLGTRDNTLRIMVSRSELDMLDIREIPRTKYKSLYSKIMKNDTS 309
 QY 313 GYKKALLLSGDD 327
 DB 310 GEYKTLKLSGDD 324

RESULT 8
 ID ANX6_MOUSE
 AC P14824;
 DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (Lipocortin VI) (p68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANXA6 OR ANX6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=89030687; PubMed=2972541;
 RA Moss S.E., Crumpton M.R., Crumpton M.J.;
 RT "Molecular cloning of murine p68, a Ca2+-binding protein of the
 RL lipocortin family".
 RL Eur. J. Biochem. 177:21-27(1988).
 CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF
 CC CA(2+) FROM INTRACELLULAR STORES.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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DR EMBL: X13460; CAA31808.1; -;
 DR PIR: S01786; S01786.
 DR HSSP: P79134; IAVC.
 DR MGD: MGI:88255; Anxa6.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 8.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 8.
 DR SMART: SM00335; ANX; 8.
 DR Annsite: PS00223; ANNEXIN; 8.
 KW Annexin: Calcium/phospholipid-binding; Repeat.
 FT INIT_MET 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 SQ SEQUENCE 672 AA; 75755 MW; 2D85C1DD235FC76 CRC64;

Query Match 56.8%; Score 932; DB 1; Length 672;
 Best Local Similarity 59.0%; Pred. No. 4e-53;
 Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

QY 13 RGVTVDFPGFDERADATLTKAMKGLGTDEESTLTLTSRNSAQRGEISAAFTLFGDRL 72
 DB 10 RGSVHDFPFDANQDAEALYTKAMKFGSDKEILITSRNKQRQRCVCSYKSLYKGLD 69
 QY 73 LDKLSELTKGKFKELVALMKPSRLDYDELKALGAGTNEKVLTEIATSRTPPELRAI 132
 DB 70 IEDLKYELTKGKFERLVGLMRPLAYCDAKEIKDAISGIGTDEKCLTEILASRTNEQMHQL 129
 QY 133 KQVTEEGSSLEDDVVGDTSGYVQRMVLLQANRDPDAGIDEAQVEDQAALFOAGEL 192
 DB 130 VAAYKDAYERDLEADIIGTSGHFQKMLVVLQGTREDDVSDLVQDDVQDLYAGEL 189
 QY 193 KNGTDEKFTITFTGTRSVSHLRKRVFDKMTISGFIETETIDRTSGNLEQLLIAYVKISR 252

Db 190 KWGTDEAQTIIYILGNRSKOHRLVDFEYLKTTKPIEASIRGELSGDFEKLMLVAVKCI 249

QY 253 SIPIYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFKRKNFATSLYSWIKGDT 312

Db 250 STEYFAERLFKAMKGLGTDRNTLIRVMVSRSELDMLDREIFRTYKSLYSWIKNDTS 309

QY 313 GDYKALLLLSGEDD 327

Db 310 GEYKALLKLCGGDD 324

RESULT 9

ANX4_HUMAN

ID ANX4_HUMAN STANDARD; PRT; 318 AA.

AC P09525; O96F33; Q9BWK1;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Annexin A4 (Annexin IV) (lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (P4-X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41) (P33/41).

DE ANX4 OR ANX4.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88309022; PubMed=2970257;

RA Grundmann U., Anann E., Abel K.-J., Kuepper H.A.;

RT "Isolation and expression of cDNA coding for a new member of the phospholipase A2 inhibitor family.";

RL Behring Inst. Mitt. 82:59-67(1988).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92155721; PubMed=1346776;

RA Tait J.F., Smith C., Frankenberry D.A., Miao C.H., Adler D.A., Distèche C.M.;

RT "Chromosomal mapping of the human annexin IV (ANX4) gene.";

RL Genomics 12:313-318(1992).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97239215; PubMed=9084877;

RA Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T., Matsumoto I.;

RT "Characterization of human p33/41 (annexin IV), a Ca²⁺ dependent carbohydrate-binding protein with monoclonal anti-annexin IV antibodies, AS11 and AS17.";

RL Biol. Pharm. Bull. 20:224-229(1997).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE-Eye, and Uterus;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5]

RN SEQUENCE OF 26-55: 98-123 AND 279-307.

RP MEDLINE=89066652; PubMed=2974032;

RX Ann N.G., Teller D.C., Blenkowski M.J., McMullen B.A., Lipkin E.W., de Haen C.;

RA "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor.";

RT J. Biol. Chem. 263:18657-18663(1988).

RN [6]

RN SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.

RP MEDLINE=89118212; PubMed=2975506;

RX Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T., Hendrickson L.E., Fujikawa K.;

RA "Placental anticoagulant proteins: isolation and comparative characterization of four members of the lipocortin family.";

RT Biochemistry 27:6268-6276(1988).

RN [7]

RN X-RAY CRYSTALLOGRAPHY.

RX MEDLINE=91073383; PubMed=2254922;

RA Freeman P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;

RT "Crystallization and preliminary x-ray crystallographic studies of human placental annexin IV.";

RL J. Mol. Biol. 216:219-221(1990).

CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).

CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.

CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

CC -1- SIMILARITY: Contains 4 annexin repeats.

CC -----

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CC -----

DR EMBL; M19383; AAC41689.1; ALT_INIT.

DR EMBL; M82809; AAA51740.1; -.

DR EMBL; D78152; BAA11227.1; ALT_INIT.

DR EMBL; BC00182; AAH00182.1; ALT_INIT.

DR EMBL; BC011659; AAH11659.1; ALT_INIT.

DR HSP; P13214; IANN

DR SWISS-2DPAGE; P09525; HUMAN.

DR PMMA-2DPAGE; P09525; -.

DR Genew; HGNC:542; ANXA4.

DR MIM; 106491; -.

DR InterPro; IPR01464; Annexin.

DR Pfam; PF00191; annexin. 4.

DR PRINTS; PR00196; ANNEXIN.

DR PRODOM; PD000143; Annexin; 4.

DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 4.

DR Annexin; Calcium/phospholipid-binding; Repeat.

FT INT_MET 0

FT REPEAT 22 82 ANNEXIN 1.

FT REPEAT 94 154 ANNEXIN 2.

FT REPEAT 178 238 ANNEXIN 3.

FT REPEAT 253 313 ANNEXIN 4.

FT CONFLICT 95 95 R -> Q (IN REF. 1).

SQ SEQUENCE 318 AA; 35751 MW; 16819E01500350F7 CRC64;

Query Match 56.2%; Score 923; DB 1; Length 318;

Best Local Similarity 58.3%; Pred. No. 6.2e-53;

Matches 183; Conservative 53; Mismatches 78; Indels 0; Gaps 0;

Qy 14 GTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSRNAQROETSAAEKTLFGDRL 73

Db 5 GTVKAASGFNAMEADAQTLRKAMKGLGTDEDAIISVLAYRNTAQROETAYKSTGRDL 64

QY 74 DLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
 DB 65 DLKSELSCNFEQIVGMMTPVLYDVQELRRAMKAGTDEGLIEILASRTPEELRRIS 124
 QY 134 QYEEYEGSSLEDDVVDTSYGYQRMVLLVLLQANRPDAGIDAEQVQDAQALFQAGEUK 193
 DB 125 QYQQYGRSLIEDDTSDFQFVRLVSLVSLAGGDEGNLYDDALVRQDAQDLYEAGEKK 184
 QY 194 WGTDEKFTITFGTSVSHLRKVFQKYMISGFOIETDRTSGNLEOLLAVVKSIRS 253
 DB 185 WGTDEKFTITVLCSSRNRLHLLVDFEYKRISSKDEQSIKSETSGSFEDALLAIVKCMRN 244
 QY 254 IPAYLAETLYAMKAGTDDHTLIIRVWVSRSRSEIDLFNIRKFKRNPATSLYMIKGDTS 313
 DB 245 KSAYFAEKLYKSMKGLGTDDNTLIIRVWVSRAEIDMLDIRAFKRLYKSLYFIKGDTS 304
 QY 314 DYKALLLSGEDD 327
 DB 305 DYKVVLLVLCGGDD 318

RESULT 10
 ANX4_PIG STANDARD; PRT; 318 AA.
 AC P08132; Q29306;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (protein II) (P32.5) (Placental anticoagulant protein I) (PAP-II)
 DE (PP4-X) (35-beta calcimedlin).
 GN ANX4 OR ANX4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestinal epithelium;
 RX MEDLINE=87275850; PubMed=2956093;
 RA Weber K., Johansson N., Plessmann U., Van P.N., Soling H.-D., Ampe C.,
 RA Vandeckerckhove J.;
 RT "The amino acid sequence of protein II and its phosphorylation site
 RT for protein kinase C: the domain structure Ca2+-modulated lipid
 RT binding proteins";
 RL EMBO J. 6:1599-1604(1987).
 RN [2]
 RP SEQUENCE OF 1-126 FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library: analysis of 839 clones";
 RL Mamm. Genome 7:509-517(1996).
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 CC EMBL; F14682; CAA23194.1; -.

DR PIR; A27107; LUPG4.
 DR HSSP; P13214; IANN.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR PRODOM; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
 KW Acetylation.
 FT INIT_MET 0 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION (PROBABLE).
 FT MOD_RES 6 6 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 318 AA; 35697 MW; FA7D9CE2B7C631E8 CRC64;

Query Match 56.1%; Score 921; DB 1; Length 318;
 Best Local Similarity 58.6%; Pred. No. 8.3e-53;
 Matches 184; Conservative 51; Mismatches 79; Indels 0; Gaps 0;

QY 14 GTVDFPPGDERADAETLRKAMKGLTDEESILTLLTSNSNAQRQISAAFKTLFGRDLL 73
 DB 5 GTVKAASGFNAEDAQTLRKAMKGLTDEDAIISVLAYRSTAQROIRTYAKSTIGRDLL 64
 QY 74 DLKSELTKGFEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
 DB 65 DLKSELSCNFEQIVGMMTPVLYDVQELRRAMKAGTDEGLIEILASRTPEELRRIS 124
 QY 134 QYEEYEGSSLEDDVVDTSYGYQRMVLLVLLQANRPDAGIDAEQVQDAQALFQAGEUK 193
 DB 125 QYQQYGRSLIEDDTSDFQFVRLVSLVSLAGGDEGNLYDDALVRQDAQDLYEAGEKK 184
 QY 194 WGTDEKFTITFGTSVSHLRKVFQKYMISGFOIETDRTSGNLEOLLAVVKSIRS 253
 DB 185 WGTDEKFTITVLCSSRNRLHLLVDFEYKRISSKDEQSIKSETSGSFEDALLAIVKCMRN 244
 QY 254 IPAYLAETLYAMKAGTDDHTLIIRVWVSRSRSEIDLFNIRKFKRNPATSLYMIKGDTS 313
 DB 245 KSAYFAEKLYKSMKGLGTDDNTLIIRVWVSRAEIDMLDIRAFKRLYKSLYFIKGDTS 304
 QY 314 DYKALLLSGEDD 327
 DB 305 DYKVVLLVLCGGDD 318

RESULT 11
 ANX6_RAT STANDARD; PRT; 672 AA.
 AC P48037;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
 DE (Calcium-binding protein CATA 65/67).
 GN ANX6 OR ANX6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95331313; PubMed=7607247;
 RA Fan H., Josic D., Lim Y.P., Reutter W.;
 RT "cDNA cloning and tissue-specific regulation of expression of rat
 RT calcium-binding protein 65/67. Identification as a homologue of
 RT annexin VI";
 RL Eur. J. Biochem. 230:741-751(1995).
 CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF

CC CA(2+) FROM INTRACELLULAR STORES.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X86086; CAA60040.1; -
 CC PIR; S65683; S52844.
 CC HSSP; P79134; 1AVC.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 8.
 CC PRINTS; PR00196; ANNEXIN.
 CC ProDom; PD000143; Annexin; 8.
 CC SMART; SM00335; ANX; 8.
 CC PROSITE; PS00223; ANNEXIN; 7.
 CC Annexin; Calcium/phospholipid-binding; Repeat.
 KW INIT_MET 0 BY SIMILARITY.
 FT REPEAT 28 88
 FT ANNEXIN 1.
 FT REPEAT 100 160
 FT ANNEXIN 2.
 FT REPEAT 184 244
 FT ANNEXIN 3.
 FT REPEAT 259 319
 FT ANNEXIN 4.
 FT REPEAT 371 431
 FT ANNEXIN 5.
 FT REPEAT 443 503
 FT ANNEXIN 6.
 FT REPEAT 532 592
 FT ANNEXIN 7.
 FT REPEAT 607 667
 FT ANNEXIN 8.
 SQ SEQUENCE 672 AA; 75622 MW; BBEE798ASCABI511 CRC64;

 Query Match 56.1%; Score 921; DB 1; Length 672;
 Best Local Similarity 58.7%; Pred. No. 2.1e-52;
 Matches 185; Conservative 48; Mismatches 82; Indels 0; Gaps 0;
 13 RGVTFDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAPKTLFGDRL 72
 10 RGVHDFADFDANQDAEALYAMKGFSGDKESILELITSRNKOROEICQSKYSGKDL 69
 73 LDDKSELTKGFEKLIVALKMPSRLYDAYELHAKLGAGTNEKVLTEIIASRTPEELRAI 132
 70 IADLKVELTKGFERLIVLMRPLAYCDAKEIKDAISGIGTDEKCLIEILASKTNEQHOL 129
 133 KQVTEEEYGSSEDDVVDGTSYGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 192
 130 VAAKDAYERLESDDIIGDTSGHFOKMLVLLQGTRENDVYVSEDVQQDLYEAGEL 189
 193 KWTDEEKFIIFGTRSVSHLRKVFDEKYMVTISGFOIETIDRETSGNLEQLLAVKGSIR 252
 190 KWTDEAQFVILGNRSKQHLRVFDEYKLTGTPFIASIRGELSCGDEKMLAVKCI 249
 253 SIPAYLAETLYAMKAGCTDHTLIRVMVSRSEIDLFRKFRKFNATSLYMIKGDTS 312
 250 STPEYFAERLFKAMKGLGTRDNTLIRVMVSRSELDMLDIRFTRKYEKSLYMIKNDTS 309
 313 GDYKALLLLSGDD 327
 310 GEYKALLKLGDD 324

 RESULT 12
 ANX4_MOUSE
 ID ANX4_MOUSE STANDARD; PRT; 318 AA.
 AC P97429;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV).

GN ANX4 OR ANX4.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HeJ;
 RA Sable C.L., Shannon J., Riches D.W.H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U72941; AAB40697.1; -
 CC HSSP; P13214; 1ANN.
 CC MGD; MGI:86030; Anxa4.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 4.
 CC PRINTS; PR00196; ANNEXIN.
 CC ProDom; PD000143; Annexin; 4.
 CC SMART; SM00335; ANX; 4.
 CC PROSITE; PS00223; ANNEXIN; 4.
 CC Annexin; Calcium/phospholipid-binding; Repeat.
 KW INIT_MET 0 BY SIMILARITY.
 FT REPEAT 22 82
 FT ANNEXIN 1.
 FT REPEAT 94 154
 FT ANNEXIN 2.
 FT REPEAT 178 238
 FT ANNEXIN 3.
 FT REPEAT 253 313
 FT ANNEXIN 4.
 SQ SEQUENCE 318 AA; 35858 MW; 53FAC7AD8006BC0D CRC64;

 Query Match 55.8%; Score 916; DB 1; Length 318;
 Best Local Similarity 57.3%; Pred. No. 1.8e-52;
 Matches 180; Conservative 58; Mismatches 76; Indels 0; Gaps 0;
 14 GTVTFDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAPKTLFGDRL 73
 5 GTVKAASGFNATEDAQTLRKAMKGLGTDEDAIIGLILAYNTAQRQEIIRSAVKSTIGDRI 64
 74 DDLKSELTKGFEKLIVALKMPSRLYDAYELHAKLGAGTNEKVLTEIIASRTPEELRAI 133
 65 EDLKSLSNFEQVILGLMTPTVLVDQELRRAMKAGTDEGCLTEILASRTPEEIRIN 124
 134 QWTEEEYGSSEDDVVDGTSYGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGELK 193
 125 QTYOQOYGRSLEEDICSDTSFQFQVIVFLSAGDEGNYLDDALMKDAQOELYEAGER 184
 194 WGTDEEKFIIFGTRSVSHLRKVFDEKYMVTISGFOIETIDRETSGNLEQLLAVKGSIR 253
 185 WGTDEVKFLSILCSNRNHLHVDFEYKRIQKDEQSIKSTSGSFEDALLAVKCMRS 244
 254 IPAYLAETLYAMKAGCTDHTLIRVMVSRSEIDLFRKFRKFNATSLYMIKGDTS 313
 245 KPSYFAERLYKSMKGLGTDNTLIRVMVSRSELDMLDIRASFRKLYGKSLYFIKGDTS 304
 314 DYKALLLLSGDD 327
 305 DYKALLLLSGDD 318

RESULT 13

ANX4_BOVIN
 ID ANX4_BOVIN STANDARD; PRT; 318 AA.
 AC PI3214;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
 DE (PP4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41)
 DE (P33/41).
 DE ANXA4 OR ANX4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89050088; PubMed=2847715;
 RA Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
 RT "Cloning and characterization of a cDNA encoding bovine endonexin
 (chromobindin 4).";
 RL Chromem. Biophys. Res. Commun. 156:660-667(1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96205957; PubMed=8631806;
 RA Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;
 RT "Characterization of carbohydrate-binding protein p33/41: relation
 with annexin IV, molecular basis of the doublet forms (p33 and p41),
 and modulation of the carbohydrate binding activity by
 phospholipids.";
 RL J. Biol. Chem. 271:7679-7685(1996).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA Sutton R.B., Sprang S.R.;
 RL Submitted (SEP-1995) to the PDB data bank.
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RX MEDLINE=98070213; PubMed=9405281;
 RA Zanotti G., Malpeli G., Gliubich F., Folli C., Stoppini M., Olivi L.,
 RA Savola A., Berni R.;
 RT "Structure of the trigonal crystal form of bovine annexin IV.";
 RL Biochem. J. 329:101-106(1998).
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 calcium and phospholipid.
 CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL: M22248; AAA30507.1; -;
 DR EMBL: X13627; CAA31954.1; -;
 DR EMBL: D78178; BAA11243.1; -;
 DR PIR: A31578; LUBO4.
 DR PDB: 1ANN; 29-JAN-96.
 DR PDB: 1AOW; 14-JAN-98.
 DR PDB: 1I4A; 25-APR-01.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4;
 OS Canis familiaris (Dog).

Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.

KW INIT_MET 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 94 94 L -> V (IN REF. 2).
 FT CONFLICT 210 210 E -> K (IN REF. 2).
 FT HELIX 15 26
 FT HELIX 33 40
 FT TURN 41 42
 FT HELIX 45 59
 FT HELIX 63 70
 FT HELIX 73 83
 FT HELIX 86 98
 FT HELIX 105 114
 FT HELIX 117 131
 FT HELIX 135 142
 FT HELIX 145 155
 FT TURN 156 156
 FT TURN 167 182
 FT TURN 183 185
 FT HELIX 189 198
 FT HELIX 201 215
 FT HELIX 219 226
 FT HELIX 229 257
 FT HELIX 264 274
 FT TURN 275 278
 FT HELIX 279 290
 FT HELIX 294 301
 FT HELIX 304 314
 SQ SEQUENCE 318 AA; 35757 MW; 86BDBDF349D774FD CRC64;

Query Match 55.78; Score 914; DB 1; Length 318;

Best Local Similarity 58.08; Pred. No. 2.4e-52;

Matches 182; Conservative 51; Mismatches 81; Indels 0; Gaps 0;

QY 14 GTVTDFPGFDERADAETLRKAMKGLGTDBESILTLTSRNSAQORQISAAFKTLFGRLD 73
 DB 5 GTVKAASGFNAEDAOTLRKAMKGLGTDEDAIINVLAIRSTAQRQEIATYKTTIGRDL 64
 QY 74 DDLKSELTKFKELIALMKPSRLYDAYELKHALKAGTNEKVLTEIIASRTPEELRAIK 133
 DB 65 DDLKSELNFGFEQVILGMPTTVLYDVQELRKAMKAGTDEGCLIEILASRTPEELRIN 124
 QY 134 QYVEEVGSLEDDVVGDTSGYYQRMVLVLOANRDPDAGIDEAOVEQDAQALFOAGELK 193
 DB 125 QYVQYQYGSLEDDIRSDTSFQFQVLSLSAGGRDESNYLDDALMRQDAQDYAGEKK 184
 QY 194 WGTDEKFTITFQTRSVSHLRKVFQKYMITSQFQIEETIDRETSGNLEQLLAVVKSIRS 253
 DB 185 WGTDEVKELTVLCSRNRNHLHVDFEVKRIAKDIEQSIKSETSGSFEDALLAIVKCMRN 244
 QY 254 IPAYLAETLYAMKAGTDDHTLIRVWVSREIDLFNIRKPKNFATSLYSIKGDTSG 313
 DB 245 KSAFAERLYKMKGLGTDDTLIRVWVSRAETDMLDIRANFKRLYKSLYSFKGDTSG 304
 QY 314 DYKALLLLSGDD 327
 DB 305 DYRKVLLILGGDD 318

RESULT 14

ANX4_CANFA
 ID ANX4_CANFA STANDARD; PRT; 318 AA.
 AC P50994;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule
 DE membrane associated protein) (ZAP36).
 DE ANXA4 OR ANX4.
 OS Canis familiaris (Dog).


```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Mongrel; TISSUE=Pancreas;
RA Fukuda S.-I.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D38223; BAA07398.1; -.
CC HSP; P13214; IANN.
CC InterPro; IPR001464; Annexin.
CC Pfam; PF00191; annexin; 4.
CC PRINTS; PR00196; ANNEXIN.
CC ProDom; PD000143; Annexin; 4.
CC SMART; SM00335; ANX; 4.
CC PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INIT MET 0
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
SQ SEQUENCE 318 AA; 35681 MW; 42EF5B89179BA863 CRC64;

Query Match 54.9%; Score 901; DB 1; Length 318;
Best Local Similarity 57.0%; Pred. No. 1.6e-51;
Matches 179; Conservative 54; Mismatches 81; Indels 0; Gaps 0;

QY 14 GTVTDFPGRADAEATLRKAMKGLGTDEESTLLTTSRNSNAQROEISAFAKTLFGRDLL 73
Db ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5 GTVKPASGFSATEDAQLRKAMKGLGTDEDAIISVLAPNTSQREIRTAAYKSTIGRDL 64
QY 74 DDLKSELTKGKEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLPEITIASRTPEELRAIK 133
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
65 DDLKSELGSENFVIGMITPTVLYDVQELRRAMKSGTGDEGLLEILASRTPEELRCIN 124
QY 134 QVYEEYGSLSDDVVGDTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFOAGELK 193
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
125 QTYQYQYGRSLDVIIRSDTSFMFORVLSLGSAGRGDEGNFLDDALMRQDAQDLYAGEKK 184
QY 194 WGTDEKPTITFTGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLBOLLVAVKSTRS 253
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
185 WGTDEKFLTVLCSNRNHLHVDEYKRIQSKDIEQGIKSETSGSFEDALLVAVKMRN 244
QY 254 IPAYLAETLYYAMKAGGDDDETLIRVMVSRSEIDLEFNTRKFRNFATSLYSWKIDTSG 313
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245 KSAYFAERLYKSMKGLGTDNTLIRVMVSRRAIDMDIRESFKRLYGLSLYSFKIGDTS 304
QY 314 DYKRALLLSGDD 327
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
305 DYKRVLLICGDD 318

RESULT 15
ANX6_CHICK STANDARD; PRT; 671 AA.
ID ANX6_CHICK

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AC P51901;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
GN ANXA6 OR ANX6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94092130; PubMed=8267590;
RT "Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthier R.E.;
RT Characterization, cloning and expression of the 67-kDa annexin from
RT chicken growth plate cartilage matrix vesicles.";
RL Biochem. Biophys. Res. Commun. 197:556-561(1993).
CC -!- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF
CC CA(2+) FROM INTRACELLULAR STORES (BY SIMILARITY).
CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: Contains 8 annexin repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S67466; AAB29337.2; -.
CC PIR; JC2029; JC2029.
CC HSP; P79134; IAVC.
CC InterPro; IPR001464; Annexin.
CC Pfam; PF00191; annexin; 8.
CC PRINTS; PR00196; ANNEXIN.
CC ProDom; PD000143; Annexin; 8.
CC SMART; SM00335; ANX; 8.
CC PROSITE; PS00223; ANNEXIN; 5.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT REPEAT 27 87 ANNEXIN 1.
FT REPEAT 99 159 ANNEXIN 2.
FT REPEAT 183 243 ANNEXIN 3.
FT REPEAT 258 318 ANNEXIN 4.
FT REPEAT 370 430 ANNEXIN 5.
FT REPEAT 442 502 ANNEXIN 6.
FT REPEAT 531 592 ANNEXIN 7.
FT REPEAT 607 666 ANNEXIN 8.
SQ SEQUENCE 671 AA; 75218 MW; D0E02F4311A93D98 CRC64;

Query Match 54.6%; Score 896.5; DB 1; Length 671;
Best Local Similarity 57.7%; Pred. No. 7.9e-51;
Matches 184; Conservative 51; Mismatches 83; Indels 1; Gaps 1;

QY 10 QVLRGTVDTPGDFDERADAEATLRKAMKGLGTDEESTLLTTSRNSNAQROEISAFAKTLFG 69
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6 KYIRGSVKDFPGFNASQDADALCNAMKGFSGDKDAILDITSRNKRLEICQAYKSYG 65
QY 70 ROLLDDLSKELTKGKEKLIKVALMKPSRLYDAYELKHALKGAGTNEKVLPEITIASRTPEEL 129
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 KDLIADLKYETKGFERLIVLMRPPAYSDAKEIDKATAGICTDEKCLTEILASRTNOSI 125
QY 130 RAIKQVYEEYGSLSDDVVGDTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFOA 189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
126 HDLVAAVKDAYERDLEADVVGDTSGHFKKMLVLLQAGREEDVYSDVLEVDQADKLEA 185
QY 190 GELKWTDEKPTITFTGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLBOLLVAVK 249
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
186 GELKWTDEAQFIYILGRSRKQHLRWVDFEYLKISGKPIERSIRAEISGDFEKLAVVK 245

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: August 22, 2003, 21:29:22 ; Search time 31.6667 Seconds
(without alignments)
2664.733 Million cell updates/sec

Title: US-09-970-969-6
Perfect score: 1642
Sequence: 1 MACCGHMAQVLRGTVDFP.....KGTSGDYKKALLLLSGEDD 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

1:	sp_archaea.*
2:	sp_bacteria.*
3:	sp_fungi.*
4:	sp_human.*
5:	sp_invertebrate.*
6:	sp_mammal.*
7:	sp_mhc.*
8:	sp_organelle.*
9:	sp_phase.*
10:	sp_plant.*
11:	sp_rodent.*
12:	sp_virus.*
13:	sp_vertebrate.*
14:	sp_unclassified.*
15:	sp_rvirus.*
16:	sp_bacteriap.*
17:	sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1585	96.5	320	4	Q8WV69
2	1475.5	89.9	319	11	Q99LA1
3	1390	84.7	302	11	O70371
4	1042	63.5	317	13	O93445
5	932	56.8	476	11	O8CEX0
6	932	56.8	667	11	O99JX6
7	930	56.6	673	11	O8BS54
8	866	52.7	320	13	O93444
9	856	52.1	508	13	O93447
10	849	51.7	321	13	O90X16
11	847	51.6	503	11	O921F1
12	840.5	51.2	327	11	O8K2N9
13	836.5	50.9	327	6	O95L54
14	822.5	50.1	327	6	O97529
15	799	48.7	323	11	O8C1X9
16	773	47.1	463	11	O922A2

17	770	46.9	463	11	Q8VIN2
18	769	46.8	463	11	Q8BP75
19	752	45.8	324	5	Q9NL61
20	752	45.8	324	5	Q8IGJ8
21	743.5	45.3	301	11	Q921D0
22	729	44.4	323	5	Q9NL59
23	720	43.8	324	5	Q9NG55
24	715	43.5	321	5	Q8WPG9
25	714	43.5	486	5	Q8WPH0
26	709	43.2	497	5	O27512
27	705	42.9	323	5	Q9NG66
28	701	42.7	323	5	Q9NL60
29	701	42.7	324	5	Q969D3
30	694.5	42.3	339	4	Q8TBV2
31	686.5	41.8	339	11	O9C217
32	685	41.7	315	5	O95V57
33	680	41.4	317	11	Q99JG3
34	673	41.0	357	6	Q8MJBS
35	660	40.2	511	5	O9VXG3
36	657	40.0	337	13	O93446
37	655	39.9	322	5	O9VXG4
38	646	39.3	316	13	O98SH7
39	643	39.2	346	6	Q8H2M6
40	629	38.3	314	13	O92128
41	582	35.4	322	5	O27864
42	573.5	34.9	415	11	O8CCV9
43	572	34.8	209	11	O8BSL2
44	540	32.9	317	5	O27473
45	528	32.2	365	5	O9XY89

ALIGNMENTS

RESULT 1
Q8WV69 PRELIMINARY; PRT; 320 AA.
ID Q8WV69;
AC Q8WV69;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Annexin A5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC018671; AAL18671.1;
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 320 AA; 35924 MW; 45FAC411DDBA4D1A CRC64;
Query Match Score 1585; DB 4; Length 320;
Best Local Similarity 99.4%; Pred. No. 1.2e-103;
Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 MAQVLRGTVDFPGFDERADAETLRKAMKGLGTDEESILTLTTSRSNAQROEISAAPFTL 67
Db 1 MAQVLRGTVDFPGFDERADAETLRKAMKGLGTDEESILTLTTSRSNAQROEISAAPFTL 60

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QY 68 FGRDLLDDKSELTGKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
Db 61 FGRDLLDDKSELTGKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
QY 128 ELRAIKQVYEEEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVDDAQLF 187
Db 121 ELRAIKQVYEEEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVDDAQLF 180
QY 188 QAGELKNGTDEEKFIIFGRSVSHLRKVKFDKTYMTISGFOIETIDRETSGNLEQLLAV 247
Db 181 QAGELKNGTDEEKFIIFGRSVSHLRKVKFDKTYMTISGFOIETIDRETSGNLEQLLAV 240
QY 248 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
Db 241 VKSIRSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
QY 308 KGDTSGDYKKALLLSCGDD 327
Db 301 KGDTSGDYKKALLLSCGDD 320

RESULT 2
Q99LAI PRELIMINARY; PRT; 319 AA.
AC Q99LAI;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Annexin A5.
GN ANXA5.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC003716; AAH03716.1; -.
DR HSSP; P14668; ANXA5.
DR MGD; MGI:106008; Anxa5.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 319 AA; 35738 MW; 52E2C7CCEA386917 CRC64;

Query Match 89.9%; Score 1475.5; DB 11; Length 319;
Best Local Similarity 93.4%; Pred. No. 5.8e-96;
Matches 295; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 13 RGTVDTPGFDERADAEATLRKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRDL 72
Db 4 RGTVDTPGFDGRDAEVLKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRDL 63
QY 73 LDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 132
Db 64 VDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIISRTPEELSAI 123
QY 133 KQVYEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVDDAQLFQAGEL 192
Db 124 KQVYEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVDDAQLFQAGEL 183
QY 193 KNGTDEEKFIIFGRSVSHLRKVKFDKTYMTISGFOIETIDRETSGNLEQLLAVVKSIR 252

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Db 184 KNGTDEEKFIIFGRSVSHLRKVKFDKTYMTISGFOIETIDRETSGNLEQLLAVVKSIR 243
QY 253 SIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
Db 244 SIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 303
QY 313 GDYKKALLL-SCGDD 327
Db 304 GDYKKALLLSCGDD 319

RESULT 3
O70371 PRELIMINARY; PRT; 302 AA.
AC O70371;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Lipocortin V (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99262163; PubMed=10329451;
RA Wen Y., Edelman J L., Kang T., Sachs G.;
RT "Lipocortin V may function as a signaling protein for vascular
RT endothelial growth factor receptor-2/Flk-1.";
RL Biochem. Biophys. Res. Commun. 258:713-721(1999).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF051895; AAC06290.1; -.
DR HSSP; P14668; 1A8B.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 3.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
FT NON_TER 302
SQ SEQUENCE 302 AA; 33965 MW; AB9FB40934A3D007 CRC64;

Query Match 84.7%; Score 1390; DB 11; Length 302;
Best Local Similarity 92.0%; Pred. No. 5.6e-90;
Matches 276; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 12 LRGTVDTPGFDERADAEATLRKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRD 71
Db 3 LRGTVDTPGFDGRDAEVLKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRD 62
QY 72 LDDLKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 131
Db 63 LVNDKSELTKFEKLIVALKMPSRLYDAYELKHALKGAGTDEKVLTEIISRTPEELRA 122
QY 132 IKQVYEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVDDAQLFQAGE 191
Db 123 IKQVYEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVDDAQLFQAGE 182
QY 192 LKNGTDEEKFIIFGRSVSHLRKVKFDKTYMTISGFOIETIDRETSGNLEQLLAVVKS 251
Db 183 LKNGTDEEKFIIFGRSVSHLRKVKFDKTYMTISGFOIETIDRETSGNLEQLLAVVKS 242
QY 252 RSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 311
Db 243 RSPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 302

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RESULT 5

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DR PRINTS; PRO0196; ANNEXIN.  
DR ProDom; PD000143; Annexin; 8.  
DR SMART; SM00335; ANX; 8.  
DR PROSITE; PS00223; ANNEXIN; 8.  
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;  
KW Repeat.  
SQ SEQUENCE 667 AA; 75260 MW; 363088A2A55CF34 CRC64;  
  
Query Match 56.8%; Score 932; DB 11; Length 667;  
Best Local Similarity 59.0%; Pred. No. 2.9e-57;  
Matches 186; Conservative 49; Mismatches 80; Indels 0; Gaps 0;  
  
QY 13 RGVTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTLFGRDL 72  
DB 11 RGSVHDFPFEDANQDAEALYTAMKFGSDKESILELITSRNKQRQEQSYKSLYKGLD 70  
  
QY 73 LDDLSKSLTGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPPELRAI 132  
DB 71 IEDLKYELTGKFKERLIVNLMRPLAYCDAKEIKDAISGIGTDEKCLIEILASRTNEQHQL 130  
  
QY 133 KQYEEYGSLSLEDDVVGDTSGYYQRMVLLQANRPDAGIDEAQVEODAAQALFOAGEL 192  
DB 131 VAAYKDAYERDLESIIIGDTSGHFQKMLVLLQGTRENDVYSEDVQDDVQDLYEAGEL 190  
  
QY 193 KNGTDEKFTITFTGTRSVSHLRKRVFDKYMFTISGFQIEETIDRTSGNLEQLLAVVKSIR 252  
DB 191 KNGTDEAQFIYILGNRSKQHLRLVDFEYLKTKGPKTEASIRGSLSGDFEKLMLAVVKCIR 250  
  
QY 253 SIPAYLAETLYYAMKAGCTDDHTLIRVMYSRSEIDLFNIRKFKRKNPATSLYSIMKGDTS 312  
DB 251 STPEYFAERLFKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTPRYEKSLYSIMKNDTS 310  
  
QY 313 GDYKALLLSGGDD 327  
DB 311 GEYKALLKLCGGDD 325  
  
RESULT 7  
Q8BSS4  
ID Q8BSS4 PRELIMINARY; PRT; 673 AA.  
AC Q8BSS4;  
DT 01-MAR-2003 (TEMBLrel. 23, Created)  
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Annexin A6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The PANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002).  
DR EMBL; AK030728; BAC27101.1; -  
SQ SEQUENCE 673 AA; 75885 MW; DCC5FC56CBD88809 CRC64;  
  
Query Match 56.6%; Score 930; DB 11; Length 673;  
Best Local Similarity 59.0%; Pred. No. 4.1e-57;  
Matches 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;  
  
QY 13 RGVTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTLFGRDL 72  
DB 11 RGSVHDFPFEDANQDAEALYTAMKFGSDKESILELITSRNKQRQEQSYKSLYKGLD 70  
  
QY 73 LDDLSKSLTGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPPELRAI 132  
DB 71 IEDLKYELTGKFKERLIVNLMRPLAYCDAKEIKDAISGIGTDEKCLIEILASRTNEQHQL 130
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QY 133 KQYEEYGSLSLEDDVVGDTSGYYQRMVLLQANRPDAGIDEAQVEODAAQALFOAGEL 192  
DB 131 VAAYKDAYERDLESIIIGDTSGHFQKMLVLLQGTRENDVYSEDVQDDVQDLYEAGEL 190  
  
QY 193 KNGTDEKFTITFTGTRSVSHLRKRVFDKYMFTISGFQIEETIDRTSGNLEQLLAVVKSIR 252  
DB 191 KNGTDEAQFIYILGNRSKQHLRLVDFEYLKTKGPKTEASIRGSLSGDFEKLMLAVVKCIR 250  
  
QY 253 SIPAYLAETLYYAMKAGCTDDHTLIRVMYSRSEIDLFNIRKFKRKNPATSLYSIMKGDTS 312  
DB 251 STPEYFAERLFKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTPRYEKSLYSIMKNDTS 310  
  
QY 313 GDYKALLLSGGDD 327  
DB 311 GEYKALLKLCGGDD 325  
  
RESULT 8  
O93444  
ID O93444 PRELIMINARY; PRT; 320 AA.  
AC O93444;  
DT 01-NOV-1998 (TEMBLrel. 08, Created)  
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Annexin max1.  
OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
OX NCBI_TaxID=8090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99025617; PubMed=9809745;  
RA Osterloh D., Wittbrodt J., Gerke V.;  
RT "Characterization and developmentally regulated expression of four  
RT annexins in the killifish medaka."  
RL DNA Cell Biol. 17:835-847(1998).  
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR  
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.  
DR EMBL; Y11252; CAA72122.1; -  
DR HSSP; P13214; 1ANN.  
DR InterPro; IPR001464; Annexin.  
DR Pfam; PF00191; annexin; 4.  
DR PRINTS; PRO0196; ANNEXIN.  
DR ProDom; PD000143; Annexin; 4.  
DR SMART; SM00335; ANX; 4.  
DR PROSITE; PS00223; ANNEXIN; 4.  
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;  
KW Repeat.  
SQ SEQUENCE 320 AA; 35424 MW; D2ED32C8676777D CRC64;  
  
Query Match 52.7%; Score 866; DB 13; Length 320;  
Best Local Similarity 54.5%; Pred. No. 4.5e-53;  
Matches 170; Conservative 59; Mismatches 83; Indels 0; Gaps 0;  
  
QY 13 RGVTVDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAAFKTLFGRDL 72  
DB 7 RGVTVASGFNPDQAKLREAMKAGTDEAAIKYLAHRTIAORIKRAYKQSVGKDL 66  
  
QY 73 LDDLSKSLTGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPPELRAI 132  
DB 67 AEDLSSELGSHQSVVGLLMPAPYDAYELKAMKAGTGAECLEIDILLASNSNEMAI 126  
  
QY 133 KQYEEYGSLSLEDDVVGDTSGYYQRMVLLQANRPDAGIDEAQVEODAAQALFOAGEL 192  
DB 127 NEVYKKEYKTLDEAVCGDTSCMFQKRLVSLTAGRDESDKVDQAQVAKDAKIDPEAGA 186  
  
QY 193 KNGTDEKFTITFTGTRSVSHLRKRVFDKYMFTISGFQIEETIDRTSGNLEQLLAVVKSIR 252  
DB 187 RWTGDEVKFLTVLCVRRNRHLLRVDFEYKKIKSKROIEDSIKREMSGSLEDVFLATVYKCLR 246
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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to annexin A11.
GN ANXA11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC012875; AHI12875.1; -.
DR MGD; MGI:108481; Anx11.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 503 AA; 54079 MW; 33F3471BE21A0D32 CRC64;

Query Match 51.6%; Score 847; DB 11; Length 503;
Best Local Similarity 53.7%; Pred. No. 1.9e-51;
Matches 169; Conservative 59; Mismatches 87; Indels 0; Gaps 0;

QY 13 RGTVTDFPGFDERADAEIRKAMKGLGTDESLTLTSSNAOROEISAFAKTLFGDRL 72
DB 189 RGTITAAGFDPLRDAEVLKAMKGFCTDEQAIIDCLGRSNKQRQIILSFATYAGKDL 248
QY 73 LDDLKSELGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAI 132
DB 249 IKDLKSELGKFKELVALMKPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAI 132
QY 133 KOVVEEYGSLEDDVGGTSGYQYRMVLVLLQANRDPDAGIDEAOEQDAQALFOAGEL 192
DB 309 SRAKTEFQKLEEARISDTSGHGFQRLILSLSGNDESTNVDMSLVQRVDVQELYAAGEN 368
QY 193 KMTDEKFTITPTGTRSVSHLRKVFDPKMTISGFOIETIDRTSGNLEOLLVAVKRSIR 252
DB 369 RLGTDESKENAILCSRAHLVAVFNEYQYQRTGDIKSIKREMSGDLQEGMLAVYKCLK 428
QY 253 SIPAYLAETLYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKFKNFATSLYSMIKGTDS 312
DB 429 NTPAPFAERLKNAMRGAGTKDRTLIRIMVSRSELDLDIRAEYKRMKGKSLYHDITGDS 488
QY 313 GDYKKAALLLSGDD 327
DB 489 GYRKILLKICGND 503

RESULT 12
Q8K2N9 PRELIMINARY; PRT; 327 AA.
AC Q8K2N9;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to annexin A8.
GN ANXA8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
```

```
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030407; AAH30407.1; -.
DR MGD; MGI:1201374; Anxa8.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
SQ SEQUENCE 327 AA; 36724 MW; 56DB9CFAFA8C2B21 CRC64;

Query Match 51.2%; Score 840.5; DB 11; Length 327;
Best Local Similarity 57.8%; Pred. No. 2.9e-51;
Matches 177; Conservative 49; Mismatches 79; Indels 1; Gaps 1;

QY 22 FDERADAEIRKAMKGLGTDESLTLTSSNAOROEISAFAKTLFGDRLDLKSELT 81
DB 21 FNPDPDAETLYKAMKIGTNEQAIIDVLTFRSNVQRQIAKSFKAQFGKDLTETLKSELS 80
QY 82 GKFEKLIVALKMPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAIKOVVEEY 141
DB 81 GKFERLIVALKMPSRLYDAYELKHALKGAGTNEKVLFEIIRASRTPEELRAIKOVVEEY 140
QY 142 SSLEDDVGGTSGYQYRMVLVLLQANRDPDAGIDEAOEQDAQALFOAGELKMGTDDEK 200
DB 141 STLEEDIQGTSGYLERILVCLLQGSRRDVSFGVDFVGLVQDAQALHEAGEKINGTDEM 200
QY 201 FITIFGTRSVSHLRKVFDPKMTISGFOIETIDRTSGNLEOLLVAVKRSIRPAYLA 260
DB 201 FITILCTRATHLRVFEYEEKIANKCIEDISIKSGSLEEAHLTVVKTRNVSYFAE 260
QY 261 TLYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKFKNFATSLYSMIKGTDSGYKKAALL 320
DB 261 RLYAMKAGCTDDHTLIRVMVSRSEIDLNFIRKFKNFATSLYSMIKGTDSGYKKAALL 320
QY 321 LLSGED 326
DB 321 NLVGTD 326

RESULT 13
Q9SL54 PRELIMINARY; PRT; 327 AA.
AC Q9SL54;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Annexin VIII.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA White A.H., Wallis G.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF417637; AAL13308.1; -.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 327 AA; 36787 MW; 2EB178E13738CF22 CRC64;

Query Match 50.9%; Score 836.5; DB 6; Length 327;
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Db	14	TVKGSFHNVPVDAETLYKAWKGIGTNEQATIDVLTRSSAQROOIAKSFQAQSGSLUTE	73
Qy	75	DLKSELTKPEKITVALMKPSRLSDAYDELHALKGAGTNKVLTEITASRTPPEELRAIKQ	134
Db	74	TLAKSELGKERLIVALMYPYRYEAKELHDAMKGLGTKEGVITEILASRTKNLOLEIMK	133
Qy	135	VYEIEYGSSLEDVVGDTSGYQRMLVYLQANRDPDAG-IDEAQVEODAAQLFOAGELK	193
Db	134	A YEEDYGSSLEEDIQADTSYLERILVCLQGSRDDVTGFDPGLAQLDAQDLYAAGEKI	193
Qy	194	WGTDDEERFIITFGRRSHLRKKVRPKMYMTISGFOIETTIDRETSGNLEOLLAVVKSR	253
Db	194	CGTDEMKAFFILCTRSARHLMRVEEYEKIANKSIEDSIKETHGSLEEAMLTIVKCPRN	253
Qy	254	IPAYLAETLYAMKGAQTDDHTLLIRVMVSRESEIDLFNIRKFRKNFATSLSYMKIGDTSG	313
Db	254	LHCYFAERLHYAMKGAQTLDGTLIRNIVRSREIDNLNLIKGHYKMYKGTLSMSMEDTSG	313
Qy	314	DYKALLLSGED	326
Db	314	DYKNALLSLVGSD	326

RESULT 15
QBCLX9
DN ORC1X9
DBPRTIMINARY.
DPT. 323 BA

DT	01-MAR-2003 (TremBurel. 23, Created)
DT	01-MAR-2003 (TremBurel. 23, Last sequence update)
DT	01-MAR-2003 (TremBurel. 23, Last annotation update)
DE	Annexin A3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	NCBI_TaxID=10090;
RX	[1]
RQ	SEQUENCE FROM N.A.
RP	TISSUE=Kidney;
RC	MEDLINE=22354683; Pubmed=12466851;
RX	The FANTOM Consortium,
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RL	Nature 420:563-573(2002).
DR	EMBL; AK090055; BAC41070.1; ..
SQ	SEQUENCE 323 AA; 36356 MW; 9F69F57BCFAC6A85 CRC64;
Query Match 48.7%; Score 799; DB 11; Length 323;	
Best Local Similarity 49.2%; Pred. No. 2.4e-48;	
Matches 155; Conservative 63; Mismatches 97; Indels 0; Gaps 0;	
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Dd	9 RGITKPYGSPSVDAAEAIKRIAGLTGTDKTLNLITLTSRNAQROLIAKYQAAYEQEL 68 : : : : : : : : : : :
Qy	73 LDDLKSELTGKFKEKLIVALKMPSRLYDAYELKHAKLGAGTKNEKVUTEIIASRTPPEELRAI 132 : : : : : : : : : : : :
Dd	69 KDDLKGLDSGHFEHVMVALVAPALFAKOLUKSMKGTTGTDEDALIELLTRSSRMKEI 128 : : : : : : : : : : : :
Qy	133 KVYYEEYGSLDDVVYGDTSYGYORMLVLQLANRPDAGIDEAQVSDACAQFOACEL 192 : : : : : : : : : : :
Dd	129 SQAYTYVKSLGGDDISSFTSGDFRKALLTLADGRDES�KVDHLAKDKQILYNAGEN 188 : : : : : : : : : : :
Qy	193 KWGTDEKFTITIGTRSVSHLRKVFDDKYMTISGFQIEETIDRETSGNLEQQLLAVVKSIR 252 : : : : : : : : : : : :
Dd	189 KWGTDEKFTEVLCRFPQKLFTFDEYRNITSQKDIEDISKGLSGHPEDILLATVHCAR 248 : : : : : : : : : : : :
Qy	253 SIPAYLAETLYAMKAGTDDHTLIIRVMVSRSSETDLFNIRKEEFKNFATSLSYMSKTGDS 312 : : : : : : : : : : :
Dd	249 NTPAFLAEERHOALKGAGTDEFTLNIRIMVSKSEIDLDIRHEFKKHGYGLSYLSIQSDTS 308 : : : : : : : : : : : :
Qy	313 GDYKKALLLSGEDD 327 : : : : : : : : : : : :

Db 309 GDYRTVLLKIGEDD 323

Search completed: August 22, 2003, 21:35:26
Job time : 32.6667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:48:20 ; Search time 1675.67 Seconds
(without alignments)
14228.779 Million cell updates/sec

Title: US-09-970-969-5

Perfect score: 981

Sequence: 1 atggcatgtgcgcgtca.....tgctcccgagaagatgac 981

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estor:*

6: em_estpi:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hct:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_plo:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957.8	97.6	1602	11	BC032093 Homo sapi
2	874.4	89.1	1076	12	BM464122 AGNCOURT
3	868.2	88.5	1071	13	EX441583
4	858.4	87.5	1201	13	EX379189

ALIGNMENTS

RESULT 1	BC032093	Homo sapiens, clone IMAGE:3924873, mRNA.	1602 bp	linear	HTC 06-JUN-2002
LOCUS	BC032093				
DEFINITION	BC032093				
ACCESSION	BC032093.1	GI:21327830			
VERSION	HTC				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REMARK					
COMMENT					

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK plate: 26 Row: f Column: 11
 This clone has the following problem: no 5' EST match.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="3924873"
 /tissue_type="Skin, melanotic melanoma."
 /clone_lib="NIH_MGC_72"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 449 a 337 c 364 g 452 t

BASE COUNT
 ORIGIN

Query Match 97.6%; Score 957.8; DB 11; Length 1602;
 Best Local Similarity 99.8%; Pred. No. 6.9e-246;
 Matches 959; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTGTGAGCGGCTGA 80
 DB 154 TATGGCACAGGTTCTCAGAGCAGCTGTGACTGACTTCCCTGGATTGTGAGCGGCTGA 213

QY 81 TCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCTGTAC 140
 DB 214 TCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGCATCTGTAC 273

QY 141 TCTGTTGACATCCCGAAGTAAGTCTCAGCGCCAGGAAATCTCGGAGCTTTAAGACTCT 200
 DB 274 TCTGTTGACATCCCGAAGTAAGTCTCAGCGCCAGGAAATCTCTCGAGCTTTAAGACTCT 333

QY 201 GTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAAT 260
 DB 334 GTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAAT 393

QY 261 AATTGTGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGACCTTT 320
 DB 394 AATTGTGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGACCTTT 453

QY 321 GAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGA 380
 DB 454 GAAGGAGCTGGAACAAATGAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGA 513

QY 381 AGAACTGAGAGCCATCAACAAAGTTTATGAAGAAATATGCTCAAGCTTGAAGATGA 440
 DB 514 AGAACTGAGAGCCATCAACAAAGTTTATGAAGAAATATGCTCAAGCTTGAAGATGA 573

QY 441 CTTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTCTCTCTTCAGGCTAA 500
 DB 574 CTTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTCTCTCTTCAGGCTAA 633

QY 501 CAGAGACCTGTGCTGGAATGATGAAGTCAAGTGAACAGATGCTCAGGCTTTATT 560
 DB 634 CAGAGACCTGTGCTGGAATGATGAAGTCAAGTGAACAGATGCTCAGGCTTTATT 693

QY 561 TCAGGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAC 620
 DB 694 TCAGGCTGGAGAACTTAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAC 753

QY 621 AGAAGTGTCTCATTTGAGAAAGGTTTTCAGAAAGTACATGACTATATCAGGATTC 680
 DB 754 AGAAGTGTCTCATTTGAGAAAGGTTTTCAGAAAGTACATGACTATATCAGGATTC 813

QY 681 AATTGAGGAACCATTCACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTGGCTGT 740

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 QY 741 TGTGAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCTCTATTATGCTATGAA 800
 DB 874 TGTGAATCTATTTCGAAGTATACCTGCCTACCTTGCAGAGACCTCTATTATGCTATGAA 933

QY 801 GGGAGCTGGGACAGATGATCATACCTCATCAGAGTATCGTGGTTCCAGGAGTGAGATTGA 860
 DB 934 GGGAGCTGGGACAGATGATCATACCTCATCAGAGTATCGTGGTTCCAGGAGTGAGATTGA 993

QY 861 TCTGTTTAACTACATCAGGAAGGAGTTAGGAAGAAATTTGGCAGCTCTCTTTATTCATGAT 920
 DB 994 TCTGTTTAACTACATCAGGAAGGAGTTAGGAAGAAATTTGGCAGCTCTCTTTATTCATGAT 1053

QY 921 TAAGGAGATACATCTGGGAGCTATAGAAAGTCTTCTGCTGCTCTCCGGAGAAAGATGA 980
 DB 1054 TAAGGAGATACATCTGGGAGCTATAGAAAGTCTTCTGCTGCTCTGCGAGAAAGATGA 1113

QY 981 C 981
 DB 1114 C 1114

RESULT 2

BM464122

LOCUS

DEFINITION

BM464122

ACCESSION

VERSION

SOURCE

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1076)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: the I.M.A.G.E. Consortium (LLNL)
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL2235 row: n column: 14
 High quality sequence stop: 708.

FEATURES

source

Location/Qualifiers

1..1076

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_image="5540173"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Noli; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT

ORIGIN

296 a 229 c 273 g 274 t 4 others
 Query Match 89.1%; Score 874.4; DB 12; Length 1076;
 Best Local Similarity 96.9%; Pred. No. 1.4e-223;
 Matches 932; Conservative 0; Mismatches 25; Indels 5; Gaps 4;

QY

22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 81

DB

105 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGAGCGGCTGAT 164

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Qy 82 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGACACAGATGAGAGAGCATCCTGACT 141
Dy 165 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGACACAGATGAGAGAGCATCCTGACT 224
Qy 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCAGAGAAATCTCTGAGCTTTTAAGACTCTG 201
Dy 225 CTGTTGACATCCCGAAGTAATGCTCAGCGCAGAGAAATCTCTGAGCTTTTAAGACTCTG 284
Qy 202 TTTGGCAGGATCTCTCGGATGACCTGAAATCAGAACTAACTGAAATTTGAAAAATTA 261
Dy 285 TTTGGCAGGATCTCTCGGATGACCTGAAATCAGAACTAACTGAAATTTGAAAAATTA 344
Qy 262 ATTGTGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTCTG 321
Dy 345 ATTGTGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCTCTG 404
Qy 322 AAGGAGCTGGAACAAATGAAAGAGTACTGACACAAATATTGCTTCAAGGACACCTGAA 381
Dy 405 AAGGAGCTGGAACAAATGAAAGAGTACTGACACAAATATTGCTTCAAGGACACCTGAA 464
Qy 382 GAATGAGAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 441
Dy 465 GAATGAGAGCCATCAACAAAGTTTATGAAGAAATATGGCTCAAGCTGGAAGATGAC 524
Qy 442 GTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTTCTCTTCAGGCTAAAC 501
Dy 525 GTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTTCTCTTCAGGCTAAAC 584
Qy 502 AGACACCTGATGCTGAATGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 561
Dy 585 AGACACCTGATGCTGAATGATGAAGCTCAAGTTGAACAAAGATGCTCAGGCTTTATTT 644
Qy 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAACAAAGTTTATCACCATCTTTGGAAAC 621
Dy 645 CAGGCTGGAGAACTTAAATGGGGACAGATGAACAAAGTTTATCACCATCTTTGGAAAC 704
Qy 622 CGAAGTGTCTCATTTGAGAAAGGTTTGGACAAAGTACATGACTATATCAGGATTTCAA 681
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Dy 765 ATTGAGAAACCATGACCGGAGACTCTGGGAAATTTAGAGCAACTACTCCTTGCTGNT 824
Qy 742 GTGAAATCTATTGCAAGTATACCTGCTACCTTCAGAGACCCCTTATATGCTATGAAG 801
Dy 825 GTGAAATCTATTGCAAGTATACCTGCTACCTTCAGAGACCCCTTATATGCTATGAAG 884
Qy 802 GGAGCTGGGACAGATGATACCTCATCAGAGCTCATGCTTTT-CCAGGAGTGAAGTTGA 860
Dy 885 GGAGCTGGGACAGATGATACCTCATCAGAGCTCATGCTTTTCCAGNAGTGAAGTTGA 944
Qy 861 TCTGTTTAAATCA-GGAAGAGTTTGAAGAAATTTTG-CCACCTCTCTTTATTCATG 918
Dy 945 TCTGTTTAAATCAAGGAGAAATTTAGGAAGAAATTTTGCCACCTCTCTTTAAATCCCTG 1004
Qy 919 ATTAAGGAGATACATCTGGGG--ACTATGAAGAGCTCTTCTGCTGCTCCGAGAGAG 976
Dy 1005 ATTAAGGAGAAATCTCTGGGGGACTTATGAAGAAAGTTCTTCGGGGGCTCTGGGGGAAA 1064
Qy 977 AT 978
Dy 1065 AT 1066
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BX441583
LOCUS BX441583 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF019VK11 5-PRIME, mRNA sequence.
ACCESSION BX441583
VERSION BX441583.1 GI:30775951
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1071)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DF019AF06QPl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF019AF06QPl.
FEATURES
Location/Qualifiers
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/clone="CS0DF019VK11"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 291 a 229 c 274 g 272 t 5 others
ORIGIN
Query Match 88.5%; Score 868.2; DB 13; Length 1071;
Best Local Similarity 99.3%; Pred. No. 6.4e-222;
Matches 870; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 21 TATGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGACGGGCTGA 80
Dy 188 TATGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTGATGACGGGCTGA 247
Qy 81 TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGAC 140
Dy 248 TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGACATCCTGAC 307
Qy 141 TCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGAAATCTCTCAGCTTTTAAGACTCT 200
Dy 308 TCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGAAATCTCTCAGCTTTTAAGACTCT 367
Qy 201 GTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAAT 260
Dy 368 GTTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAAT 427
Qy 261 AATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGACATGAACATGCCCT 320
Dy 428 AATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTATGACATGAACATGCCCT 487
Qy 321 GAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGA 380
Dy 488 GAAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGA 547
Qy 381 AGAACTGAGAGCCATCAACAAAGTTTATGAAGAAATATATGCTTCAAGCCCTGGAAGATGA 440
Dy 548 AGAACTGAGAGCCATCAACAAAGTTTATGAAGAAATATATGCTTCAAGCCCTGGAAGATGA 607
Qy 441 CGTGGTGGGACACTTCAAGGCTACTACCAGCGGATGTTGGTGGTCTCTCCTTCAGGCTAA 500
Dy 608 CGTGGTGGGACACTTCAAGGCTACTACCAGCGGATGTTGGTGGTCTCTCCTTCAGGCTAA 667
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QY 501 CAGAGACCTGATGCTGGAATTTGATGAAGTCAAGTGAACAGATGCTCAGGCTTTATT 560
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 QY 561 TCAGGCTGGAGAACTTAATAGGGGACAGATGAAGAAAGTTATCACCATCTTTGGAA 620
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 Db 728 TCAGGCTGGAGAACTTAATAGGGGACAGATGAAGAAAGTTATCACCATCTTTGGAA 787
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 QY 621 ACGAAGTGTGCTCATTTGAGAAAGTGTTTGCACAGTACATGACTATATCAGGATTCA 680
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 Db 788 ACGAAGTGTGCTCATTTGAGAAAGTGTTTGCACAGTACATGACTATATCAGGATTCA 847
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 QY 681 AATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTTAGACCAACTACTCTTGGCTG 740
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 Db 848 AATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTTAGACCAACTACTCTTGGCTG 907
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 QY 741 TGTGAATCTATTCGAAGTATACCTGCTTACCTTGCAGAGACCTCTATATGCTATGAA 800
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 Db 908 TGTGAATCTATTCGAAGTATACCTGCTTACCTTGCAGAGACCTCTATATGCTATGAA 967
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 QY 801 GGGAGCTGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGA 860
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 Db 968 GGGAGCTGGACAGATGATCATACCTCATCAGAGTCATGTTTCCAGGAGTGAGATTGA 1027
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 Db 1028 TCTGTTTACATCAGAGAGGAGTTTATAGGAAGATTT 1063
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RESULT 4

BX379189

LOCUS

DEFINITION

clone CS0DI030YL18 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX379189 1201 bp mRNA linear EST 08-MAY-2003
 BX379189 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI030YL18 5-PRIME, mRNA sequence.
 BX379189
 EST. GI:30446777
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2353.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DI030DF090P1&cluster=2353.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DI030DF090P1.
 Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI030YL18"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /cnote="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 5 vector. Library was normalized."
 307 a 263 c 255 g 294 t 42 others

FEATURES

source

Query Match 87.5%; Score 858.4; DB 13; Length 1201;
 Best Local Similarity 94.9%; Pred. No. 2.9e-219;
 Matches 892; Conservative 15; Mismatches 27; Indels 6; Gaps 2;
 QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGGATTTGATGAGCGGCTGAT 81
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 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141
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 Db 263 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 322
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 QY 142 CTGTTGACATCCGGAAGTAACTCTCAGCCGAGGAAATCTCTCCAGCTTTTAAAGACTCTG 201
 |||||
 Db 323 CTGTTGACATCCGGAAGTAACTCTCAGCCGAGGAAATCTCTCCAGCTTTTAAAGACTCTG 382
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 QY 202 TTTGGCAGGATCTTCTGATGACCTGAAATCAGAACTAACTGGGAAATTTGAAAATTTA 261
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 Db 383 TTTGGCAGGATCTTCTGATGACCTGAAATCAGAACTAACTGGGAAATTTGAAAATTTA 442
 |||||
 QY 262 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTTG 321
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 Db 443 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTATGAACCTGAAACATGCTTTG 502
 |||||
 QY 322 AAGGAGCTGGGAAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 |||||
 Db 503 AAGGAGCTGGGAAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 562
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 QY 382 GAACCTGAGAGCCATCAACAACTTTATGAAGAAATATGCTCAGCCGAGGATGAC 441
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 Db 563 GAACCTGAGAGCCATCAACAACTTTATGAAGAAATATGCTCAGCCGAGGATGAC 622
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 QY 442 GTGGTGGGGGACACTTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 501
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 Db 623 GTGGTGGGGGACACTTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 582
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 QY 502 AGAGACCTTGATGCTGGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
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 QY 742 GTGAAATCTATTTCGAGATATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 801
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 QY 802 CGAGCTGGGACAGATGATCATACCTCTCATCAGATGATGTTTCCAGGAGTGAAGATTGAT 861
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 Db 983 GGAGCTGGGACAGATGATCATACCTCTCAGCAGAGTHATGKTTTCHAGGAGTGAAGATTGAT 1042
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 QY 862 CTGTTTAACTCAGGAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTTCCATGATT 921
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 Db 1043 CTGTTTAACTCAGGAAGGAGTTTAGGAAGAAATTTGCCACCTCTCTTTATTTCCATGATT 1099
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 QY 922 AAGGAGATACATCTGGGCACTTATGAAGCTCTTCTGCG 961
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 Db 1100 AAGGGAANA---YTKGGGCGWATAAAAACCTCTCKKSC 1136
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RESULT 5

BX417429

LOCUS

DEFINITION

BX417429 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009Y116
 linear EST 13-MAY-2003

5-PRIME, mRNA sequence.
 BX417429
 VERSION
 BX417429.1 GI:30654405
 EST.
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2353.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DE009BE080P1&cluster=2353.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DE009BE080P1.
 Location/Qualifiers
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DE009Y116"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT.6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT 310 a 260 c 297 g 295 t 39 others
 ORIGIN
 Query Match 87.2%; Score 855.2; DB 13; Length 1201;
 Best Local Similarity 95.0%; Pred. No. 2.1e-218;
 Matches 893; Conservative 10; Mismatches 30; Indels 7; Gaps 2:
 QY 22 ATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCTCGGATTTGATGCGGGCTGAT 81
 DB 206 ATGGCAGAGTTCTCAGAGGCACTGTGACTGACTTCCTCGGATTTGATGCGGGCTGAT 265
 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGCCACAGATGAGGAGAGCATCCTGACT 141
 DB 266 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTGGCCACAGATGAGGAGAGCATCCTGACT 325
 QY 142 CTGTTGACATCCGGAAGTAAGTCTCAGCGCCAGGAAATCTCGAGCTTTTAAGACACTG 201
 DB 326 CTGTTGACATCCGGAAGTAAGTCTCAGCGCCAGGAAATCTCGAGCTTTTAAGACACTG 385
 QY 202 TTGGCAGGAGTCTCTGATGACCTGAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
 DB 386 TTGGCAGGAGTCTCTGATGACCTGAATCAGAACTAACTGGAATAATTTGAAAAATTA 445
 QY 262 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACCTGAACATCGCCTG 321
 DB 446 ATTGTGGCTCTGATGAACCCCTCTCGGCTTTATGATGCTTTATGAACCTGAACATCGCCTG 505
 QY 322 AGGGAGCTGGACAAATGAAAAAGTACTGACAGAAATATTTGCTTCAAGGACACCTGAA 381
 DB 506 AGGGAGCTGGACAAATGAAAAAGTACTGACAGAAATATTTGCTTCAAGGACACCTGAA 565
 QY 382 GAATCAGAGCCATCAACAAAGTTTATGAAGAAGTAATGCTCAAGCTCGAAGATGAC 441
 DB 566 GAATCAGAGCCATCAACAAAGTTTATGAAGAAGTAATGCTCAAGCTCGAAGATGAC 625
 QY 442 GTGGTGGGGACACTTCAGGCTACTACCGAGGAGTGTGGTGGTCTCTTCAGGCTAAC 501

QY 442 GTGGTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTCTCTTCAGGCTAAC 501
 DB 628 GTGGTGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGTCTCTTCAGGCTAAC 687
 QY 502 AGAGACCCGTGATGCTGGAATGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
 DB 688 AGAGACCCGTGATGCTGGAATGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 747
 QY 562 CAGGCTGGAGAACTTAATGSGGGACAGATGAAGAAAGTTTATCACCATCTTTGGGAACA 621
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 QY 622 CGAAGTGTGCTCATTTGAGAAAGGTGTTGACAAGTACATGACTATATACAGATTTCAA 681
 DB 808 CGAAGTGTGCTCATTTGAGAAAGGTGTTGACAAGTACATGACTATATACAGATTTCAA 867
 QY 682 ATTGAGGAAACCATGACCGGAGACTTCGCGCAATTTAGAGCAACTACTCTTCGCTGTT 741
 DB 868 ATTGAGGAAACCATGACCGGAGACTTCGCGCAATTTAGAGCAACTACTCTTCGCTGTT 927
 QY 742 GTGAAATCTATTGGAAGTATACCTGCTTACCTTGACAGACCCCTTATTATGCTATGAAG 801
 DB 928 GTGAAATCTATTGGAAGTATACCTGCTTACCTTGACAGACCCCTTATTATGCTATGAAG 987
 QY 802 GGAGCTGGGACAGATGATACCCCTCATCAGAGTCAATGTTTCCAGGAGTGAGATGAT 861
 DB 988 GGAGCTGGGACAGATGATACCCCTCATCAGAGTCAATGTTTCCAGGAGTGAGATGAT 1047
 QY 862 CTGTTTACATCAG 876
 DB 1048 CTGATWACATCAG 1062

RESULT 8

LOCUS BX379218 1201 bp mRNA linear EST 08-MAY-2003
 DEFINITION BX379218 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1031YA16 5-PRIME, mRNA sequence.

ACCESSION BX379218
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li W.B., Gruber C., Jessee J. and Polayes D.
 Full-length cDNA libraries and normalization
 Unpublished

COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2353.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1031BA08QP1&cluster=2353.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1031BA08QP1.
 Location/Qualifiers
 1..1201

FEATURES

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 /note="1st strand cDNA was primed with a NotI-oligo(dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 319 a 257 c 291 g 296 t 38 others
 ORIGIN
 Query Match 85.6%; Score 839.6; DB 13; Length 1201;
 Best Local Similarity 95.3%; Pred. No. 3.3e-214;
 Matches 896; Conservative 11; Mismatches 25; Indels 8; Gaps 4;
 QY 22 ATGCACAGGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
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 DB 238 GCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGATCCTGACT 297
 QY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201
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 QY 202 TTTGCGAGGATCTTCTGGATGACCTGAAATCAGAACTAACCTGGAATTTGAAAAATTA 261
 DB 358 TTTGCGAGGATCTTCTGGATGACCTGAAATCAGAACTAACCTGGAATTTGAAAAATTA 417
 QY 262 ATTGCGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGAACATGCCCTTG 321
 DB 418 ATTGCGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACATGAACATGCCCTTG 477
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 DB 478 AAGGAGCTGGAAACAATGAAGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 537
 QY 382 GAAGCTGAGAGCCATCAAAACAAGTTTATGAAGAAGAAATATGGCTCAAGCTTGAAGATGAC 441
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 QY 442 GTGTTGGGGACACTTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 501
 DB 598 GTGTTGGGGACACTTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTCAGGCTAAC 657
 QY 502 AGAGACCTGTGCTGGAATGATCAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
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 DB 956 CGAGCTGGACAGAAAAACATACCCMAATCAGAGTCATGGGTTCCAGGAGTGAGATGAT 1015
 QY 862 CTGTTTAAATCAGGAAGGAGTTTAGGAAGAAATTTGGCCACCTCTCTTTTATTCATGATT 921
 DB 1016 CTGTTTAAATCAGGAAGGAGTTTAGGAAGATTTTGGCCCTCTC---TTTATCCAGATT 1072
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 DB 1073 ARGGGGAAATCT---GGGGTATAGAAACCCCTCTKCTGC 1109

RESULT 9

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AL542496      1201 bp      mRNA      linear      EST 12-MAY-2003
LOCUS      AL542496 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012Y114
DEFINITION      5-PRIME, mRNA sequence.
ACCESSION      AL542496
VERSION      AL542496.2 GI:30547699
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1201)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT      On Feb 15, 2001 this sequence version replaced gi:12874598.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE012BE07QP1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE012BE07QP1.
FEATURES
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        /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
        with a NotI-oligo(dT) primer. Five prime end enriched,
        double-strand cDNA was digested with Not I and cloned into
        the Not I and EcoRV sites of the pCMVSPORT 6 vector.
        Library was not normalized."
BASE COUNT      310 a 243 c 293 g 307 t 48 others
ORIGIN
Query Match      85.5%; Score 838.4; DB 9; Length 1201;
Best Local Similarity 98.2%; Pred. No. 6.9e-214;
Matches 875; Conservative 3; Mismatches 10; Indels 3; Gaps 3;
QY      22 ATGGCACAGGTTCTCAGAGGCACGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT 81
DB      167 ATGGCACAGGTTCTCAGAGGCACGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT 226
QY      82 GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTTGACT 141
DB      227 GCAGAACTCTTCGGAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCTTGACT 286
QY      142 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201
DB      287 CTGTTGACATCCGGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 346
QY      202 TTGGCAGGAGTCTCTGATGACCTGAATCAGAACTAAGTGGGAAATTTGAAAATTA 261
DB      347 TTGGCAGGAGTCTCTGATGACCTGAATCAGAACTAAGTGGGAAATTTGAAAATTA 406
QY      262 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTTATGATGCTTATGAAGTGAACATGCTTG 321
DB      407 ATTGTGGCTCTGATGAAACCCCTCTCGGCTTTTATGATGCTTATGAAGTGAACATGCTTG 466
QY      322 AAGGGAGCTGGACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB      467 AAGGGAGCTGGACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 526
QY      382 GAAGTACAGAGCCATCAACAAGTTTATGAAGAGATATATGGCTCAGCCCTGGAGATGAC 441

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527 GAACTGAGAGCCATCAACAAGTTTATGAAGAAGAATATATGCCTCAAGCCCTGGAAGATGAC 586
442 GTGCTGGGGACACACTTCAGGGTACTACACGCGCATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
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707 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 766
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767 CGAAGTGTGTCTCA-TTTGAGAAGGCTTTTGACAAGTACATACATATATCAGGATTCA 826
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740 TTGTGAATCTATTTCGAAGTATACCTGCTACCTTCAGAGACCCCTCTATTATGCTATGA 799
887 TTGTGAATCTATTTCGAAGTATACCTGCTACCTTCAGAGACCCCTCTATTATGCTATGA 946
800 AGGAGCTGGGACAGATGATACCTCATCATGAGTCATGTTTCCAGGAGTGAGATTG 859
947 AGGAGCTGGGACAGATGATACCTCATCATGAGTCATGTTTCCAGGAGTGAGATTG 1006
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RESULT 10
BX358605      1076 bp      mRNA      linear      EST 05-MAY-2003
LOCUS      BX358605 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CS0DI041YI02 5-PRIME, mRNA sequence.
ACCESSION      BX358605
VERSION      BX358605.1 GI:30382268
SOURCE      EST.
KEYWORDS      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1076)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI041BE01QP1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI041BE01QP1.
FEATURES
    source
        1..1076
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CS0DI041YI02"
        /tissue_type="PLACENTA COT 25-NORMALIZED"
        /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
        /note="1st strand cDNA was primed with a NotI-oligo(dT)

```

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
BASE COUNT 287 a 233 c 274 g 278 t 278 t 4 others
ORIGIN

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Query Match      85.2%; Score 835.8; DB 13; Length 1076;
Best Local Similarity 97.4%; Pred. No. 3.3e-213;
Matches 866; Conservative 4; Mismatches 16; Indels 3; Gaps 2;

OY 22 ATGGCAGAGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGATGCGGGCTGAT 81
DB 191 ATGGCAGAGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGATGCGGGCTGAT 250
OY 82 GCAGAACTCTCTCGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 251 GCAGAACTCTCTCGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 310
OY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTGT 201
DB 311 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTGT 370
OY 202 TTTGCGAGGATCTCTGATGACCTGAATCAAGAACTAACTGGAATAATTTGAAAAATTA 261
DB 371 TTTGCGAGGATCTCTGATGACCTGAATCAAGAACTAACTGGAATAATTTGAAAAATTA 430
OY 262 ATTGGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTTG 321
DB 431 ATTGGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTTG 490
OY 322 AAGGAGCTGGAACAAATGAAAGAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA 381
DB 491 AAGGAGCTGGAACAAATGAAAGAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA 550
OY 382 GAATGAGAGCCATCAACAAGTTTATGAAGAAGTAATGCTCAAGGCTGGAAGTCAAC 441
DB 551 GAATGAGAGCCATCAACAAGTTTATGAAGAAGTAATGCTCAAGGCTGGAAGTCAAC 610
OY 442 GTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 501
DB 611 GTGTGGGGGACACTTCAGGCTACTACAGCGGATGTTGGTGGTCTCTCTTCAGGCTAAC 670
OY 502 AGAGACCTGTATGCTGGAATGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTTATT 561
DB 671 AGAGACCTGTATGCTGGAATGATGAAGCTCAAGTTGAACAGATGCTCAGGCTTTATT 730
OY 562 CAGGCTGGAGAACTTAAATGGGGACAGATCAAGAAAGTTTATCACCATCTTTGGAACA 621
DB 731 CAGGCTGGAGAACTTAAATGGGGACAGATCAAGAAAGTTTATCACCATCTTTGGAACA 790
OY 622 CGAAGTGTGCTCATTTGAGAAAGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 681
DB 791 CGAAGTGT-TCTCATTTGAGAAAGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 849
OY 682 ATTGAGGAACCATGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTCTGCTTT 741
DB 850 ATTGAGGAACCATGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTCTGCTTT 909
OY 742 GTGAAATCTATTCGAAGTATACCTGCCTACCTTCGAGAGCCCTCTATTATGCTATGAAG 801
DB 910 GTGAAATCTATTCGAAGTATACCTGCCTACCTTCGAGAGCCCTCTATTATGCTATGAAG 969
OY 802 GGAGCTGGACAGATGATCATACCTCATCAGAGTCATGGTTTCCAGAGTGAGATTGAT 861
DB 970 GGAGCTGGACAGATGATCATACCTCATCAGAGTATGGTTTCCAGAGTGAGATTGAT 1029
OY 862 CTGTTTAAATCATCAGGAAGGTTTATGGAAGAAATTTTGCCACCTCTCTTT 910
DB 1030 CTGTTTAA--CATCAGGAGGACTTTAGGAGGATTTKCCACACTCTCTTTWT 1076
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RESULT 11
BX402751

LOCUS BX402751 1007 bp mRNA linear EST 13-MAY-2003
DEFINITION clone CS0D1084YA05 5-PRIME, mRNA sequence.
ACCESSION BX402751
VERSION BX402751.1 GI:30607254
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1007)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2353.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIAI0212G030P1&cluster=2353.r. Contact :
Peng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAI0212G030P1.

FEATURES

Location/Qualifiers
1..1007
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1084YA05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 277 a 216 c 257 g 256 t 1 others
ORIGIN

```
Query Match      84.8%; Score 832.2; DB 13; Length 1007;
Best Local Similarity 99.6%; Pred. No. 2.9e-212;
Matches 834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 22 ATGGCAGAGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGATGCGGGCTGAT 81
DB 171 ATGGCAGAGTTCTCAGAGGCACCTGTGACTGACTTCCCTGGATTGTGATGCGGGCTGAT 230
OY 82 GCAGAACTCTCTCGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB 231 GCAGAACTCTCTCGAAGGCTATGAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 290
OY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTGT 201
DB 291 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGAGCTTTTAAGACTGT 350
OY 202 TTTGCGAGGATCTCTGATGACCTGAATCAAGAACTAACTGGAATAATTTGAAAAATTA 261
DB 351 TTTGCGAGGATCTCTGATGACCTGAATCAAGAACTAACTGGAATAATTTGAAAAATTA 410
OY 262 ATTGGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTTG 321
DB 411 ATTGGGCTGTGATGAACCCCTCTCGGCTTTATGATGCTTATGAACCTGAACATGCCCTTG 470
OY 322 AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB 471 AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 530
OY 382 GAATGAGAGCCATCAACAAGTTTATGAAGAAGTAATGCTCAAGGCTGGAAGTCAAC 441
DB 531 GAATGAGAGCCATCAACAAGTTTATGAAGAAGTAATGCTCAAGGCTGGAAGTCAAC 590
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QY 442 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
 Db 591 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 650
 QY 502 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 561
 Db 651 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTATTT 710
 QY 562 CAGGCTGGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 621
 Db 711 CAGGCTGGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGAACA 770
 QY 622 CGAAGTGTGTCTCATTTGGAAGAGTGTGTTGACAAGTACATGATATATCAGGATTTCAA 681
 Db 771 CGAAGTGTGTCTCATTTGGAAGAGTGTGTTGACAAGTACATGATATATCAGGATTTCAA 830
 QY 682 ATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTT 741
 Db 831 ATTGAGGAACCAATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTCTGCTGTT 890
 QY 742 GTGAATCTATTTCGAAGTATACCTGCTGCTACCTTGACAGAGACCCTCTATTATGCTATGAAG 801
 Db 891 GTGAATCTATTTCGAAGTATACCTGCTGCTACCTTGACAGAGACCCTCTATTATGCTATGAAG 950
 QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTGTGTTTCCAGGAGTGAATTT 858
 Db 951 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTGTGTTTCCAGGAGTGAATTT 1007

RESULT 12

AL547761 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL547761 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0DI017YJ11 5-PRIME, mRNA sequence.

AL547761
 VERSION AL547761
 KEYWORDS EST.
 SOURCE 1. GI:31269590

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 On Feb 15, 2001 this sequence version replaced gi:12882128.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2353.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DI017CE06QP1&cluster=2353.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI017CE06QP1.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI017YJ11"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 311 a 252 c 305 g 306 t 27 others

BASE COUNT

ORIGIN

AL517516 1201 bp mRNA linear EST 12-MAY-2003
 LOCUS AL517516 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
 DEFINITION

Query Match 84.8%; Score 831.6; DB 9; Length 1201;
 Best Local Similarity 95.0%; Pred. No. 4.6e-212;
 Matches 911; Conservative 11; Mismatches 26; Indels 11; Gaps 6;
 QY 22 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTTATGAGCGGGCTGAT 81
 Db 208 ATGGCACAGGTTCTCAGAGCACTGTGACTGACTTCCCTGGATTTTATGAGCGGGCTGAT 267
 QY 82 GCAGAAACTCTTCGGAAGGCTATGAAGGCTTCGGACACAGATCAGAGAGCATCCTGACT 141
 Db 268 GCAGAAACTCTTCGGAAGGCTATGAGGCTTCGGACACAGATCAGAGAGCATCCTGACT 327
 QY 142 CTGTTGACATCCCAGAAATATGCTCAGCGCCAGGAAATCTCTCAGCTTTTAAAGACTCTG 201
 Db 328 CTGTTGACATCCCAGAAATATGCTCAGCGCCAGGAAATCTCTCAGCTTTTAAAGACTCTG 387
 QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTCGAAAAATTTGAAAAATTA 261
 Db 388 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTCGAAAAATTTGAAAAATTA 447
 QY 262 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTTATGAACTGAAACATGCTTGG 321
 Db 448 ATTGTGGCTCTGATGAAACCTCTCGGCTTTATGATGCTTTATGAACTGAAACATGCTTGG 507
 QY 322 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
 Db 508 AAGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 567
 QY 382 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGGCTCAAGCCCTGGAAGATGAC 441
 Db 568 GAACTGAGAGCCATCAACAAAGTTTATGAAGAGAAATATGGCTCAAGCCCTGGAAGATGAC 627
 QY 442 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 501
 Db 628 GTGGTGGGGACACTTCAGGGTACTACACGGGATGTTGGTGGTCTCTCCTTCAGGCTAAC 687
 QY 502 AGAGACCCCTGATGCTGGAATGATGAAGCTCAAGTTTATGCTCAAGCTCAAGCTTTATTT 561
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 QY 742 GTCAAACTATTTCGAAGTATACCTGCTACCTTGCAGAGACCTCTATTATGCTATGAAG 801
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 QY 802 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTGTGTTTCCAGGAGTGAATTTGAT 861
 Db 987 GGAGCTGGGACAGATGATCATACCCCTCATCAGAGTGTGTTTCCAGGAGTGAATTTGAT 1044
 QY 862 CTGTTTAACTATCAGGAGGAGTTTAGGAAGAATTTTCCACCTCTCTTTATTCATGATTT 921
 Db 1045 CTGTTT-ACMTCAGGAAGGAGTTTAGGA--GAATTTGCCACCTCTCTCTTTATTCATGATTT 1101
 QY 922 AAGGGAGATACATCTGGGACTATAGAAGGCTTCTGCTGCTCTCCGGAGAGATGA 980
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CS0DA003YF05 5-PRIME, mRNA sequence.
AL517516
AL517516.2 GI:30534896
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12781009.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DA003C03Q0P1&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DA003C03Q0P1.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA003YF05"
/tissue_type="NEUROBLASTOMA"
/notes="Vector: "Homo sapiens NEUROBLASTOMA"
with a NotI-oligo(dT) primer. Five prime end enriched, into
double-strand cDNA was digested with Not I and cloned
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 317 a 257 c 303 g 297 t 27 others
ORIGIN
Query Match 84.5%; Score 828.6; DB 9; Length 1201;
Best Local Similarity 93.5%; Pred. No. 3e-211;
Matches 880; Conservative 14; Mismatches 40; Indels 7; Gaps 3;

QY 22 ATGGCACAGGTTCTCAGAGGCTATCAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 81
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 204 ATGGCACAGGTTCTCAGAGGCTATCAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 263
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 82 GCAGAACTCTCGGAGGCTATCAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 141
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 264 GCAGAACTCTCGGAGGCTATCAAGGCTTGGGCACAGATGAGGAGCATCCTGACT 323
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 142 CTGTTGACATCCCGAGTAGTATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAAGACTCTG 201
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 324 CTGTTGACATCCCGAGTAGTATGCTCAGCGCCAGGAATCTCTCAGCTTTTAAAGACTCTG 383
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 202 TTTGGCAGGATCTCTCGGATGACCTGAATCAGAACTAACTGGAATTTGAAATTA 261
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 384 TTTGGCAGGATCTCTCGGATGACCTGAATCAGAACTAACTGGAATTTGAAATTA 443
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 262 ATTGTGGCTCTGATGAACCTCTCGGCTTTATGCTTTATGAACCTGAACATGCTCTG 321
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 444 ATTGTGGCTCTGATGAACCTCTCGGCTTTATGCTTTATGAACCTGAACATGCTCTG 503
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 322 AAGGGAGCTGGACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 381
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 504 AAGGGAGCTGGACAAATGAAAGTACTGACAGAAATTTATGCTTCAAGGACACCTGAA 563
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 382 GAAGTGGAGCCATCAACCAAGTTTATGAAGAGAAATATGCTTCAAGGAGATGAC 441
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 564 GAAGTGGAGCCATCAACCAAGTTTATGAAGAGAAATATGCTTCAAGGAGATGAC 623
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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QY 442 GTGGTGGGGACACTTCCAGGGTACTACCAGGGGATGTTGGTGTCTTCTTCAGGCTAAC 501
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 502 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 684 AGAGACCCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 743
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 562 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAGTTTATCACCATCTTTTGGGAACA 621
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 622 CGAAGTGTGCTCATTTGAGAAAGGTTTGGACAAGTACATGATATATCAGGATTTCAA 681
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 804 CGAAGTGTNTCATTTGAGAAAGGTTTGGACAAGTACATGATATATCAGGATTTCAA 863
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 682 ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTCTGCTTT 741
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 864 ATTGAGAAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCTTCTGCTTT 923
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 742 GTCAATCTATTTCGAAGTATACCTGCTTACCTTGCAGAGACCCCTCTA-TTATGCTATGAA 800
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 924 GTCAATCTATTTCGAAGTATACCTGCTTGCAGAGACCCCTCTATTTATGCTATGAA 983
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 801 GGGAGCTGGACAGATGATCATACCTTCATCAGAGTCTGTTTCCAGGAGTGAAGATTGA 860
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 984 GGGAGCTGGACAGATGATCATACCTTCATCAGAGTCTGTTTCCAGGAGTGAAGATTGA 1040
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 861 TCTGTTTAAATCAGGAGGAGTTTAGGAAGATTTTGGCACCCTCTCTTTATTCATGAT 920
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1041 ATCTGTTTAMWCAAGGAGGAGTGTAGGAAGATTTTCCACACCTCTCTTTATTCATGAT 1097
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 921 TAAGGAGTATACATCTCGGACATATAAGAAAGCTCTTCTGTC 961
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1098 TSAGGAGAAAMACTGGGGCTATATAAACAACCTCTTCGGS 1138
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 14
AL541412 1201 bp mRNA linear EST 12-MAY-2003
LOCUS AL541412 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE006YJ10
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL541412
VERSION AL541412.2 GI:30545565
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12872460.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE006YJ10&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE006YJ10.
Location/Qualifiers
1. 1201
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FEATURES
source

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/clone_lib="Homo sapiens PLACENTA"
/Note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      315 a      256 c      289 g      303 t      38 others
ORIGIN

Query Match      83.8%; Score 822; DB 9; Length 1201;
Best Local Similarity 94.3%; Pred. No. 1.8e-209;
Matches 886; Conservative 18; Mismatches 29; Indels 7; Gaps 5;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
Db 196 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 255
QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGCAGACAGATGAGAGAGCATCTGACT 141
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QY 262 ATTTGGGCTCTCATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAACATGCACTG 321
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QY 322 AAGGAGCTGGAAACAAATGAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA 381
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QY 382 GAACCTGAGAGCATCAACAACTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGAC 441
Db 556 GAACCTGAGAGCATCAACAACTTTATGAAGAAGATATGGCTCAAGCCTGGAAGATGAC 615
QY 442 GTGGTGGGGACACTTCAGGGTACTACCAAGGATGTTGGTGTCTCTCTCAGGCTTAC 501
Db 616 GTGGTGGGGACACTTCAGGGTACTACCAAGGATGTTGGTGTCTCTCTCAGGCTTAC 675
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QY 800 AGGAGCTGGGACAGATGATATACCCCTCATCAGAGTCAATGG-TTTCAGGAGTGAAT 858
Db 976 AGGAGCTGGGACAGATGATATACCCCTCATCAGAGTCAATGGTTTTCYAGGAGTGAAT 1035
QY 859 GATCTGTTTAAATCAGAGGAGTTTAGGAAGAAATTTTGCACCTCTCTTTATTCATG 918
Db 1036 GATCTGTTT-AMATCAGGAGGAGTTWRGAGAAATTTKCCACACTTC---TTATTCATG 1091

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QY 919 ATTAAGGAGATACATCTGGGGACTATATAAGAAGCTCTTC 958
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RESULT 15
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LOCUS        5-PRIME. mRNA sequence.
DEFINITION   AL583578 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE004YD21
ACCESSION   AL583578
VERSION      AL583578.2 GI:30606551
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1022)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 16, 2001 this sequence version replaced gi:12932676.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DE004CB1Q1p1cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE004CB1Q1P1.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/Note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      282 a      219 c      261 g      255 t
ORIGIN

Query Match      83.6%; Score 820.4; DB 9; Length 1022;
Best Local Similarity 99.1%; Pred. No. 4.3e-209;
Matches 840; Conservative 1; Mismatches 5; Indels 2; Gaps 2;

QY 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGCTGAT 81
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QY 82 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGCAGACAGATGAGAGAGCATCTGACT 141
Db 236 GCAGAACTCTTCGGAAGGCTATGAAGGCTTGGCAGACAGATGAGAGAGCATCTGACT 295
QY 142 CTGTTGACATCCGCAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 201
Db 296 CTGTTGACATCCGCAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAAGACTCTG 355
QY 202 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 261
Db 356 TTTGGCAGGATCTTCTGGATGACCTGAAATCAGAACTAACTGGAATAATTTGAAAAATTA 415
QY 262 ATTTGGGCTCTCATGAACCCCTCTCGGCTTTATGATGCTTATGAATGAACATGCACTG 321
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Qy	322	AAGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATATTGCTTCAAGGACACCTGAA	381
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Qy	382	GAATGAGAGCCATCAACAAGTTTATGAAGAATATGGCTCAAGCCTGGAAGATGAC	441
Db	536	GAATGAGAGCCATCAACAAGTTTATGAAGAATATGGCTCAAGCCTGGAAGATGAC	595
Qy	442	GTGCTGGGGACACTTCAGGCTACTACCAGCGGATGTTGGTGGTCTCCTTCAGGCTAAC	501
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Qy	502	AGACACCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT	561
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Qy	682	ATTGAGGAACCATTTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCCTGT	741
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Qy	742	GTGAAATCTATTGGAAGTATACCTGCTTACCTTCAGAGACCCCTCTATTATGCTATGAAG	801
Db	895	GTGAAATCTATTGGAAGTATACCTGCTTACCTTCAGAGACCCCTCTATTATGCTATGAAG	954
Qy	802	GGAGCTGGGACAGATGATACCTCATACAGTCTGTTTCCAGGAGTGAGATTGAT	861
Db	955	GGAGCTGGGACAGATGATACCTCATACAGTCTGTTTCCAGGAGTGAGATTGAT	1013
Qy	862	CTGTTTAA	869
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 Job time : 1678.67 secs

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